

QUANTITATIVE IMAGE ANALYSIS OF CARTILAGE HISTOLOGY

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Introduction

Osteoarthritis (OA) is often assessed by histologic appearance, using the 14-point histological-histochemical grading scale (HHGS) devised by Mankin et.al [1]. On this scale (normal = 0), cartilage is graded based on structural compromise (0-6 points), loss of metachromatic matrix staining (0-4), cellularity abnormality (0-3), and violation of tidemark integrity (0-1). To date HHGS scorings have been dependent on human observer subjectivity, and thus susceptible to inter- and intra-observer variability [2].

The present study reports a novel image analysis procedure for fully automated and fully objective assessments of HHGS score (Figure 1), based on quantified cartilage parameters, programmed in a widely available software environment (Matlab®).

Methods

For structural abnormality of cartilage histology sections, a method is required to quantify cleft / defect depth (Figure 2). The smooth pre-OA cartilage surface is approximated by piecewise quadratic curve fits. The program calculates cleft / defect depth, from which HHGS structural defect scores are generated based on cleft depth : cartilage thickness ratio. The decrease in proteoglycan content in cartilage, which is indicated by reduced Safranin-O staining, is quantified by averaging saturation values for near-red pixels (safranin-O positive), and assigning zero saturation values to non-red pixels.

Hematoxylin stained nuclei are detected by neighborhood thresholding of HSI Intensity image and size filtering (Figure 3). Cellular cloning, a possible feature present in OA cartilage, is detected by utilizing tree clustering to group cells located in close proximity. Separate clusters are grouped until the average distance of all members in two clusters exceeds a specified value (1/8 of cartilage thickness). For tidemark violation, the presence versus absence of penetrating blood vessel is detected by size filtering and shape-detection operations on identified holes in the cartilage specimen.

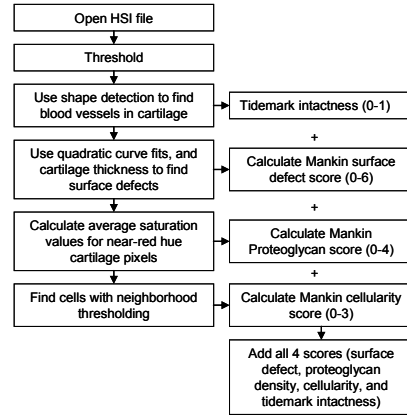


Figure.1 Algorithm for the automated HHGS scoring program.

Results and Discussion

The automated image analysis results agree well with human reader HHGS scorings, while avoiding inter-observer variability (Figure 4). Moreover, unlike the selective “spot sampling” approach employed in conventional histology, the algorithm’s speed and its ability to operate on operator-defined (contiguous) regions of interest permit continuous spatial mapping of cartilage abnormality.

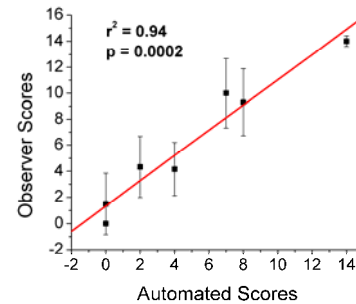


Figure. 4 Observer HHGS values versus computer-generated automated scores. Standard deviations due to inter-observer variability are indicated.

References

1. Mankin et al. (1971). JBJS. 2. Ostergaard et al. (1997). Arth & Rheum.

Acknowledgments

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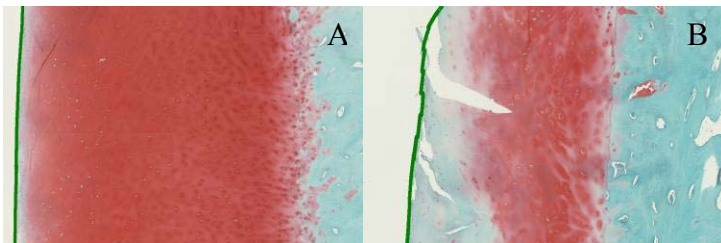


Figure.2 Safranin-O / Fast green stained cartilage specimens with smooth curve fits (Green line). (A) non-OA specimen (B) OA specimen with HHGS surface defect scores of 0 and 3, respectively.

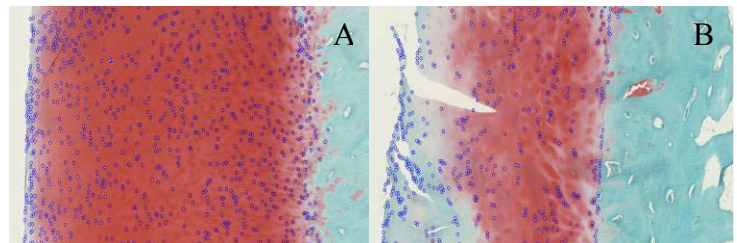


Figure.3 Cells detected by the program on. (A) non-OA and (B) OA specimen, with cellularity scores of 0 and 3, respectively.