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Computer Analysis of Knee by Magnetic Resonance Imaging Data

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Abstract

The examination of knee cartilage degradation by magnetic resonance imaging (MRI) data is essential due to the reduction in physical activity of the population and a rising number of patients with osteoarthritis(OA). The main aim of this publication is to show a new approach for analyzing knee tissue by MRI data. The present paper investigates the problems of relaxation times calculation, medical image segmentation and statistical texture features calculation. Proposed paper describes an approach for medical image segmentation, relaxation times calculation and statistical texture features calculation. An important aspect of analysis of articular cartilage relaxation times changing is illustrated in the experimental part. The experimental part of the publication also describes the dependence between organic structure and relaxation times. The proposed approach the obtained results can be useful for early OA diagnostics.

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Keywords: Early diagnosis of osteoarthritis; Magnetic resonance imaging; Medical imaging; Knee joint; Cartilage; Image segmentation; Relaxation time

1. Introduction

Osteoarthritis(OA) is one of the most common knee joint diseases[1]. In America, every tenth adult has OA. Osteoarthritis takes place when the knee joint cartilage wears-out. Magnetic resonance imaging is used to image soft tissue (for example, cartilage is a soft tissue). A doctor who uses simple MRI images can't see all the information which is contained in the MRI image file (usually DICOM formats). For example, he can't see the early stage of

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osteoarthritis. Therefore, computer analysis of knee by magnetic resonance imaging data is very important. The purpose of this analysis is to provide the doctor with the quantitative information about articular cartilage. This information allows the doctor to make early osteoarthritis diagnosis and allows for more precise estimation of the cartilage changes. This paper proposes new methods for knee cartilage OA diagnostics by MRI data.

2. Problem statement

The quantitative information about articular cartilage is very useful, because it provides an opportunity to control the treatment process and examine the effectiveness of medicaments. A doctor, who has quantitative information about articular cartilage state, can estimate the influence of medicaments on cartilage and compare the effectiveness of different medicaments.

Also, the estimation of the articular cartilage changes is very useful, because of early OA diagnostic. A doctor who uses computer analysis for estimating articular cartilage changes has the ability to make early OA diagnosis. At the first OA stage, it is more likely to cure osteoarthritis without any surgical intervention.

Before cartilage analysis it is important to extract cartilage from MRI data[2,3,4,5]. For this purpose, it is useful to perform MRI data segmentation. After that, we can perform segmented object recognition in order to find articular cartilage. So, these are the main problems:

- MRI data segmentation
- Segmented object classification
- Articular cartilage segmentation and recognition
- Articular cartilage analysis
- Early OA stage displaying

3. Proposed approach

Before we can solve the described problems, it is important to know exactly which parameters and features could be used for articular cartilage analysis, recognition and segmentation. This paper proposes to use:

- Physical parameters - relaxation times (T1,T2), proton density and MRI signal[6]
- Statistical texture features – contrast, correlation, dissimilarity, energy, entropy and et al.

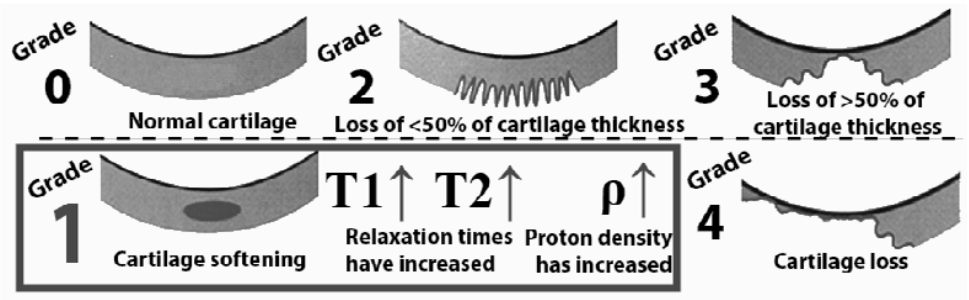

Fig. 1. Outerbridge classification.

Physical parameters can be useful for first OA grade detection. OA has five grades[7,8] as shown in Fig. 1. The early OA diagnostic is of great importance for people with the early grade of OA. Articular cartilage degeneration is usually recoverable at the first grade of OA. Unfortunately, the first grade of OA is invisible to the doctor who uses usual grayscale MRI images.

However, it is known that cartilage softening take place at the first grade of OA. During cartilage softening, proton density and relaxation times increase[9], as shown in Fig. 1.

These physical features can be useful for first OA grade detection. Statistical texture features can be useful for usual analysis of grayscale MRI images. It is possible to classify different tissues by statistical texture features: contrast, correlation, energy entropy, homogeneity, maximal probability, variance etc. (see Fig. 2).

