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COMPARISON OF MRI SEQUENCES FOR THE AUTOMATIC SEGMENTATION OF KNEE STRUCTURES

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INTRODUCTION

Medical imaging is increasingly being used to make person-specific musculoskeletal models within the biomechanics field. Specifically, magnetic resonance imaging (MRI) images are used for extracting anatomical structures such as bone and cartilage [1]. However, manual segmentation of these structures is a bottleneck for further advancement in the field. Automatic segmentation has the potential to change this. However, MRI image characteristics are very different according to sequences, so it is important to select an optimal sequence for automatic segmentation [2]. This study aims to find the most suitable MRI sequence for segmentation through edge evaluation.

METHODS

Analysis was performed using the T1, PD, and SPGR sequences scanned from the knee of the same participant (Fig. 1). After selecting the same location in each sequence of images, the cortical bone, cancellous bone, and cartilage edges were manually drawn on the selected images. After generating a normal vector at the edge line of the cortical bone, the points (E_{CT}: between cartilage and tissue, E_{BC}: between bone and cartilage, E_{BB}: between cortical and cancellous bone, E_{BT}: between bone and tissue), where the normal vector meets the obtained edge line were calculated (Fig. 2).

Fig. 1 Three MRI sequences from the same subject. (T1: T1 weighted, DP: proton density, SPGR: spoiled gradient recalled acquisition in the steady state)

We designed the metric to evaluate the edge characteristic. The metric is calculated as the ratio of the average of both regions through which the normal vector passes, at each point selected. The evaluation was conducted using data from a total of 10 healthy participants.

RESULTS AND DISCUSSION

As a result of the experiment using the evaluation metric (Table 1), the E_{BB} and E_{BT} was the most distinct in the T1 sequence. Also, the SPGR sequence showed the most distinct edge at E_{BC} and E_{CT}.

Since it is difficult in practice to scan multiple sequences on the same participant, we only used three sequences known to have good contrast for bone and cartilage. Therefore, further studies on additional sequences are required. In addition, we experimented with only a single image in a femur region. An evaluation using more data in various bone areas is required through future research.
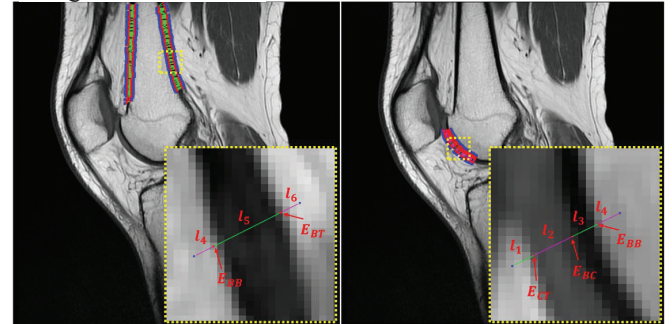
Fig. 2 Evaluation of edge characteristics using the proposed method.

CONCLUSIONS

For the quantitative evaluation of edges, our proposed metric will be a useful method for selecting sequences for automated MRI segmentation studies.

REFERENCES

1. Sozan MA, et al., *Diagnostics* **12**: 1-16, 2022
2. Bruce F, et al., Neuroimage **23**: 69-84, 200

Table 1 Experimental results using proposed metrics (10 subjects)

Subject	T1				PD				SPGR			
	E_{BB}	E_{BC}	E_{CT}	E_{BT}	E_{BB}	E_{BC}	E_{CT}	E_{BT}	E_{BB}	E_{BC}	E_{CT}	E_{BT}
1	3.47±1.41	1.70±0.57	1.62±0.57	3.83±1.64	1.30±0.49	2.32±1.41	1.26±0.81	2.48±0.92	1.55±0.57	4.81±1.91	3.53±2.88	1.77±0.74
2	4.33±1.05	1.84±0.30	2.38±0.49	4.96±1.14	2.18±0.77	2.97±1.86	1.36±0.71	2.87±0.72	1.63±0.70	3.60±2.44	3.56±2.12	1.78±0.59
3	3.24±1.23	1.33±0.18	1.50±0.32	4.50±2.38	1.57±0.41	3.99±0.95	1.61±0.29	2.80±0.65	1.51±0.48	4.31±1.23	3.05±2.07	3.58±1.07
4	2.73±0.89	1.60±0.22	1.53±0.37	4.15±1.72	1.38±0.37	3.81±0.59	1.24±0.23	2.93±0.86	1.52±0.47	4.42±1.15	4.27±2.19	2.49±1.05
5	4.04±1.18	2.09±0.45	1.59±0.48	4.58±1.90	2.10±0.65	3.84±0.79	1.61±0.63	3.75±1.21	1.93±0.57	3.26±1.02	1.58±0.47	3.04±0.81
6	3.98±1.29	2.19±0.50	1.60±0.58	5.11±1.97	2.18±0.46	6.45±0.78	1.24±0.24	2.40±0.44	1.61±0.55	3.82±1.48	1.59±0.46	2.30±0.65
7	2.92±1.24	1.67±0.15	1.46±0.41	3.19±1.10	1.46±0.35	3.34±0.38	1.41±0.38	2.24±0.80	1.70±0.55	3.22±1.05	1.61±0.47	2.10±0.78
8	3.71±0.96	2.54±0.57	1.61±0.33	5.04±1.97	1.86±0.64	4.42±0.87	1.34±0.24	3.68±1.08	1.67±0.67	4.42±1.52	3.08±1.67	2.09±0.73
9	3.66±1.20	2.17±0.51	1.63±0.53	4.14±1.58	2.55±0.93	4.37±1.36	1.65±0.35	2.22±0.55	1.51±0.50	4.88±1.45	2.19±1.52	1.53±0.46
10	3.89±1.28	2.05±0.30	1.74±0.45	4.65±1.74	2.34±0.63	4.93±1.47	1.47±0.40	3.13±0.82	1.76±0.63	3.74±1.01	1.82±0.33	2.56±1.07

Note.- Mean ± Standard deviation