A Fully Automated Multi-Tissue Multi-Sequence Knee Segmentation Pipeline For Studying Soft Tissue And Bony Structures in 3D

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INTRODUCTION: Magnetic resonance imaging (MRI) has been frequently used for the noninvasive qualitative and quantitative assessment of the knee joint, in particular, to assess injuries to the anterior cruciate ligament (ACL), torn medial and/or lateral menisci and articular cartilage. 3D evaluations of the anatomy and structural properties (e.g., relaxometry) of these structures and their associated injuries are constrained by the need for manual segmentation. Segmentation for model development from MRI images is very time-consuming and arduous even for experienced segmenters hindering the assessment of large-scale data. Deep-learning is a popular approach to automate the 3D segmentation process from medical images. The majority of prior autosegmentation works have either been focused on a singular structure such as knee articular cartilage or ACL and/or only focused on limited sequences only used in research. To address those limitations, we have developed a deep-learning-based autosegmentation pipeline capable of segmenting major knee soft tissue (i.e., ACL, menisci, and articular cartilage) and bony (i.e., femur, tibia, patella and fibula) structures from commonly used clinical sequences (i.e., PD: proton density-weighted and DESS: double-echo steady-state). Such a pipeline would facilitate quantitative assessments of the whole knee joint and ultimately help identify the intrinsic and extrinsic factors responsible for high-risk knee anatomy, which can directly impact the strategies for minimizing the risk of common knee injuries.

METHODS: Following IRB approval, longitudinal MRIs of both surgically treated and healthy contralateral knees of subjects (n= 159; age: 19.8± 5.2 years, 57% female) enrolled in IRB and FDA-approved BEAR clinical trials were obtained (i.e., PD-SPACE and DESS, scanned by 3T Siemens Trio or Prisma magnets). We built a comprehensive data set of 338 knee MRI scans for each sequence, acquired from multiple time points between 3 to 72 months post-surgery. Using commercial image processing software (Mimics v21), bones (femur, patella, tibia, fibula), as well as the soft tissues (ACL, lateral and medial menisci, medial and lateral tibial cartilages, femoral cartilage, and patellar cartilage) encompassing the knee joint, were manually segmented by an experienced examiner on a subset of 100 MRIs. A modified 3D U-Net was trained on the manually segmented MRIs to create a baseline network to speed the segmentation process for each MR sequence. The baseline model was used to segment the rest of the dataset which was manually checked and corrected. The final manually corrected dataset was split into train (80%, n=281) and test (20%, n=57) sets stratified by subjects for the final training. The network is trained for 1000 epochs with a logarithmically decremental learning rate. The network was supplemented with data augmentation techniques during the training phase and with a postprocessing step to improve the segmentation dice compared to the prior run. Anatomical similarity to manually corrected and annotated ground truth was assessed with the Dice coefficient and Hausdorff distance. Statistical tests (paired t-test) were performed to compare model performance across PD and DESS MRI sequences.

RESULTS: The final model-generated segmentations for both PD and DESS scans were anatomically similar to the ground truth annotations (Figure 1). For the PD-SPACE MRIs, the average Dice was 0.98 (0.93 to 0.99) and the average surface distance was 0.5 mm (0.44 to 0.80) across all labels (Figure 1). For DESS MRIs, the average Dice was 0.94 (0.88 to 0.98) and the average surface distance was 0.7 mm (0.50 to 1.21) across all labels (Figure 1). On average the model performed better on PD than DESS across all labels for the Dice coefficient (0.007 to 0.05; $P<0.001$); and reported a significant difference in the Hausdorff distance for bony structures (0.004 to 0.41 mm; $P<0.001$). There were no significant differences in the soft tissue segmentations between the two sequences.

DISCUSSION: PD and DESS are commonly used MRI sequences to evaluate knee injuries in clinical settings. The observed superior performance of our multi-tissue segmentation model on these common clinical sequences highlights the potential of the current approach to be integrated into clinical care, offering robust 3D assessments with a minimum burden. Such an approach facilitates the translation of advanced quantitative approaches (e.g., 3D relaxometry) from labs into clinics. The utilized iterative manual segmentation and model training helped reduce the time to manually segment one scan from 1 day to 20 mins, and the final network took about 30 seconds to generate accurate labels for each scan. The current data supports the ability of the proposed deep-learning pipeline to generate 3D models of critical soft tissue and bony structures of the knee joint with high accuracy yet at a fraction of the time it takes a human annotator. Future work involves expanding the current model to other sequences and multisite data with the ultimate goal of developing robust pipelines for 3D evaluation of knee shape and tissue structural properties.

SIGNIFICANCE: Automated segmentation of major knee soft tissue and bony structures from MRI to create a 3D representation of knee joint can produce new insights regarding knee, and tissue health and ultimately help with evidence-based treatment strategies and timely return to sports activities.
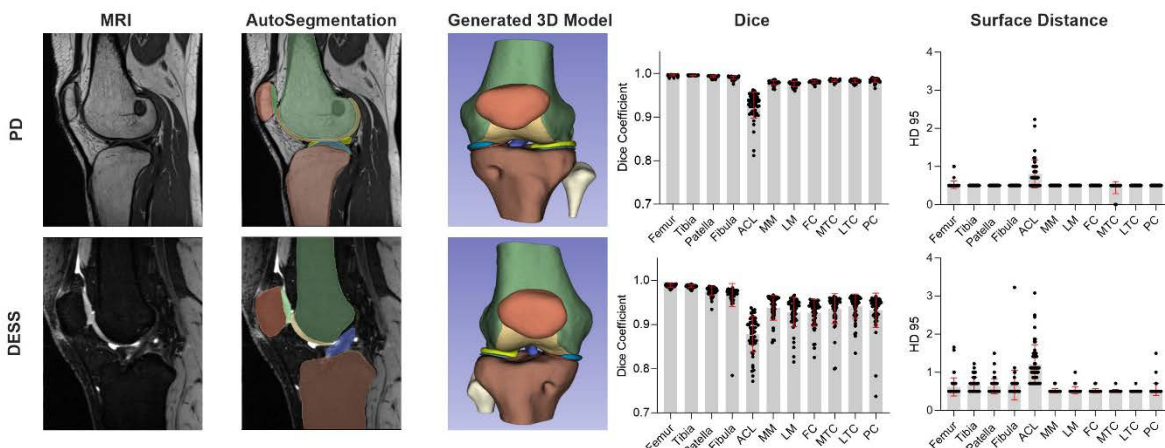

Figure 1. Automatic segmentation and model development from PD (top) and DESS (Bottom) sequences. MM: Medial Meniscus, LM: Lateral Meniscus, FC: Femoral Cartilage, MTC: Medial Tibial Cartilage, LTC: Lateral Tibial Cartilage, PC: Patellar Cartilage.