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02-BRAIN

#54226 : Interplay between segmentation and quantification in quantitative magnetic resonance imaging

Preferred format : Oral presentation

Keywords: qMRI, segmentation, UHF

Please indicate a primary category for the abstract:: Relaxometry

Please indicate a secondary category for the abstract:: Reproducibility & validation

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Introduction

Region segmentation is a critical part of MRI data processing. In quantitative MRI (qMRI) and particularly in ultra-high field (UHF) imaging clean segmentation is hindered by the interplay between the segmentation procedure and the underlying quantitative values. The complication arises due to the data often being used as input for the segmentation is subsequently employed with the segmentation output to represent structural and functional properties [1]. There is potentially a bidirectional dependency, where quantitative values influence segmentation, and vice versa. A critical question is then, how large is this interplay between quantification and segmentation?

Methods :

To provide a measurable estimate of the influence of using qMRI maps for segmentation on the subsequently extracted median quantitative values, we have used two UHF multiparameter mapping (MPM) datasets acquired at GIGA-CRC Human Imaging with a 7T Terra scanner. The two datasets: sTx-MPM (85 participants) and pTx-MPM (50 participants) were acquired using three (T1-, PD-, and MT-weighted) whole-brain 3D FLASH-based multi-echo sequences with isotropic resolution of 0.6 mm, six echoes for PDw and T1w, and four echoes for MTw. Two major differences between MPM acquisitions comprised: first, using 1Tx/32Rx Nova Medical coil for sTx-MPM, and 8Tx/32Rx Nova Medical coil with k-t points excitation for pTx-MPM, and second, using SE-STE-EPI based B1+ mapping for sTx-MPM, and AFI-based one for pTx-MPM. Full description of acquisition parameters is available elsewhere [2]. The magnitude images were denoised with LCPCA-based algorithm [3]; then quantitative maps (R1, R2*, and PD) were created using hMRI toolbox (0.6.1) [4] and subjected to nonlinear transformation into MNI space (ANTsPy 0.4.2) matching the space of MASSP prior labels. The transformed qMRI maps were used in MASSP segmentation [5] to provide masks of 31 subcortical structures in left and right hemispheres. This intertwined quantitative values with segmentation, as MASSP uses both prior label maps, and quantitative maps to delineate structures. Alternatively (Fig. 1), the

same transformed maps were used with MASSP prior labels for segmentation in an atlas-based manner, thus disentangling the effects of segmentation and quantification (except for the coupling previously introduced at the MNI coregistration step). Median values of R1 and R2* were calculated for each ROI from the MASSP segmentation and from the MASSP-atlas based segmentation after pooling values from left and right ROIs. Two-way mixed effects single-rater type [6] Intraclass Correlation Coefficients (ICC) were calculated for the two segmentation types to assess the consistency of relaxation rate measurements. The ICC significance and confidence intervals were assessed with a Bonferroni-corrected (for 14 ROIs and 2 metrics tested) p-value threshold of 0.05. Mean relative difference was calculated for each dataset (sTx-MPM and pTx-MPM) and for each ROI similarly to Bland-Altman approach as the averaged ratio of difference between two measurements to the mean of two measurements. The latter was compared to the ratio of difference between protocol-specific means to mean of protocol-specific means.

Results :

The median values of R1 and R2* extracted from two types of segmentations were highly consistent. All the calculated ICCs significantly differed from zero with the ICC-related p-value lower than Bonferroni-corrected 0.05 threshold. The estimated ICCs ranged from 0.839 to 0.996 for R1 (Fig. 2, A) and from 0.764 to 0.993 for R2* (Fig. 2,B). No direct correlations between ICC and structure volume were observed. The average segmentation-related difference in pTx-MPM protocol varied from 0.02% to 9.56% for R1 (Fig. 3,A), and from 0.83% to 14.89% for R2* (Fig. 3,B). Similar difference in sTx-MPM varied from 0.03% to 15.34% for R1 and from 0.86% to 20.98% for R2* (Fig. 3). At the same time, the difference between sTx-MPM means and pTx-MPM means in atlas-based segmentation varied from 13.79% to 25.62% for R1, and from 1.99% to 11.94% for R2* (Fig. 3).