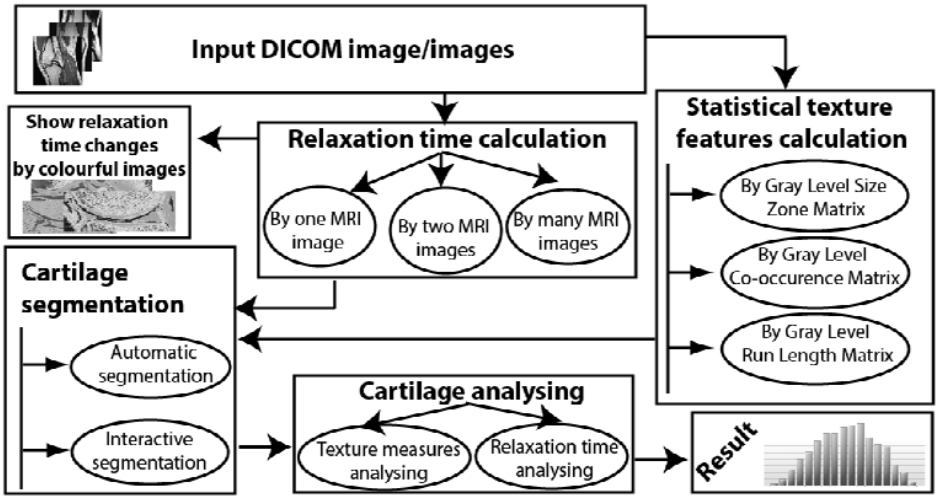

Fig. 2.Common flowchart.

Proposed approach consists of four important stages (see Fig. 2):

- Relaxation time calculation
- Statistical texture features calculation
- Cartilage segmentation
- Cartilage analysis

3.1. Relaxation time calculation

The relaxation time – is a physical feature of the tissue's protons[10]. After RF exposure the proton absorbs energy and changes energetic state[11]. But after relaxation time, the proton returns to the initial state (for more detail, see my previous publication[12]).

Relaxation times (T1 and T2) can be calculated by one MRI image, two MRI images[13] or many MRI[14] images. The relaxation time calculations methods are described in my previous publication[12]. The relaxation time calculation by many images is the most precise method.

Using this method, we can model tissue's proton relaxation process (see Fig. 3). In the Fig. 3 is shown eight MRI images which have different TE (Echo Time).

Therefore, these eight images contain information about proton energetic state at different moments in time. Thank to this information, it is possible to approximate relaxation process as shown in Fig. 3.

It is possible to solve the approximation problem by using partial derivatives and the least square method (1):

$$S(M_0, T2) = \sum_{i=1}^{n} (SI_i - M_0 * \exp(\frac{-TE_i}{T2}))^2 \rightarrow \min$$

$$\begin{cases} \frac{\partial S}{\partial M_0} = -2\sum_{i=1}^{n} (e^{\frac{-TE_i}{T2}} * (SI_i - M_0 * e^{\frac{-TE_i}{T2}})) = 0 \\ \frac{\partial S}{\partial T2} = -\frac{2}{T2^2} * M_0 * \sum_{i=1}^{n} (e^{\frac{-TE_i}{P2}} * (SI_i - M_0 * e^{\frac{-TE_i}{P2}}) * TE_i) = 0 \end{cases} \quad (1)$$

where:

M_0 – initial magnetization,
T2 – relaxation time,
S – MRI signal,
SI – intense value of image pixel,
TE – Echo Time,
n – count of images.

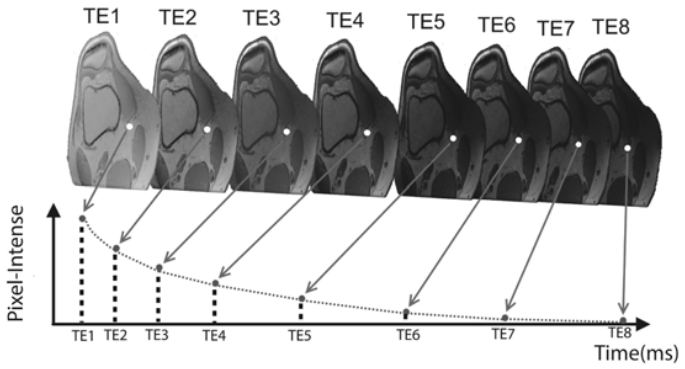

Fig. 3. Many MRI images, which reflect one slice (T2 relaxation process).

