Segmentation of the Knee for Analysis of Osteoarthritis

A Robust Algorithm for the Definition of Subchondral Evaluation Regions

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Abstract. Osteoarthritis changes the load distribution within joints and also changes bone density and structure. Within typical timelines of clinical studies these changes can be very small. Therefore precise definition of evaluation regions which are highly robust and show little to no inter- and intra-operator variance are essential for high quality quantitative analysis. To achieve this goal we have developed a system for the definition of such regions with minimal user input.

1 Introduction

Our task is to evaluate changes in bone mineral density (BMD) and bone structure in patients with osteoarthritis based on CT datasets. Usually MRI scans and radiographs of the joint gap are used as diagnostic imaging procedures. However, CT is better suited for the quantification of changes in BMD and bone structure which may add significant information for the diagnosis of osteoarthritis.

The aim is to define evaluation regions largely independent of the user perfoming the analysis. To achieve this we need to automatically identify at least one salient anatomical feature.

One such feature is the growth plate. During development of the foetus the epiphyses and diaphyses of tibia and femur are initiated as separate structures which are joined during growth. This process causes a visible break in the texture of the cancellous bone called the growth plate. Even though the trabecular structure and shape of the bone change during lifetime, the texture change at the growth plate does not. Our system first segments the growth plate. A further step restricts the volumes of interest (VOIs) to areas adjacent to the joint gap between tibia and femur, since we anticipate the biggest BMD changes in the subchondral bone VOIs.

Together with the eigenvectors of the moments of inertia of the anatomical structure we can define position and orientation of our VOIs in a robust and repeatable manner.

2 Materials and methods

CT data for this study were acquired on a Siemens Somatom Sensation 64 scanner at 120 kV and 255 mAs. Each scan includes a calibration phantom which allows for quantitative analysis once the segmentation steps are complete. Images are reconstructed with 434 slices and 512 by 512 pixels with an isotropic resolution of 0.5 mm and a medium U40u kernel.

Step 1: Automatic detection of the calibration phantom. We segment the periosteal and endosteal areas of the femur and tibia using an adaptation of an algorithm described in [1, 2].

Step 2: To segment the growth plate (Fig. 1) we have implemented a new segmentation algorithm which combines statistical gray value information and a constraint on the shape of the growth plate.

The user sets one seed point somewhere in the central region of the growth plate. Relative to this point we define a band of voxels with a width of 60 slices in the z-direction of the image. The algorithm divides this band further into individual columns oriented in z-direction. In each column we find the voxel whose gray value deviates most from its neighbors within a given distance (Fig. 3(a)).

The seed point is transformed into the first link from which we grow a chainmail data structure as described in [3]. Each point or "link" in the chainmail has 4 neighbors whose maximum and minimum distances are limited by the data structure. We iteratively search for the closest point found in step one of the algorithm. If there is a point within reach then a new link is added and its position fixed. If no point is found to be close enough then a link is added but left 'floating free'. Free floating links add their mobility when they are processed so their neighboring links are able to connect to points further away. In a post processing step the position of floating points is interpolated between neighboring links. Then the edges are trimmed because the growth plate is only visible in the center region of the bone (Fig. 3(b)).

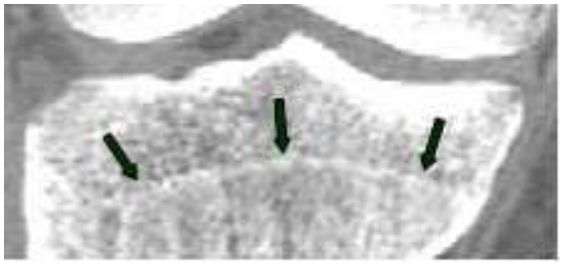
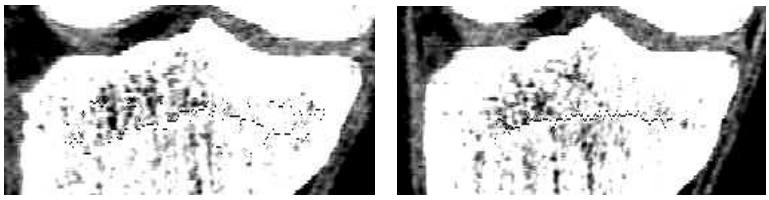


Fig. 1. The tibia growth plate (indicated by arrows)

Fig. 2. Growth plate segmentation (window level adjusted for better contrast)



(a) Voxels of greatest gray value deviation (dark dots).

(b) After chainmailing, relaxation and trimming.

Step 3: To define the VOIs we also segment the joint gap by calculating distance maps for the femur and tibia. Then we perform two walks: One starting from the surface voxels of the femur to the tibia and one in the opposite direction.

We define a voxel as belonging to the joint gap if during both walks it has the following property: All neighboring points, which are farther away from the starting anatomical structure than the voxel under consideration are equally close (or closer) to the target structure.

Step 4: VOIs are defined between the periosteal surface bordering the joint gap and the growth plate which is extended by a plane. This plane is fitted through the mass center of the growth plate (Fig. 3).

3 Results

Preliminary results were evaluated from analysis and comparison of the results of the same datasets by three operators (inter-operator variability) and also by repeated analysis of single datasets by one operator (intra-operator variability). The only possible variation is the seed point of the growth plate, since the bone and joint gap segmentation are done fully automatic. Thus only the variation of

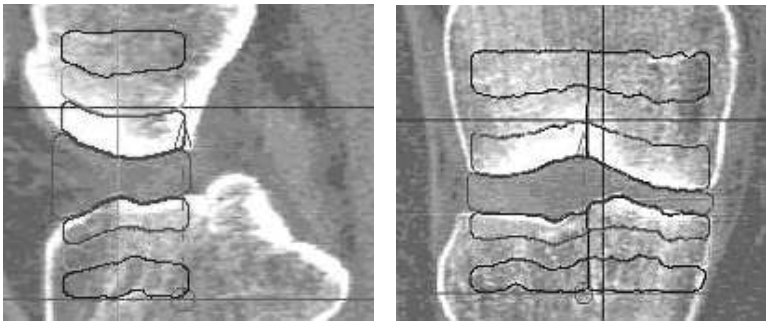


Fig. 3. Joint gap and three subchondral VOIs per structure (lateral and coronal view)

the center of mass of the growth plate enters as an operator dependent variable into the positioning of the VOIs.

In both experimental setups deviation of the center of mass averaged 1 ± 0.8 voxels. Thus we conclude that the definition of the VOIs as described above is repeatable and robust.

4 Discussion

We have demonstrated a way to define VOIs within the knee in a robust and repeatable way using a novel segmentation algorithm for 'noisy' structures. The center of mass of the growth plate coupled with the eigenvectors of the moments of inertia of the anatomical structures provide salient features for the attachment of the VOIs.

Together with the fully automatic definition of the joint gap we have managed to decouple the positioning of the VOIs largely from the dependence of operator input.

In the future we will perform more extensive precision analysis with more datasets and larger number of operators. We will add evaluation algorithms, which will perform e.g. trabecular morphology analyzes within the defined VOIs. Due to the high precision the developed methodology seems a promising tool for the analysis of osteoarthritis induced bone changes in longitudinal studies.

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