Discussion :

The high ICCs obtained for all the ROIs and metrics indicate the robustness of the selected segmentation method [5] to changes in the quantitative values (Fig. 4). For median regional R1 values the impact of protocol-dependent qMRI values is for most ROI much larger than the impact of segmentation, as indicated by the quantification of the relative protocol-dependent differences in qMRI values and segmentation-related differences. Conversely, the protocol-dependency of R2* values is generally small, but the impact of protocol-dependent qMRI is comparable to the impact of segmentation.

Conclusion :

Automatic segmentation of subcortical structures making use of the quantitative values has a negligible effect on the resulting median values of quantitative metrics in the selected ROIs. A much higher impact is exerted by the differences in the imaging protocol. Support: EU JPND, FNRS, ULiège, FEDER, Stop-Alzheimer Foundation

Data and Code Availability Statement (Information not included in the word counting) :

Code is available upon reasonable request to Mikhail Zubkov No data are available for this abstract

References (Information not included in the word counting) :

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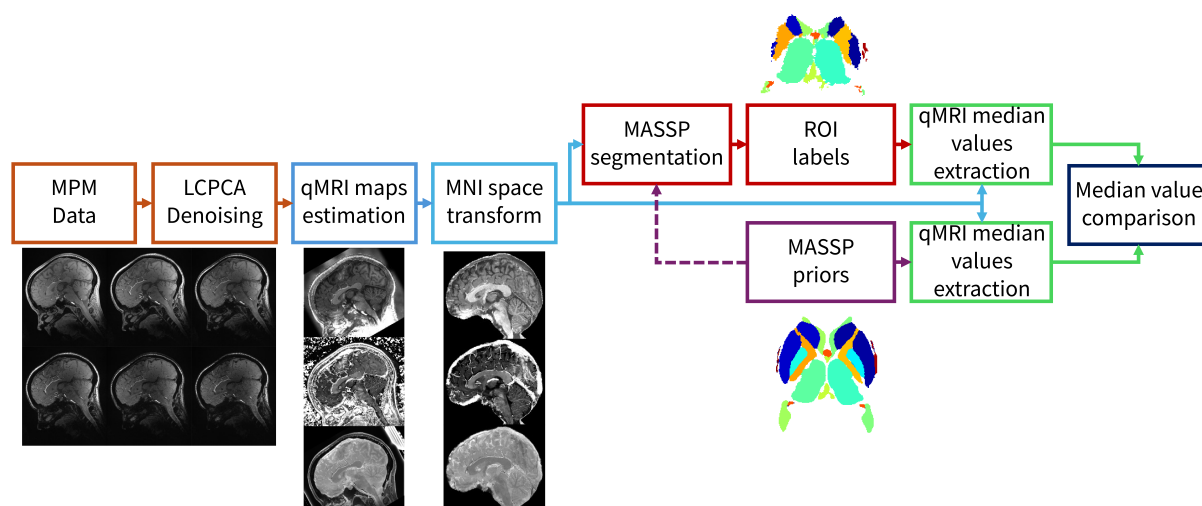


Figure 1. Data processing pipeline resulting in two sets of median values per region: one with stronger, and another with weaker segmentation and quantification coupling