3.2. Statistical texture features

Grayscale MRI images have different texture features based on:

- Spatial frequencies
- Statistical characteristics (GLCM matrix, histogram)
- Structural elements (GLRLM matrix)

For textures features calculation it is advised to use a special matrix or a histogram. In this paper, special attention is paid to the GLCM matrix[15]. Depending on matrix direction, there can be four types of this matrix: vertical, horizontal, diagonal (45 degrees) and diagonal (135 degrees). GLCM matrix preparation for texture features calculation has 4 steps:

- Gray image pixels values quantization – all new image pixels values must be in the range (from 0 to GLCM matrix size)
- GLCM matrix calculation – GLCM matrix shows neighboring elements combination frequency
- GLCM matrix symmetrisation
- GLCM matrix normalization – matrix values must be in the range (from 0 to 1)

After that it is possible calculate some textures features (a),(b),(c):

a. Contrast(CON):

$$CON = \sum_{i,j=0}^{N-1} P_{i,j}(i-j)^2 \tag{2}$$

b. Homogeneity(HOM):

$$HOM = \sum_{i,j=0}^{N-1} \frac{P_{i,j}}{1+(i-j)^2} \tag{3}$$

c. Entropy(ENT):

$$ENT = \sum_{i,j=0}^{N-1} P_{i,j}(-\ln P_{i,j}) \tag{4}$$

where:

P – GLCM matrix value (after normalization), that shows probability of combined neighbouring elements,
i and j – GLCM matrix indexes, which show quantized image pixels values of neighboring elements,
N – GLCM matrix size.

3.3. Knee tissue segmentation

Tissue segmentation can be either interactive or automatic. Interactive segmentation cannot work without user input, but automatic segmentation can be helpful when we have a lot of information. Thus, this paper focuses on automatic segmentation. Experiments show that automatic segmentation can be done by Watershed algorithm together with Prewitt or Sobel operators as shown in Fig. 4. The results of the developed method are shown in this Fig. 4. This developed method is based on Watershed algorithm.

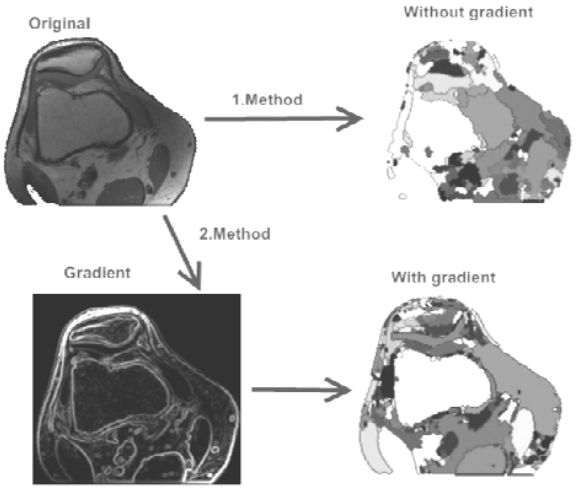

Fig. 4. Automatic segmentation.

3.4. Tissue analysis

It is possible to use the dispersion method for the analysis of changes in tissue relaxation times.

The dispersion is calculated as follows (5):

$$D = \overline{X^2} - \left(\overline{X}\right)^2 = \frac{1}{n}\sum_{i=1}^{n} X_i^{\,2} - \left(\frac{1}{n}\sum_{i=1}^{n} X_i\right)^2 \tag{5}$$

where:

D – the dispersion,
X - relaxation time (T1 or T2),
$\overline{X}$ -the average relaxation time,
$\overline{X^2}$ - the square of the mean value,
n – count of values ,
i – index of the current value.

The dispersion method analyzes relaxation time values of all segmented tissue pixels and calculates dispersion. The biggest dispersion shows that tissue structure has heterogeneous structure. Sick cartilage tissue has heterogeneous structure. So, it is possible to use dispersion methods for analyzing the tissue degeneration.

4. Experimental results

4.1. Histogram analysis

After successful cartilage segmentation it is possible to check all cartilage pixels and create a histogram of relaxation times. Experimental results show that we can detect OA grade form the shape of the histogram (Fig. 5, Fig. 6). So, early OA stage detection problem can be solved by using histograms of relaxation times.

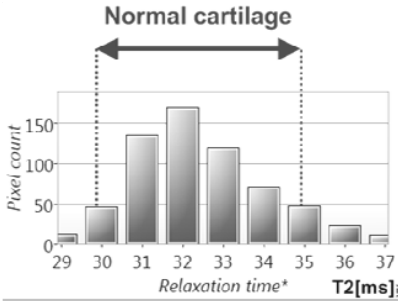

Fig 5. Healthy cartilage.

