Rapid, open-source, cross-platform 3D multiparametric mapping for multisite neuroimaging

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Synopsis

Motivation: To address the unmet need for a cross-platform, multiparametric technique to facilitate data harmonization across different sites.

Goal(s): To implement and evaluate a fully transparent 3D multiparametric mapping for multisite neuroimaging.

Approach: A multiparametric mapping technique, 3D-QALAS, was implemented in Pulseq. The acquired T1 and T2 maps were compared within-scanner, cross scanners, software versions, sites, and vendors.

Results: The Pulseq implementation exhibited significantly higher reproducibility than vendor-native implementations, particularly for T2 values, in both phantom and in vivo studies. This approach enabled ADNI-compliant field-of-view sizes with 1mm isotropic resolution within 5 minutes, while maintaining a cross-platform coefficient of variation below 4%.

Impact: An open-source implementation across different vendors and scanners, along with a consistent reconstruction and fitting pipeline, improved measurement reproducibility. This approach facilitates data harmonization, version control and error-propagation assessment, making it also suitable for extracting quantitative information for downstream analysis.

Introduction

Open-source science is desirable for enhancing transparency and reproducibility in neuroimaging studies, particularly since multi-site studies require consistent data acquisition, reconstruction, and analysis across various platforms[1]. Traditional closed-source, vendor-specific environments may hinder this consistency[2, 3]. To increase the cohort size, and thereby the statistical power, multi-site studies such as ABCD[4], HBCD[5], and HBN[6] collect MRI data from different scanner vendors and models. However, multi-site data cannot be naively pooled together for analysis due to large inter-scanner differences. This variability in vendor-specific acquisition sequences and reconstruction algorithms contribute to the "reproducibility crisis" in neuroimaging.

Towards addressing this open problem, we introduce a rapid, open-source, cross-platform multiparametric technique, aiming to optimize control over the entire MRI acquisition to reconstruction process. We hypothesized that using identical wave shapes, gradient timing, and consistent reconstruction and parameter fitting procedures will improve reproducibility across different platforms.

Methods

Process overview and study setup

Figure 1A shows the workflow overview. Pulse sequence was implemented with Pulseq[7] (v1.4.0) in MATLAB. The sequence was executed on Siemens scanners using the Siemens Pulseq interpreter[7], and on the GE scanner using the TOPPE interpreter[8]. Adjustments were made to the gradient raster timing, delays, and waveforms to enable all scanners to execute the sequence near identically. The raw k-space data were reconstructed offline using identical procedures in MATLAB. Data were acquired using various 3T MRI scanners from multiple sites and manufacturer as listed in **Figure 1B**. A NIST/ISMRM phantom (serial number: 136-0001) and a healthy volunteer underwent scanning sessions on each of these scanners.

Sequence and data acquisition

We used a multiparametric technique called 3D-quantification using an interleaved Look-Locker acquisition sequence with a T2 preparation pulse (3D-QALAS)[9, 10] as shown in Figure 2. 3D-QALAS incorporates five FLASH readouts, interleaved with a T2 preparation pulse and an inversion pulse. Acquisition parameters were as follows: orientation, sagittal; TR, 4500ms; TE, 2.29ms; TI, 110/1010/1910/2810/3710ms; echo spacing, 5.8 ms; flip angle, 4 degrees; echo train length, 127; and bandwidth, 326 Hz/pixel.
For phantom (**Figure 2B**): FOV, 192x168x168; Matrix, 192x168x56; TA, 4min 21sec. Phantom temperature was measured using MRI readable thermometer[11].
For invivo (**Figure 2C**): FOV, 256x240x208 (ADNI-compliant); Matrix, 256x240x208; R=6;TA, 4min 48sec. After normalizing k space data, L1 penalized non-linear conjugate gradient reconstruction with wavelet and TV regularization was performed[12, 13]. The five source images were passed to voxel-wise Bloch simulations with B1 correction and inversion efficiency estimation[14], and the T1 and T2 values were obtained. Vendor-native 3D-QALAS acquisitions were also acquired. Inversion recovery T1 and single-echo spin echo T2 mapping was also performed on phantom.

Evaluation

For phantom data, spherical ROIs were placed in the spheres to measure relaxation times for each sphere. For in vivo data, SynthSeg implemented on Freesurfer v7.4 was used to segment images and estimate the regional T1 and T2 values for each scan[15, 16]. Coefficient of variation (CV), Bland-Altman plots were used to assess within-scanner repeatability and reproducibility across scanner models, software versions and vendors.

Data sharing

We adhere to the guidelines set by the ISMRM Reproducibility Committee. Pulse sequence, reconstruction and analysis code and raw data can be accessed from https://anonymous.4open.science/r/Pulseq-qalas-0E64.

