A PROPOSED WORKFLOW FOR QUALITY CONTROL AND REPRODUCIBLE DATA ANALYSIS OF HEATHCARE-ACQUIRED QUANTITATIVE MR USING XNAT

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Introduction: NCITA[1] is creating a national coordinated infrastructure to accelerate the translation of quantitative MR (qMR) cancer imaging biomarkers for clinical use. qMR imaging biomarkers require standardised processes for image acquisition, quality control (QC) and data analysis and have capacity to improve therapy development and add patient benefit[2]. Here, we demonstrate an end-to-end workflow in which quantitative analyses are performed on qMR datasets stored on XNAT[3]. Specifically, we perform T1 mapping and tracer-kinetic model fitting on DCE-MRI data using the open-source analysis toolkit Madym[4]. However, this workflow is generalisable to any analysis/software package that can be scripted to run automatically in a Docker container. We demonstrate that clinically-acquired research qMR data from the NHS or multi-centre clinical trials can be processed using XNAT into a form suitable for rapid data acceptance/rejection and further data processing, without requiring local data download and offline processing at individual research institutions.

Methods and Results: *Prerequisites:* An XNAT server (version 1.8+) with the container plug-in installed. For a proof-of-principle analysis during development we (1) installed a local version of XNAT running on a virtual machine using Vagrant and Virtual Box; (2) built and installed the container plug-ins from source.

Build and pull Docker images containing analysis software: A Docker image running a python tool to check data for discrepancies from the acquisition protocol was built and pulled onto XNAT. For DCE-MRI analysis we used Madym, which can be downloaded pre-installed in a Docker image and adapted for use in the XNAT container plug-in[5].

Set-up XNAT project and upload configuration files: Previous steps need only be set-up once and can be re-used for multiple projects. Creating and uploading configuration files at the project level ensures consistency of analysis across data within the project, while allowing each project to have analyses tailored to its specific needs.

Acquire study data: Clinical imaging data have been acquired using research DCE-MRI protocols implemented at The Christie Hospital. Images were exported directly from the scanner to a research PACS (Conquest DICOM[6]) with automated de-identification in accordance with DICOM Supplement 142 via a pseudo-anonymisation service (RSNA Clinical Trial Processor[7]). From here the data can be transferred to the XNAT node at The University of Manchester.

Run analysis: Using XNAT we performed: (1) protocol checking to confirm the expected scans were received for the session; (2) Conversion from DICOM to NIFTI images for further processing; (3) Quantitative baseline T1 mapping; (4) Arterial input function detection; (5) Tracer-kinetic DCE model fitting (any model available in Madym).

Figure 1: Proposed end-to-end workflow for qMRI using XNAT

Discussion and Conclusion: This pipeline demonstrates the main requirements of an automated end-to-end workflow, securely moving NHS clinically-acquired research qMR data via a research database to an academic research repository in a form suitable for data QC assessment, analysis and storage. In future work the XNAT-OHIF viewer will be used to define ROIs and assess summary outputs[8]. Note that while the setup steps require a level of technical expertise using XNAT, data QC and analyses can be run simply through the XNAT browser interface. Each step requires minimal intervention and there is a potential for a wide range of well-defined quantitative data acquisition and analyses to be performed. We have demonstrated the ability to perform rapid QC and analysis of quantitative data acquired on patients in a healthcare setting. This infrastructure will be available for qMR standardisation in multi-centre clinical trials via the planned NCITA MRI Core Lab.

References: [1] McAteer MA et al. BJC 2021; 11–4. [2] O'Connor JPB, et al. Nat Rev Clin Oncol. 2017;14(3):169–86. [3] Herrick et al. NeuroImage, 2016; 124(B): 1093-1096;
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[6] https://ingenium.home.xs4all.nl/dicom.html [7] https://mircwiki.rsna.org/index.php?title=CTP-The_RSNA_Clinical_Trial_Processor [8] https://wiki.xnat.org/documentation/x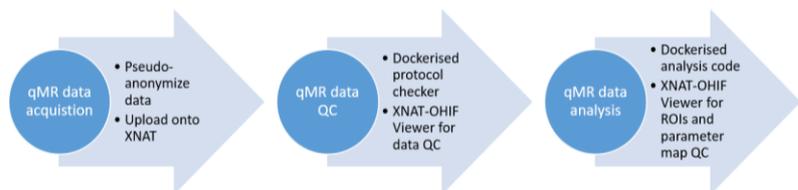nat-ohif-viewer/xnat-ohif-viewer-122978433.html