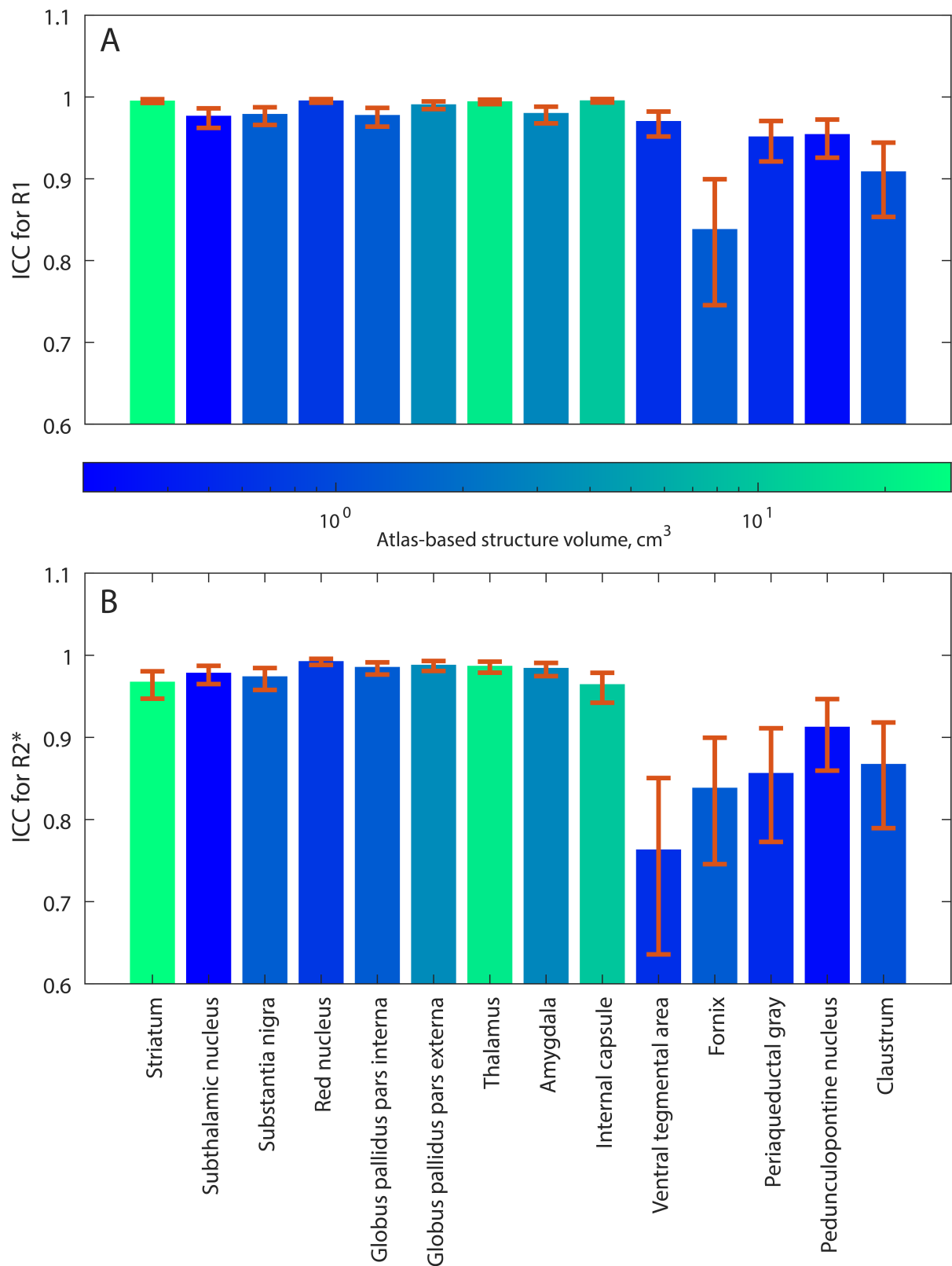


Figure 2. ICC values between MASSP-based and atlas-based segmentations with confidence intervals for R1 measurements (A) and R2* (B)

