Fully Automated Online Reconstruction, Registration, and Analysis Pipeline for 3D Magnetic Resonance Fingerprinting

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Target Audience: Clinicians and researchers interested in the point-of-care viability and potential of 3D Magnetic Resonance Fingerprinting.

Purpose: Although 3D Magnetic Resonance Fingerprinting (3D-MRF) allows for rapid acquisition of quantitative parameter maps, the process of preparing quantitative maps for radiologists to interpret is usually far slower With multiple offline steps, fingerprinting maps are rarely available via PACS or at the scanner. These manual reconstructions often discard crucial spatial and header information needed by PACS, or comparison packages like FSL, reducing the value of a quantitative modality like MRF. To address these limits, we implemented an online fully-automated pipeline capable of reconstructing 3D-MRF data and returning T1, T2, M0, and B1 maps in both subject and MNI-152 space, while remaining fully DICOM-compatible. The immediate availability of MNI space quantitative maps was then leveraged to automatically generate comparison reports of atlas regions versus population norms while the subject was still in the bore.

Methods: To create a modular, scalable system, Docker images communicating via ISMRM-RD pipes were created and hosted within a remote Kubernetes cluster. Raw data was sent to the cluster via the Framework for Image Reconstruction Environment (FIRE, Siemens) prototype through an SSH jump node. MRF maps were reconstructed first by a Gadgetron module and passed to a second Gadgetron module generating synthetic T1w and T2w maps. These maps were then passed to a Python/FSL module, which registered the synthetic images to MNI-152 space and applied the resulting nonlinear warps to the MRF maps. Finally, the MNI space maps were analyzed using the Harvard-Oxford subcortical atlas to calculate regional statistics from the quantitative maps for comparison against historical subject specific or aggregate population data retrieved from the cloud. The MRF quantitative maps in both subject-space and MNI-space, as well as the region report, were piped back to the scanner console where they could be viewed, exported to DICOMs, or sent to a PACS database.



Existing raw datasets acquired with a prototype FISP 3D-MRF sequence on a 3T scanner (MAGNETOM Vida, Siemens Healthcare, Erlangen, Germany) with varying fields of view and spatial resolutions from 3 healthy volunteers and 3 brain tumor patients were retroreconstructed as an initial test of the proposed system. Postprocessing times for each module were recorded. As a proof of concept for the regional statistics reports, we generated regional comparisons against "expected" values derived from 60 test-retest MRF datasets acquired from 10 healthy volunteers. Regional means and distributions were plotted against population means and distributions. Data were color-coded as "typical" (within population Q1/Q3 quartiles), "inconclusive" (within population 10%/90% percentiles), or "atypical" (all other values).

Results: Automated reconstruction, registration, and report generation were successful for the six retrospective datasets evaluated, with results returned to the scanner 205.8±38.2 seconds after data acquisition was completed. For the three healthy subjects, all regions were successfully identified as either "typical" (58 of 60) or "inconclusive" (2 of 60) in the statistical reports, with MNI registration exhibiting a strong match. For the three brain tumor patients, the statistical reporting indicated substantially higher rates of "atypical" (9 of 60) or "inconclusive" (13 of 60) regional results. MNI registrations for the two metastatic tumor patients remained strong. Meanwhile, the registration from a GBM patient exhibited nonlinear errors proximal to the tumor, which likely impacted region accuracy. Notably, this was flagged as "atypical" by the associated report.

Discussion: Automated generation and storage of MNI-space quantitative maps for each reconstructed dataset should substantially simplify future population-based research methods. For example, MNI-space images allow for immediate comparison against a subject's past scans or even against other subjects. These images can be performed without any additional registration, ROI creation, or other manual intervention. Additionally, while still requiring substantial validation, the fully-automated generation of regional reports represents an initial attempt at simplified anomaly detection while still at the scanner console. We hope these reports can eventually serve as an "early warning" about potential anomalies, allowing technicians to acquire additional imaging immediately, avoiding a repeat visit.

Conclusion: A fully-automated online analysis pipeline is presented for 3D-MRF, capable of returning quantitative T1, T2, M0, and B1 maps in both subject-space and MNI-152 space, as well as automatic intra- or inter-subject statistical reporting using MNI-space atlas regions. Images and reports are returned to the scanner in real-time.Both raw and MNI-registered quantitative maps are compliant with DICOM and NIFTI tools like FSL and 3DSlicer. Images and reports can be saved to PACS directly, simplifying clinical adoption for radiologists and other clinicians.

