Precision medicine approach to Osteoarthritis: Automatic cartilage segmentation

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Introduction

BACKGROUND

- Osteoarthritis (OA) is the degeneration of protective cartilage within the knee joint, leading to disability in older adults.
- Literature suggests that various Single Nucleotide Polymorphisms (SNPs), a type of genetic biomarker, are linked to OA susceptibility.
- Limitations include difficulty in detecting major SNPs and the use of rudimentary single time point MRI images to associate biomarkers with OA progression.
- The broad goal is to correlate more precise MRI findings of OA progression to SNPs identified from available bio-samples.

OBJECTIVES

- Validate the use of Python machine learning to automatically segment cartilage volumes in lieu of time-intensive manual segmentation.
- Conduct genotyping on SNPs that are linked to increased risk of OA.

Methods

- The dataset was provided by the Osteoarthritis Initiative (OAI), a longitudinal and prospective observational study that serves as a participant biospecimen and knee MRI image database.
- Participant (n~1200) left and right knee MRI images were organized at baseline and 24-month timepoints.
- Femoral, tibial, and patellar cartilage volume measurements for each knee at both timepoints were made by executing the IWOAIUnet2DNormalized segmentation model in the DOSMA Python package.
- Identified an array of generic loci associated with cartilage loss and ran DNA PCR analysis to determine whether available bio-samples from the OAI dataset contained any of these patterns which would be useful in the predictive modeling tool.

Results

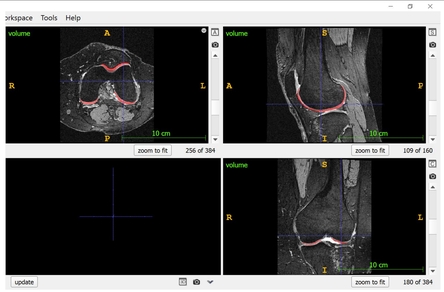


Figure 1: MRI cartilage volume automated segmentation utilizing IWOAI challenge algorithm.

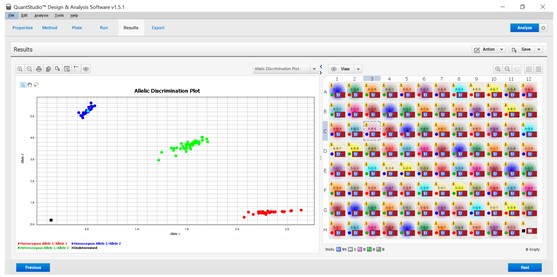


Figure 2: Single nucleotide polymorphism genotyping utilizing OAI database.

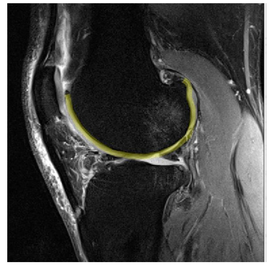
Discussion/ Conclusion

- Completion of ~1200 participant cartilage volume segmentation of baseline and 24 month follow up and SNP genotyping.
- Existing data on SNP genotype and osteoarthritis association based on radiographic findings, which is less sensitive for disease progression compared to MRI imaging findings.
- Analysis of association of SNP genotypes and MRI quantification will be performed for selection of the clinically applicable OA susceptibility loci.
- Stratification of OA risk by SNP genotyping may be used for imaging surveillance, individual treatment decision, and clinical trial subgroup analysis.

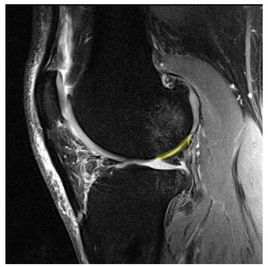
Future Directions

- Femoral, tibial, and patellar cartilage volumes obtained in this study will be used to compute volume loss over the 24-month follow up.
- Cartilage volume loss by the MRI morphometry will be associated with the participant's genotype to identify key SNPs.
- These key SNPs will serve as principal biomarkers to guide the surveillance of high-risk patients prone to develop OA to suggest OA prevention and intervention clinical trials.
- Additional imaging biomarker will be obtained: % full thickness cartilage loss and will be associated with SNPs as well.

Femur subchondral bone



Area of full thickness cartilage loss



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