#47635 : To Pool or Not to Pool? Comparability of Multi-Protocol Ultra-High-Resolution qMRI in Healthy Brain Aging

Preferred format : Oral presentation

Keywords: qMRI, ageing, UHF

Primary Sub-Category: Morphology

Secondary Sub-Category: Reproducibility and Validation

• COMPETITION: I would like to participate in the General Audience Pitches Competition and, if accepted, I will submit a short video >> https://esmrmb2025.org/general-audience-pitches/: No

Introduction

High resolution imaging associated with ultra-high field (UHF) MRI provides promising advances for brain imaging. A particularly powerful UHF tool is quantitative MRI (qMRI) which aims to remove the protocol dependency by measuring parameters related to the biophysical properties of the tissues. Few studies have employed large cohorts to infer age-related changes of UHF qMRI parameters [1–4]. A limitation of existing studies is that each has been restricted to its own scan protocol. This constrains further expansion of the cohorts that could be done by pooling multiple datasets. We combine an open UHF qMRI dataset [1] with locally-acquired data and explore how pooling affects the observed age dependencies, and which biases occur between protocols. We focus on small subcortical structures as their delineation is almost exclusive to UHF MRI.

Methods :

The sample comprised three cohorts of healthy subjects from different sources referred as AHEAD, sTx-MPM and pTx-MPM. The AHEAD data came from an openly available dataset [1] previously acquired on a Philips Achieva 7T. The other two cohorts' data sources were the studies conducted at local site on a 7T Siemens Terra. The total dataset comprised 223 subjects (128F, 95M, mean 44.9 y). The AHEAD study (60F, 45M, mean 42.4 y) used a 1-Tx/32-Rx coil and an MP2RAGEME acquisition [5] with two inversion times (TI1/TI2 670.0/3675.4 ms), 4 echoes (TE of 3.0/11.5/19.0/28.5 ms), and SENSE acceleration with R=2 in one direction. No B1 mapping was performed. The sTx-MPM study (53F, 32M, mean 48.6 y) employed a 1-Tx/32-Rx coil and an MPM protocol [6] with three (T1-, PD-, MT-weighted) whole-brain 3D FLASH multi-echo sequences (TR 19.5 ms, FA PDw/MTw/T1w 5/5/20°, 6 echoes for PDw and T1w, TE 2.3 to 14.2 ms, and same first 4 echoes for MTw, GRAPPA acceleration in two directions with R=2 in each, and a 4 ms, 140° Gaussian MT-pulse, 2 kHz off-resonance. SE-STE-EPI was used for B1 mapping [7]. The pTx-MPM study (15F, 18M, mean 43.4 y) adhered to a similar protocol, but used a 8-Tx/32-Rx coil, kt-points excitation pulses [8], a 4 ms, 130° Gaussian-shaped MT-pulse, 3 kHz off-resonance, and AFI based B1 mapping [9]. The AHEAD pipeline comprised the LCPCA denoising [10], standard MP2RAGE calculation of the T1 [11], single-exponential fitting of the echo decay for the R2*, and TGV-QSM [12]. The output maps (R1, R2*, and QSM) were then used for the Multi-contrast Anatomical Subcortical Structures Parcellation (MASSP) [13] to provide the ROI for statistical analyses. The data in sTx-MPM and pTx-MPM cohorts were processed through similar pipelines comprising LCPCA denoising, hMRI-toolbox [14] for quantitative parameter calculation [14], and MASSP. Potential errors were assessed via calculating the number of non-unique R2* values and entropy [15] in the ROI. Linear models were built for each of the median qMRI metrics in each subcortical ROI with age, age2, and sex being the regressors [1–3]. Significance of the observed age dependency, protocol-related bias or age-protocol interaction was determined at a false discovery rate-corrected [16] threshold of 0.05.

Results :

