Texture Analysis in Quantitative Osteoporosis Assessment

Characterizing Micro-architecture in High Resolution Peripheral Quantitative Computed Tomography

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Abstract. High resolution peripheral quantitative quantitative computed tomography (HR-pQCT) permits in-vivo assessement of trabecular microstructure at an isotropic voxel size of 82 μm. The new imaging modality has potential in the differentiation of certain forms of osteoporosis based on the associated microstructural patterns. In this paper we propose an approach that assesses bone microarchitecture based on texture features extracted from the trabecular bone. The method is based on a three-dimensional gray level co-occurence matrix descriptor, and a k-medians clustering in the feature space to indicate characteristic categories of texture. The distribution of the microarchitecture classes allows for a differentiation between osteoporotic and healthy subjects. We report initial results for the repeatability of the clustering method and the feasibility of the differentiation between healthy and osteoporotic bone for 6 subjects.

1 Introduction

Osteoporosis is a metabolic bone disease leading to an increased risk of fracture [1]. Low bone density and alterations in bone microarchitecture both contribute to increased fracture risk. Adequate diagnosis is the key to effective intervention. Osteoporosis remains clinically silent until the first fragility fractures occur [2]. The diagnosis and fracture risk assessment is currently based on bone mineral density (BMD) as observed by dual x-ray absorptiometry (DXA), which has certain limitations [3]. In particular the very specific, divergent bone metabolism associated with various pathophysiological subtypes of osteoporosis can not be differentiated by DXA alone. Thus, we consider texture analysis of high resolution peripheral quantitative computed tomography (HR-pQCT) data with an in-vivo resolution of 82 μm as an important new approach with high potential in the differentiation of certain forms of osteoporosis.

In this paper we propose an approach that assesses bone micro-architecture based on texture features that are extracted from the spongiosa region in HR-pQCT volumes. A three-dimensional gray level co-occurrence matrix serves as a descriptor. A clustering in the resulting feature space indicates texture categories which appear repeatedly in the entire training set. Their distribution is used for the differentiation between osteoporotic and healthy subjects. It mimics the medical experts observation of distinct patterns in the regions, expected to correlate with different forms of the disease. Unlike current BMD assessment, this approach could indicate differentiation between different stages of osteoporosis or potentially identify sub-types of the disease. This differentiation could have a clinical impact by aiding treatment option decisions and leading to establishment of a novel biomarker which complements traditional BMD by DXA.

2 Methods

We first extract from training images local texture features that describe the micro-architecture quantitatively. These features are then clustered to derive categories of local texture. Unseen data is then processed by partitioning the entire volume into the respective classes identified by the training set. The method is divided into two main steps: (i) feature extraction with a three-dimensional gray level co-occurrence matrix, and (ii) k-medians clustering and classification of the extracted features of the trabecular bone.

2.1 Texture Analysis

To describe bone texture, quantitative feature extraction is performed using a three-dimensional gray-level co-occurrence matrix (3D GLCM) on the HR-pQCT volumes. The GLCM is a commonly used approach in medical imaging [4, 5]. In the volumetric case there are 13 different directions and we are using 4 voxel distances $d = \{1, 2, 4, 8\}$. To extract textural information from the GLCM, 12 different statistical Haralick texture measures [6] are computed for each direction. With linear scaling the original 12 bit-depth of the volume is normalized to 8 gray-levels. For every second point in the volume the local descriptor is calculated for a cubic neighborhood of $15 \times 15 \times 15$ voxels. On these overlapping subcubes a normalized symmetrical 3D GLCM with a re-quantization size of $Q = 8$ is performed. The number of gray levels Q determines the size of the GLCM and thus directly effects computational costs. The re-quantization to fewer gray levels in medical images has an advantage of reducing the noise-induced effects. For feature reduction and to avoid directional dependency, we calculate the angular mean and angular independent variance over all 13 matrices representing the directions.

2.2 K-medians Clustering to Obtain Texture Categories

After calculating the descriptor for each point in the spongiosa region of the HR-pQCT volume, we cluster feature vectors to capture sets of points with comparable characteristics. In this work we employ standard k-medians clustering. Instead of the squared Euclidian distance we utilize the Manhatten distance (L_1 norm). K-medians has been shown to be more sensitive to outliers for high dimensional features [7]. In our experiments it exhibited higher reproducibility and more feasible results than k-means. After a preliminary study and visual validation by a medical expert, we experimented with $4 \leq k \leq 6$.

2.3 Quantitative and Qualitative Validation

To validate the repeatability, we divided the available data into 2 disjoint sets: A, and B. We performed unsupervised learning of the clusters on one set (e.g., A), and applied the resulting classifier to the other set (e.g., B), and vice versa. The repeated measurements were evaluated by the Dice coefficient [8]. To describe the differentiation between the different groups a histogram of the cluster volume was performed, and the resulting distribution was compared to healthy and osteoporotic cases.

3 Results

We performed experiments on six HR-pQCT volumes of the distal radius having a size of $512 \times 512 \times 110$ with an isotropic resolution of $82\,\mu$m. Three of the subjects were healthy volunteers and three were patients diagnosed as osteoporotic. For the k-medians clustering we compared 4 different parameter settings. Settings 1 and 2 use all 96 extracted texture features $d = \{1, 2, 4, 8\}$ with two different numbers of clusters $k = \{5, 6\}$. Settings 3 and 4 use a reduced feature space $d = \{4, 8\}$ with $k = \{5, 6\}$. We report initial quantitative results regarding 3 questions. Firstly, does the unsupervised differentiation of texture patterns in the bone result in a repeatable clustering? Put another way, can we expect the texture classes to represent true classes in the data? Second, can we use the frequency of the texture classes to differentiate between healthy and osteoporotic subjects? Finally, which texture classes are captured by the procedure, and do they correspond to texture classes intuitively described by medical doctors.

