

Registration of histology to quantitative MRI of femoral head cartilage for volumetric comparison

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Summary

We present a method for the registration of histology to quantitative MRI (qMRI) of the *full* femoral head via an intermediate CT scan (Figure 1). Previous examples in literature cut the specimen for histology prior to MRI to aid registration [1]. A method for registration to MRI of the *full* femoral head allows comparisons of histology to *in vivo* scans.

Introduction

Histological analysis is the current reference standard for evaluating cartilage health [2]. qMRI offers a method of assessing the quality of cartilage *in vivo* [3]. Comparison of these data modalities provides increased validation of qMRI, furthering applications in clinical diagnosis and orthopedic modelling. Such a comparison at the femoral head presents difficulties, as the spherical shape of the specimen limits recognisable features for image registration.

Methods

This project received approval from our local HREC (18670). All participants provided written informed consent. Femoral head specimens from hip replacement surgeries were scanned *ex vivo* with MRI (T1p 600µm isotropic voxel), and photon counting CT (resampled to 100µm isotropic). Twelve parallel, 5µm thick histology sections were taken from a sample of the femoral head every 50µm. Sections were evaluated using Safranin O-fast Green [4] staining and scanned at 40 times magnification. A custom algorithm written in MATLAB semi-automatically registered histology sections to an oblique slice of the CT scan. The algorithm preprocessed the histology image before matching image features to slices of the CT volume, taken at regularly spaced orientations and positions. The number of matched features was used to determine the best CT slice for registration. The processed histology image was non rigidly registered to the best CT slice (Figure 1b). By composing the histology to CT transformation with a rigid transformation between CT and MRI volumes (Figure 1d), a direct transformation between the histology section and the

MRI volume was found. Image registrations were validated using DICE coefficients [5].

Results and Discussion

When comparing a processed histology section to a random CT slice, the average number of matched features was low ($M=3.7$, $SD = 2.0$), however a ‘good’ match would typically have more than 20 matched features. The DICE coefficient between the processed histology image and the thresholded CT image was 0.73. A DICE score above 0.7 is considered a good agreement between images [5]. Adjacent histology sections registered to parallel CT slices had DICE coefficients ranging between 0.69 and 0.77. Many matched features and strong DICE coefficients across multiple parallel histology sections and CT slices strongly suggest that the positioning and orientation of the registration is accurate.

Conclusions

A pipeline for the comparison of histology of the femoral head to MRI via an intermediate CT scan has been outlined. The results of parallel image comparisons indicate that this method registers a histology ROI to MRI data within one voxel with a high degree of confidence.

Acknowledgments

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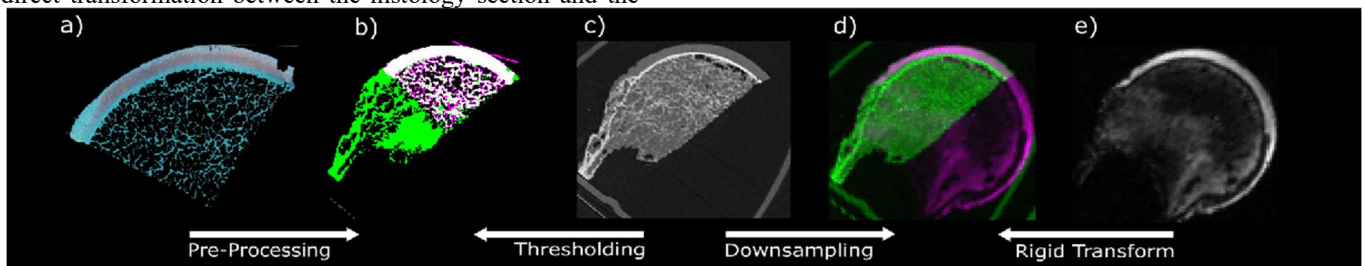


Figure 1: Pipeline showing histology (a) to MRI (e) registration process via an intermediate CT scan (c). (b) shows the histology to CT registration step, where a preprocessed histology image is transformed onto a thresholded CT image. (d) shows the CT to MRI registration step, where a downsampled CT volume is registered to the MRI volume via rigid transformation.