Results

Phantom study

Figure 2 displays representative images and maps from each scanner, with ROI analysis presented in **Figure 3**. The Pulseq implementation demonstrated significantly higher reproducibility in T2 values, as indicated by lower CVs, compared to the vendor-native implementation (4.9% vs. 3.4%, p=.71 for T1; 17% vs. 2.3%, p<.001 for T2).

In vivo study

Figure 4 presents the representative maps from each scanner and provides a brain region-wise analysis. Pulseq showed cross-platforms CVs of 3.0% for T1 and 1.7% for T2. The Pulseq implementation again showed higher reproducibility than the vendor-native implementation (8.5% vs. 4.0%, p=.29 for T1; 5.0% vs. 3.8%, p=.0052 for T2).

Discussion

Consistency in measurement steps was achieved across sites and vendors, not only at a high level (FOV, matrix, TR, TE, etc.) but also at a more detailed level (wave shape, pulse timing, etc.). Such uniform and fully transparent implementation across different vendors and scanners, along with a consistent reconstruction and fitting pipeline, ensures comprehensive control over the measurements. The achieved significant improvement in reproducibility should boost the statistical power of future large-scale neuroimaging studies. In later stages of this project, we aim to incorporate additional vendors such as Philips, Canon, and United Imaging.

Conclusion

Open-source, vendor-agnostic, rapid 3D multiparametric mapping provided relaxation times with less than a 4.0% variation across different scanners, software, and vendors, with improved cross-vendor reproducibility for both in phantom and in vivo data compared to vendor-native implementations.

Acknowledgements

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Figures

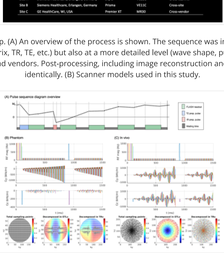

Figure 1. Process Overview and Study Setup. (A) An overview of the process is shown. The sequence was implemented identically across scanners and vendors, not only at a high level (FOV, matrix, TR, TE, etc.) but also at a more detailed level (wave shape, pulse timing, etc.) using Pulseq, executed on different scanners, software platforms, and vendors. Post-processing, including image reconstruction and parameter fitting, was performed offline identically. (B) Scanner models used in this study.

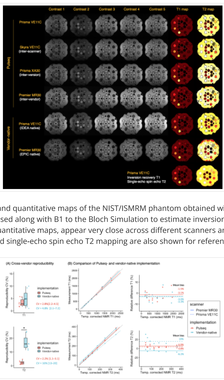

Figure 2. Sequence implementation (A) The QALAS sequence comprises of five equally spaced FLASH readouts, interleaved with IR and T2prep pulses. These five images are used to derive T1 and T2 maps through Bloch simulations. (B and C) A center-out Cartesian sampling method was adopted for this sequence. (B) For phantom scans, a full sampling with elliptical scanning technique was used. (C) For in vivo scans, to reduce the scan duration, an R=6 variable density under-sampling was applied to facilitate compressed sensing acceleration and to enable future motion correction capabilities.

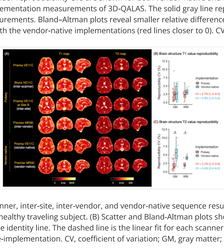

Figure 3. Representative source images and quantitative maps of the NIST/ISMRM phantom obtained with 3D-QALAS. The 3D-QALAS acquires five contrast-weighted images, which are passed along with B1 to the Bloch Simulation to estimate inversion efficiency, T1, and T2 values. The source contrast-weighted images, as well as the quantitative maps, appear very close across different scanners and software. Inversion recovery T1 mapping and single-echo spin echo T2 mapping are also shown for reference.

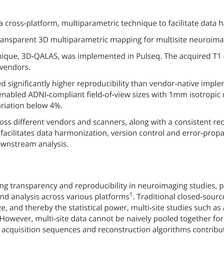

Figure 4. Phantom results. (A) Inter-vendor reproducibility CVs are shown for both vendor-native and Pulseq implementation. (B) Scatter plots demonstrate the linearity of the Pulseq implementation measurements of 3D-QALAS. The solid gray line represents the identity line, which corresponds to the temperature-corrected NMR measurements. Bland–Altman plots reveal smaller relative differences to NMR measurements with the Pulseq implementation than with the vendor-native implementations (red lines closer to 0). CV, coefficient of variation.

Figure 5. In vivo results. Only the inter-scanner, inter-site, inter-vendor, and vendor-native sequence results are shown in the figure for simplicity. (A) Representative quantitative maps from a healthy traveling subject. (B) Scatter and Bland-Altman plots showing cross-platform agreement. Each dot represents a brain region. The solid line is the identity line. The dashed line is the linear fit for each scanner. (C) Inter-vendor reproducibility is shown for Pulseq- and native-implementation. CV, coefficient of variation; GM, gray matter; WM, white matter.