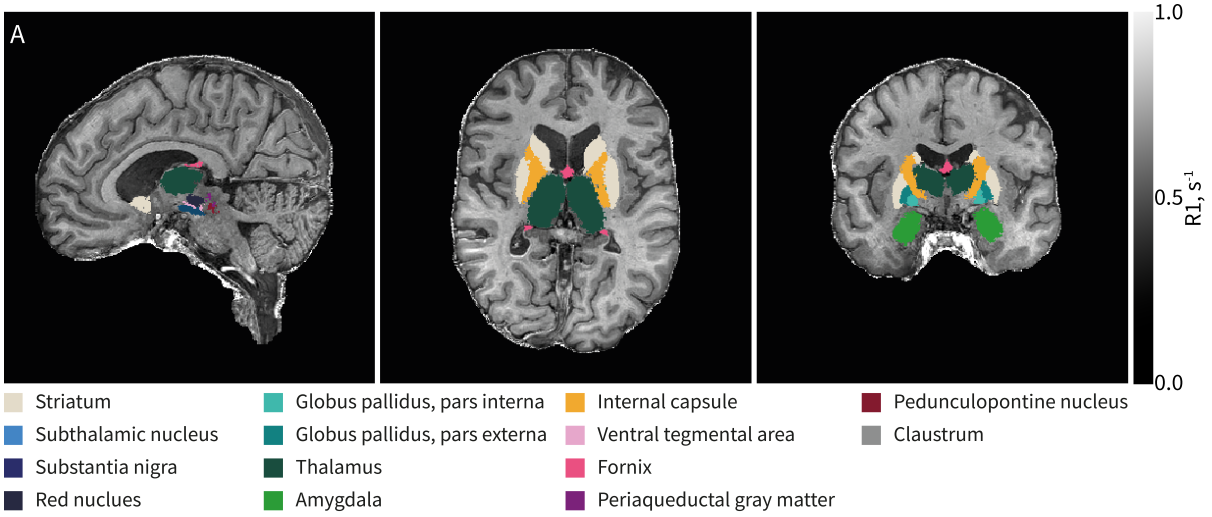
High resolution (0.6 mm) maps of qMRI parameters (R2*, PD, and R1) were obtained, allowing parcellation and ROI volume calculation (Fig 1). Quality assurance has suggested excluding the ventricles and few subjects per ROI from further analyses (Fig 2). The GLM analyses showed significant age and age2 dependency in R1, R2* and subcortical ROI volume for most ROIs. Most of the models indicated significance in protocol-related variable and interactions between protocol- and age- related variables (Fig 3).

Discussion :

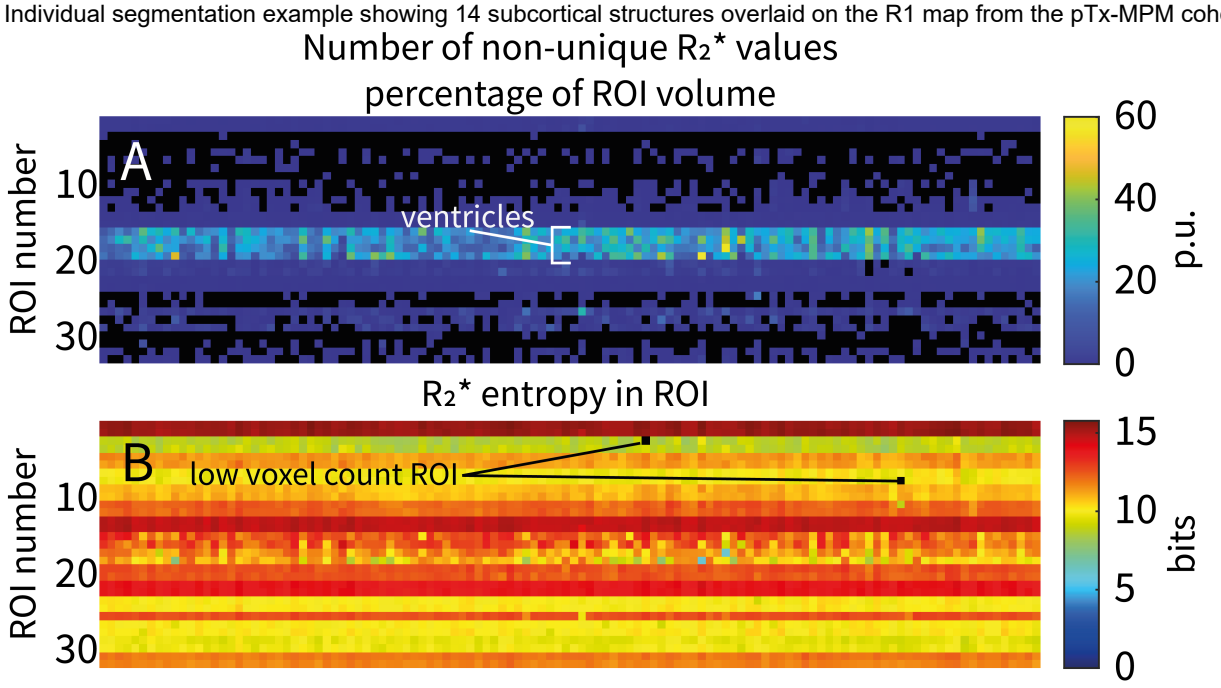
Age-related changes in the pooled dataset exhibit the inverted U-shape dependence in all qMRI metrics, which arises from age-related myelin loss and iron accumulation in the brain tissue [17]. Comparing AHEAD and local data suggests compatibility of age-related profiles for R2* and ROI volume measurements, having the lowest number of significant age-protocol interactions, and less so for the R1 measurements. Generally, the age dependencies (i.e., the GLM slopes) stay consistent, but the absolute values (i.e., the GLM intercepts) vary across protocols. R1 was strongly (up to 31% difference) affected by the protocol, potentially due to difference in B1 or bias in B1 measurements [14]. The B1 mapping exhibited systematic B1 difference (Fig 4) in average B1 between sTx and pTx protocols, which could be caused by biases in AFI and SE-STE-EPI B1 mapping [18], resulting in systematic R1 difference. The R2* calculation reduced dependency on B1 mapping can explain it exhibiting less biases and interactions in the pooled dataset, making it stable across UHF qMRI protocols.

