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Background/Aim

Changes in myocardial (heart-muscle) tissue such as scar and epicardial adipose tissue (EAT) show associations with various cardiovascular diseases. Both can be assessed by magnetic resonance imaging (MRI) using 3D Late Gadolinium Enhancement (LGE) Dixon sequences. The manual evaluation of these biomarkers is still time consuming and integration into routine clinical practice remains challenging. The aim of this project was to develop a machine-learning (ML) based semi-automated post processing workflow for quantitative myocardial tissue characterization together with a data curation platform for data collection, model training and validation.

Methods

A total of 80 3D LGE Dixon images were segmented manually to create a training dataset. Manual segmentations of Right ventricular (RV) scar tissue and Ventricular EAT were performed using open-source post processing softwares CEMRGApp and 3D Slicer. For the data curation platform, concrete requirements were defined after an analysis of the clinically relevant use cases and iteratively reconsidered throughout the project. Docker was used for interoperability and platform independence. MongoDB served as the database for metadata storage, and Python for implementing underlying application logic. The user interface was built in React and model training was performed using the nnU-Net framework.

Results:

A first version of the platform was successfully tested by the clinical members of the project. A prototype pipeline was established for model training and semi-automated segmentation. Automated segmentation of an individual case using the developed machine learning model was possible within 2s/case. The model achieved a Dice-similarity coefficient of 0.72 on the test dataset.

Discussion:

Our platform extends existing post-processing workflows for tissue characterization by connecting data management and quality assurance. While a significant speed up could be achieved for quantifying tissue parameters, clinical supervision of the ML-model's output is still necessary. The established prototype pipeline could serve as a blueprint for semi-automated quantitative tissue characterization on other datasets. The platform's accessibility via a graphical user interface (GUI) ensures utilization by medical professionals in addition to data scientists.

Limitations:

The model is based on a relatively small sample size and requires further evaluation on broader datasets in the future.