16th International Workshop on Osteoarthritis Imaging: Oral Presentations

NODESTUDIO, A VISUAL PROGRAMMING FRAMEWORK FOR MUSCULOSKELETAL MRI ANALYSIS

M.A. Mendoza, Z. Huo, Y. Diao, Y. Jin, J. Huang, N.K. Bangerter

Imperial College London, London, England

INTRODUCTION: As research advances with ever increasing complexity and quantity of algorithms for MRI, it becomes increasingly difficult to research, consolidate, and access algorithms without considerable effort to either implement or integrate software repositories in a clinical researcher's analysis pipeline. To this end, we have developed a framework with the aim of improving the accessibility of sophisticated musculoskeletal MR imaging processing techniques and facilitating the creation of new multi-platform image processing pipelines. This software application offers an intuitive, visual method for the development of analysis pipelines for MR reconstruction, segmentation, data visualization, and quantitative analysis. We hope this framework will encourage the collaboration of researchers by facilitating the traditionally difficult task of integrating MR algorithms into clinical imaging processing pipelines.

OBJECTIVE: 1) An open-source node-based imaging processing web platform, called NodeStudio, was created to facilitate the design, development, and standardization of musculoskeletal MRI signal processing pipelines. 2) It supports a comprehensive, flexible ecosystem of tools, libraries, and resources to support researchers to push the state-of-the-art in MRI research. 3) It is designed to allow researchers to easily build, design and deploy advanced algorithms and techniques using a visual programming node editor.

METHODS: NodeStudio was developed to enable researchers to build complex imaging processing pipelines visually using a computation graph. A visual computation graph is a method for the design of complex algorithms without writing a single line of code. Instead of writing code, the user can visually assemble node networks in a cross-platform web application. NodeStudio gives rapid feedback that reflects network changes. It is designed to be simple to use and doesn't require the knowledge of Python or any standard programming languages. This platform also supports multi-vendor MRI data, the integration of custom Python code, and the integration of third-party packages the deep learning framework DOSMA. As a tool for MSK, the platform supports several techniques for quantitative MR analysis.

RESULTS: We demonstrated the use of NodeStudio to create a quantitative MR analysis pipeline for the T2 values of meniscus cartilage using a qDESS T2 mapping algorithm and a DOSMA-based segmentation mask generation node. In the pipeline shown in Figure 1, the T2 values for femoral cartilage for a single sample subject was found to be 35.21 ± 9.03, in line with standard values, as shown in the stats node.
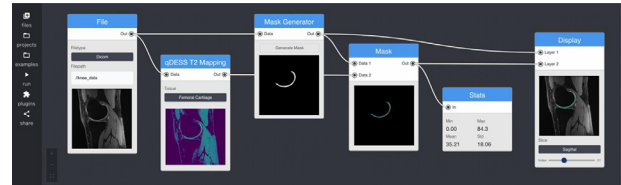

Figure 1: Example of a Quantitative MR Analysis Pipeline with NodeStudio User Interface

CONCLUSION: We have developed a framework to reduce the complexity of MR reconstruction, segmentation, data visualization, and quantitative analysis. NodeStudio allows clinical researchers to visualize and facilitate the development of MR analysis pipelines. We hope this framework will provide a new standard for clinical MRI research.

AGREEMENT AND SENSITIVITY TO BETWEEN-GROUP DIFFERENCES OF U-NET-BASED, AUTOMATED CARTILAGE T2 ANALYSES - DATA FROM THE OA-BIO PROJECT

A. Wisser [*], F.W. Roemer [**], F. Berenbaum [***], F. Eckstein [*], S. Maschek [*], W. Wirth [*]

[*] *Chondrometrics GmbH, Freilassing, Germany & Paracelsus Med. University, Salzburg, Austria*
[**] *University Hospital & University of Erlangen, Erlangen, Germany & Boston University School of Medicine, Boston, MA, USA*
[***] *Sorbonne University, INSERM, APHP Hôpital Saint-Antoine and 4Moving Biotech, Paris, France*

INTRODUCTION: Previous studies reported a high agreement for cartilage segmentations from high resolution 3D gradient echo MRIs using deep learning techniques when compared to manual cartilage segmentations with Dice similarity coefficients (DSC) of up to ~0.90. Only few studies applied deep learning techniques to multi-echo spin echo (MESE) MRI for cartilage T2 analysis and also reported a somewhat lower agreement (DSC up to 0.75).

OBJECTIVE: a) to evaluate the agreement between U-Net-based vs. manual cartilage segmentations of the weight-bearing femorotibial joint using MESE MRIs from Osteoarthritis Initiative (OAI) healthy reference cohort (HRC) participants and b) to evaluate, whether U-Net cartilage segmentations allow to reproduce the differences in cartilage T2 times