Conclusion :

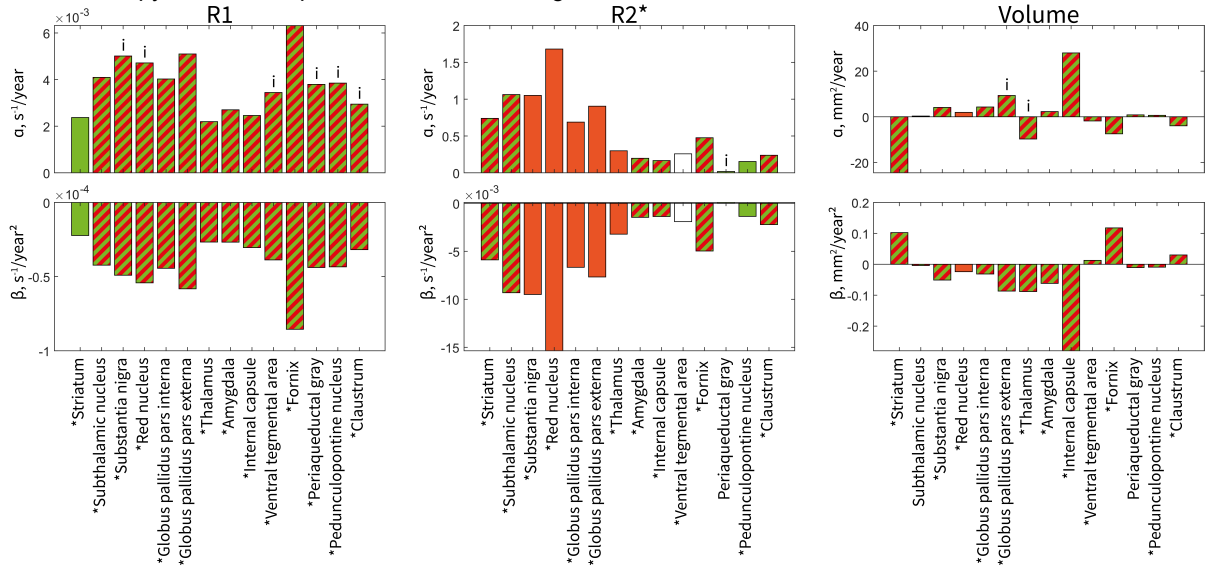
Pooling UHF qMRI datasets reveals inconsistency in absolute values of qMRI metrics across different protocols due to biases in B1 mapping. R2* and ROI volume display more inter-protocol stability, but R1 can also be used for determining age-related dependencies if protocol difference is accounted for.



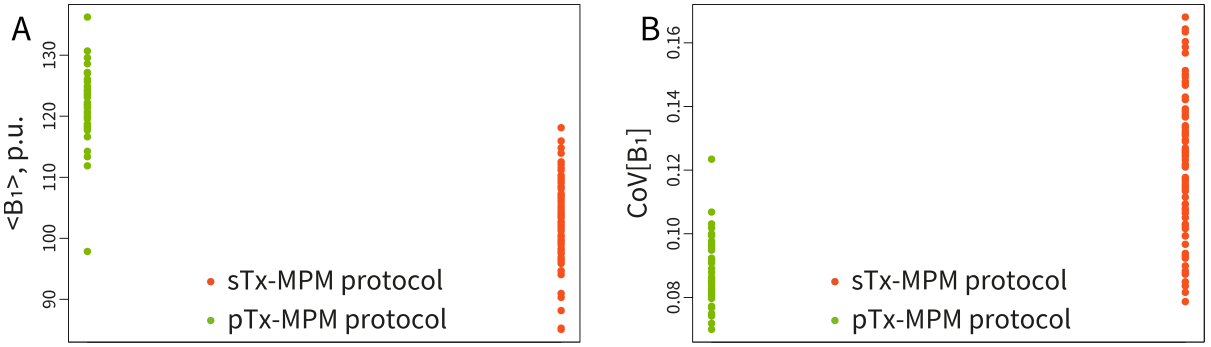
Individual segmentation example showing 14 subcortical structures overlaid on the R1 map from the pTx-MPM cohort.



Quality assurance for the locally acquired data. The number of ROIs is higher than in Fig 1 due to the quality metrics calculation prior to averaging left and right. A. Non-unique values in ventricles result from the qMRI fitting converging to boundary values. B. Low entropy values are sporadic and indicate single-voxel ROI.



GLM analyses summary. Top: linear age term (α), bottom: quadratic age term (β). Age-related significance is indicated by asterisk. Red indicates significant bias of qMRI metrics in sTx-MPM against AHEAD data, green– of pTx-MPM. i symbol indicates significant interaction between age-related and protocol-related terms.



A - Measured B1 values averaged across all ROI. B - Coefficient of variation of the measured B1. A demonstrates the pTx-MPM protocol to produce higher B1 values, B demonstrates the pTx-MPM protocol to produce more uniform B1 distribution.

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