In Fig. 2(a) the results of the k-medians clustering are illustrated. The six texture categories corresponding to the feature clusters are feasible and distinguishable between each other. Minimal changes are visible according to the performance of the clustering. Dice similarity coefficients show also high levels of repeatability for our experiments with mean values of texture class overlap ranging from 0.906–0.990 and a standard deviation from 0.002–0.063. In Fig. 1 two examples of osteoporotic and healthy bone are depicted. The texture class images in Fig. 1(b, e) show differences in the distribution of texture classes, corresponding to the visible microstructural differences in the texture patterns

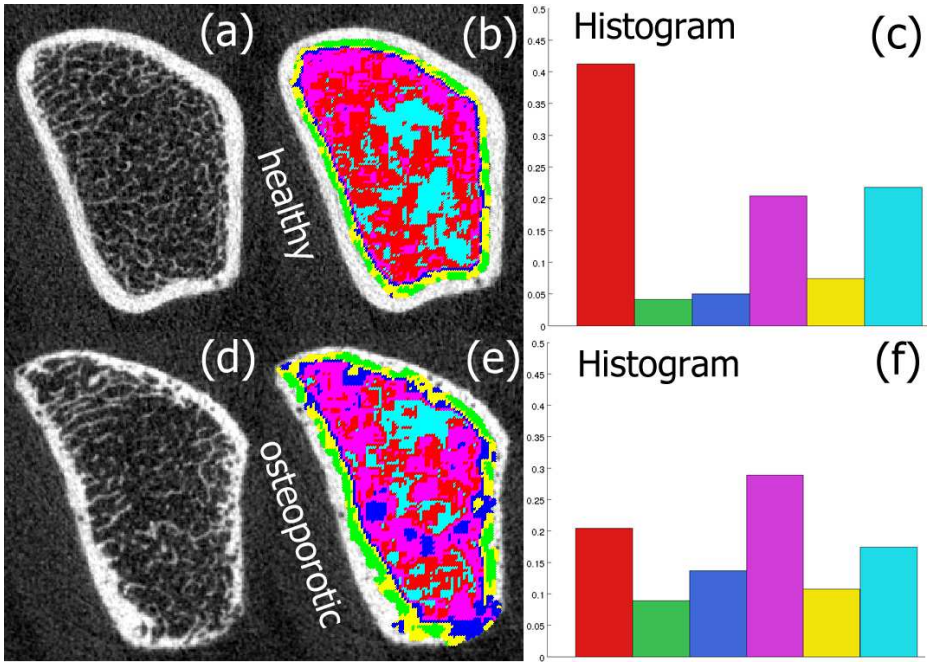

Fig. 1. Clustering comparison: healthy vs. osteoporotic bone microarchitecture: (a) is a healthy and (d) is a osteoporotic bone image slice, where k-means clustering with $k = 5$ was performed, shown in (b, e). In (c) the histogram of the k-means clustering result is illustrated, performed on the entire volume of the healthy bone (a). (f) represent the histogram of the osteoporotic case.

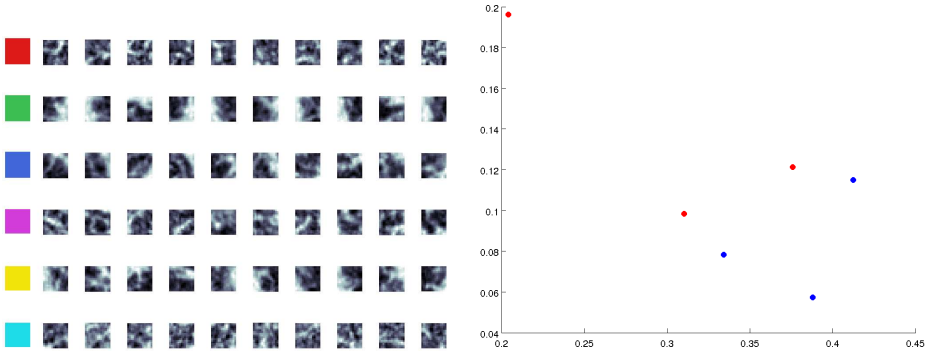

Fig. 2. Left: Prototype examples for six microarchitecture classes learned from the data. The patches show the ten nearest neighbors of each cluster centroid in the feature space; Right: Differentiation of osteoporotic (red dots) and healthy (blue dots) subject: x-axis is the cancellous buffer zone (red), y-axis is the cortical transition (yellow/green).

of Fig. 1(a, d). The Histograms vary between the osteoporotic and healthy subjects, as illustrated in Fig. 1(c, f). The cyan areas represent parts of the cancellous bone compartment which are poor in trabecular structure and rich in bone marrow. Trabecular core regions (magenta) are surrounded by trabecular buffer zones (red). Green and yellow indicate the outer border of the trabecular compartment and can be seen as a cortical transition zone with very thick trabeculae. Trabecular core and buffer zones are separated from the yellow/green cortical transition zone by a blue border region. The inverse relationship between the ratio of the cortical transition zone (yellow/green) and the cancellous buffer zone (red) and its correlation to osteoporotic versus healthy subjects indicate a potential differentiating power of the histogram features (Fig. 2(b)).

4 Conclusion

In this paper we investigate the differentiation between osteoporotic and healthy subjects according to their three-dimensional micro-architecture observed in HR-pQCT data. We learn spongiosa micro-architecture categories in an unsupervised manner and evaluate the repeatability of the resulting categories. Results indicate that the approach is applicable to define and classify micro-structural patterns of trabecular bone, and that the distribution of the micro-architecture classes exhibit a trend that allows for differentiating healthy and osteoporotic bone.

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