

The Improvement of Region-Of-Interest Statistics in Musculoskeletal MRI

V. Juras^{1,2}, S. Zbyn¹, P. Szomolanyi^{1,2}, I. Frollo², and S. Trattnig¹

¹MR Centre of Excellence, Medical University of Vienna, Vienna, Austria, ²Institute of Measurement Science, Slovak Academy of Sciences, Bratislava, Slovakia

Introduction:

Improvements in MR hardware and sequence design enable the biochemical analysis of articular cartilage (AC) structural components *in vivo*, in reasonable scan times. There is a number of biochemical parameters routinely used in clinical MR practice (T_1 , T_2 , ADC, $T_{1\rho}$). In musculoskeletal MRI, the most common way to diagnose an injury, or tissue impairment, is the visual reading of 2D or 3D images and possible employment of ROI evaluation [1-4]. The aim of this study was to show that the implementation of the fitting error estimation (R^2 , RMSE, MSE, MAE) as a weighting coefficient can significantly improve the accuracy of the statistical analysis performed on selected ROIs. We hypothesized that the data weighted by estimated error can increase the significance of statistical difference and enable to distinguish between different cartilage tissue types much easier, especially in case of lower image quality caused by noise.

Materials and Methods:

The MR images from 15 patients with MACT transplants were used (3 females, 13 males; mean age, 37.8; range, 21-54 years). The MACT transplantation was performed on either the medial femoral condyle (12 patients) or on the lateral femoral condyle (3 patients). The postoperative interval was in the range of 3-42 months. MR examinations were performed on a 3.0 T MR scanner (Trio, Siemens Erlangen, Germany) equipped with a gradient system with the strength of 40 mT/m and MR signal was acquired using an 8-channel phased array knee coil. The T_2 relaxation times were calculated from MR data obtained with the multiple spin-echo technique, with a repetition time (TR) of 2.060 seconds and six echo times (TE): 16.4, 32.8, 49.2, 65.6, 82.0, and 96.4 milliseconds. Additional sequence parameters were set as follows: FOV of 180×200 mm², 320×288 pixels matrix, slice thickness of 1 mm with a distance factor of 100%, bandwidth of 130 Hz/pixel and 18 slices. Total scan time was 6 minutes and 43 seconds; phase and slice resolution was set to 90%. T_2 maps were calculated using the mono-exponential, three-parametric fitting IDL (RSI, Boulder, CO) algorithm using *mpcurvefit* written by C.B. Markwardt (NASA/GSFC Code 662, Greenbelt, MD 20770). To simulate a noise in magnitude MR images, a Rice distribution of noise was used for each TE image before the fitting routine was employed. Every intensity level was calculated as the curve of noise distribution with the appropriate noise level (σ). Artificial noise was then added to each pixel with different noise levels defined with respect to the percentage (from 0 to 50% in 1% steps) of random value from a normalized Rice distribution. Afterwards, P-values (T-test used for the comparison of the difference between normal and repair cartilage ROIs as depicted on Fig. 1) were compared between non-corrected and corrected means. Corrected means were determined as weighted averages, whereas the fitting errors estimates (R^2 , RMSE, MAE, MSE) were used as the weighting coefficients.

Results:

The mean global value of T_2 in transplant cartilage tissue was 62.47 ± 7.42 ms (range, 50.7 to 70.0 ms) and in healthy cartilage was 49.28 ± 5.99 ms (range, 40.0 to 60.0 ms). The difference between these values was statistically significant ($P < 0.001$). In images with 50% noise, SNR decreased to 17.95 ± 4.11 and 15.61 ± 3.96 in repair and native cartilage, respectively, and mean CNR was only 0.26 ± 0.06 . With regard to statistical significance, with up to 35% noise added in TE images, the P-value between native and transplant cartilage was still lower than 0.05. With a higher noise level, the difference was no longer statistically significant. After the RMSE and MSE corrections were applied as weighting factors, the difference in T_2 was statistically significant only up to 31% of noise level (similarly to non-corrected comparison). When R^2 was used as a weighting coefficient, the statistical significance was maintained up to the 47% noise level (Fig. 2).

Discussion/Conclusion:

The results clearly showed that the use of error estimates from fitted curves as weighting coefficients may increase the statistical validity of individual ROIs and maintain statistical significance even in noisy measurements. It has been shown that coefficient of determination (R^2) is the most effective correction factor in comparison to RMSE, MSE and MAE. Since the calculation of R^2 consists of simple mathematical operations, it does not require extensive processor time. In this study, the implementation of error estimates calculation increased the total calculation time by less than 5%. The results of this study showed that using the R^2 as a weighting parameter in the ROI evaluation in musculoskeletal MRI may crucially improve the differentiation of native and transplant cartilage tissue even in images suffering of low SNR. This has a great potential to improve the non-invasive monitoring of the post-operative status of patients with cartilage transplants using MR systems with lower B_0 .

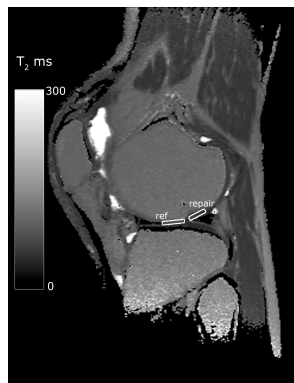


Fig. 1: T_2 map with 0% noise level showing ROI selection on MACT transplant (trans) and native cartilage tissue (ref). Colorbar is labeled with T_2 values in ms.

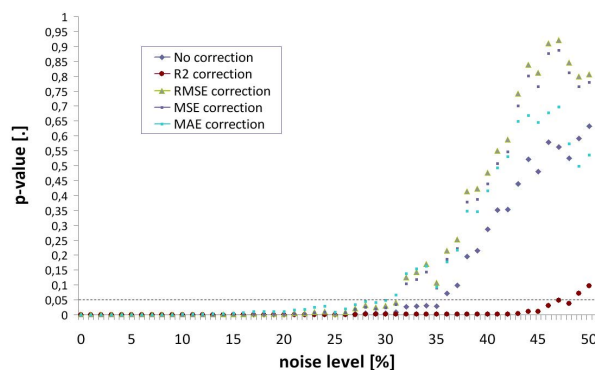


Fig. 2: Plot of noise level in % against P-value calculated in sense of Student T-Test as a difference between normal and transplant cartilage tissue. Statistical significance boundary level ($P = .05$) is depicted by the horizontal dashed line. It is shown that ROI correction using R^2 is very feasible and is able to maintain the statistical significance to almost doubled noise in TE images.

References:

- [1] Burstein, D. et al. Investigative Radiology, (35) 10, pp 622-638, 2000;
- [2] Trattnig, S. et al. Journal of Magnetic Resonance Imaging, (26) 4, pp 974 - 982, 2007;
- [3] Welsch, G. et al. Journal of Magnetic Resonance Imaging, (28) 4, pp 979 - 986, 2008;
- [4] Eckstein F. et al. NMR in Biomedicine, (19) 7, pp 822 - 854, 2006.