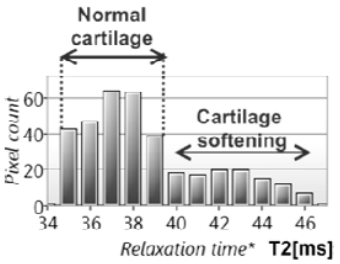

Fig 6. OA first grade.

4.2. Dispersion cartilage analysis

Six patients participated in this experiment. Only patient P6 does not have OA, as shown in Fig. 7. The healthy cartilage has homogeneous structure and has small dispersion.

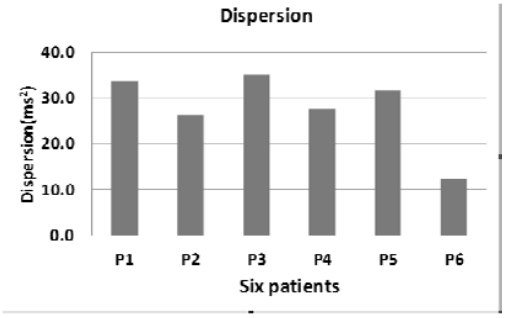

Fig. 7. Dispersion cartilage analysis.

4.3. Modulating the relaxation process by many MRI images

This experiment has shown that various organic structures have a different relaxation process. In the Fig. 8 we can see that muscle T2 relaxation process is faster than bone relaxation process. Different tissues have various relaxation times. Therefore, tissues classification problem can be solved by using the relaxation times.

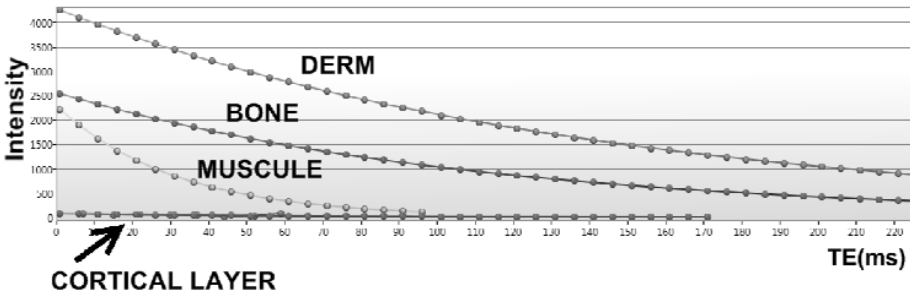

Fig. 8. T2 relaxation process.

4.4. Statistical texture features

The classification of knee tissues is an important problem. In order to solve this problem, we can use texture features. This experiment shows the knee tissues texture features values (see Fig. 9).

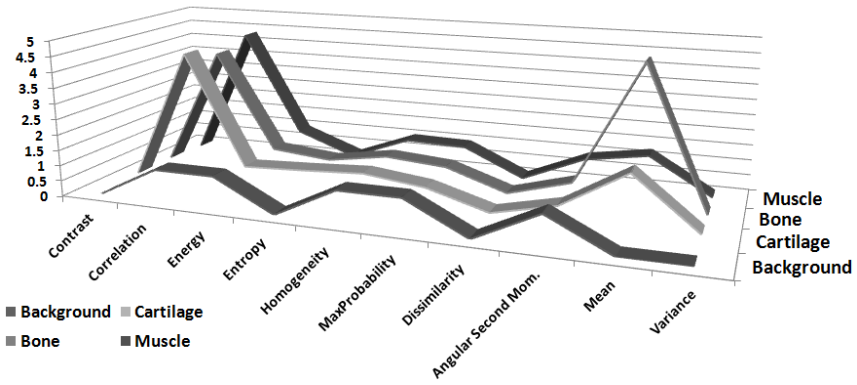

Fig. 9. Statistical texture features.

Different tissues have different features. For example, bone tissues have very high mean value, but cartilage and muscles have high correlation. Thus, tissues classification problem can be solved by using tissues texture features values.

5. Conclusion

Computer analysis of a knee by magnetic resonance imaging data is a very complicated task. This task consists of many steps: calculation of parameters and features, segmentation of the important information, analysis of the extracted region parameters and features. In this paper a method is proposed for parameter and features calculation. The tissue's texture statistical features can be calculated by using a GLCM matrix, while the tissue's protons physical parameters can be calculated by special relaxation time calculation methods. These parameters and features are useful for tissue classification and cartilage degeneration level control. The experiments have shown that different tissues have various relaxation times and unequal texture statistical features. This paper shows that the proposed method could be used to help doctors make an early OA diagnosis and compare cartilage changes by quantitative cartilage parameters.

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