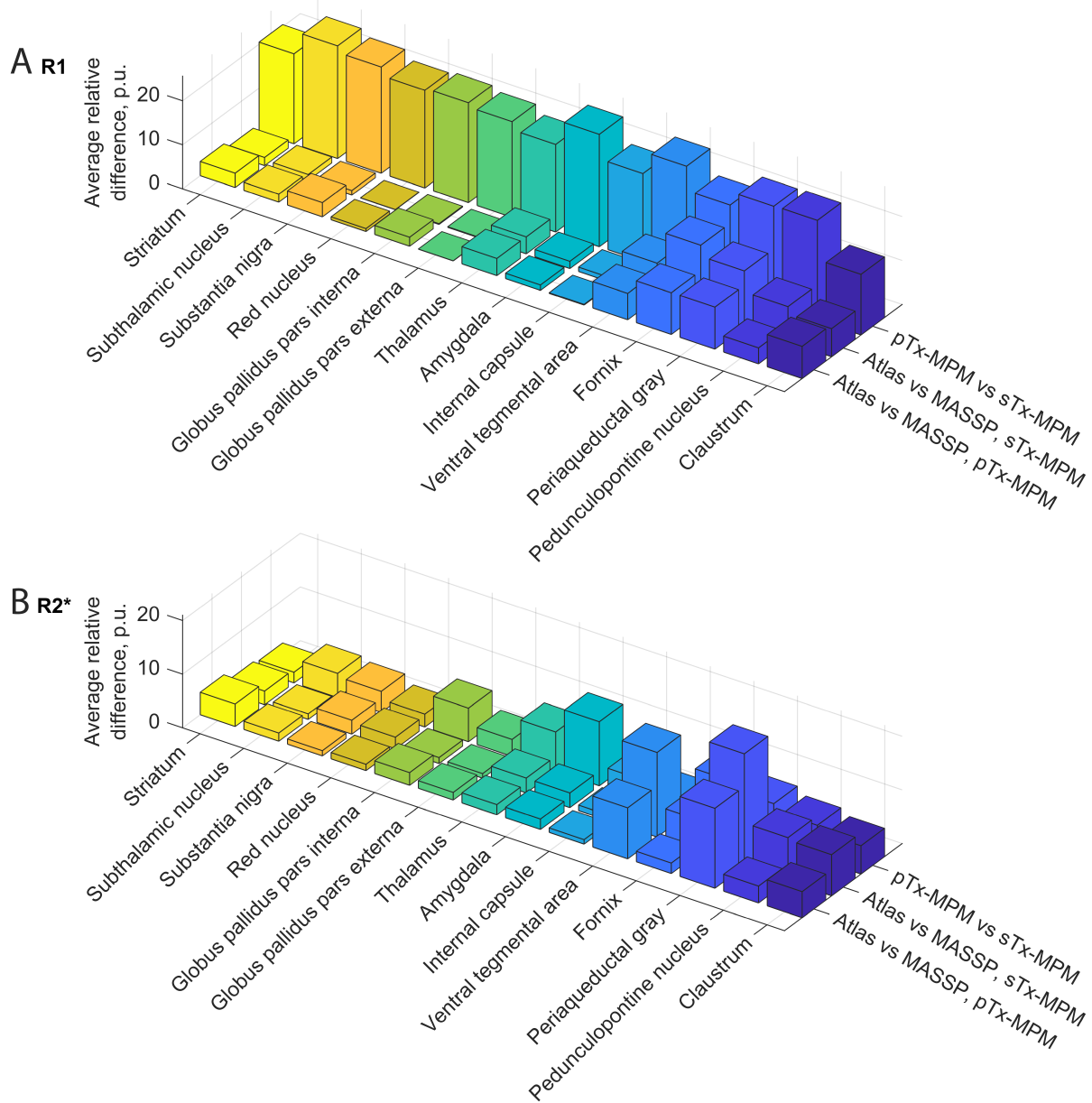


Figure 3. Participant-averaged average segmentation-related and protocol-related differences for R1 (A) and R2* (B)

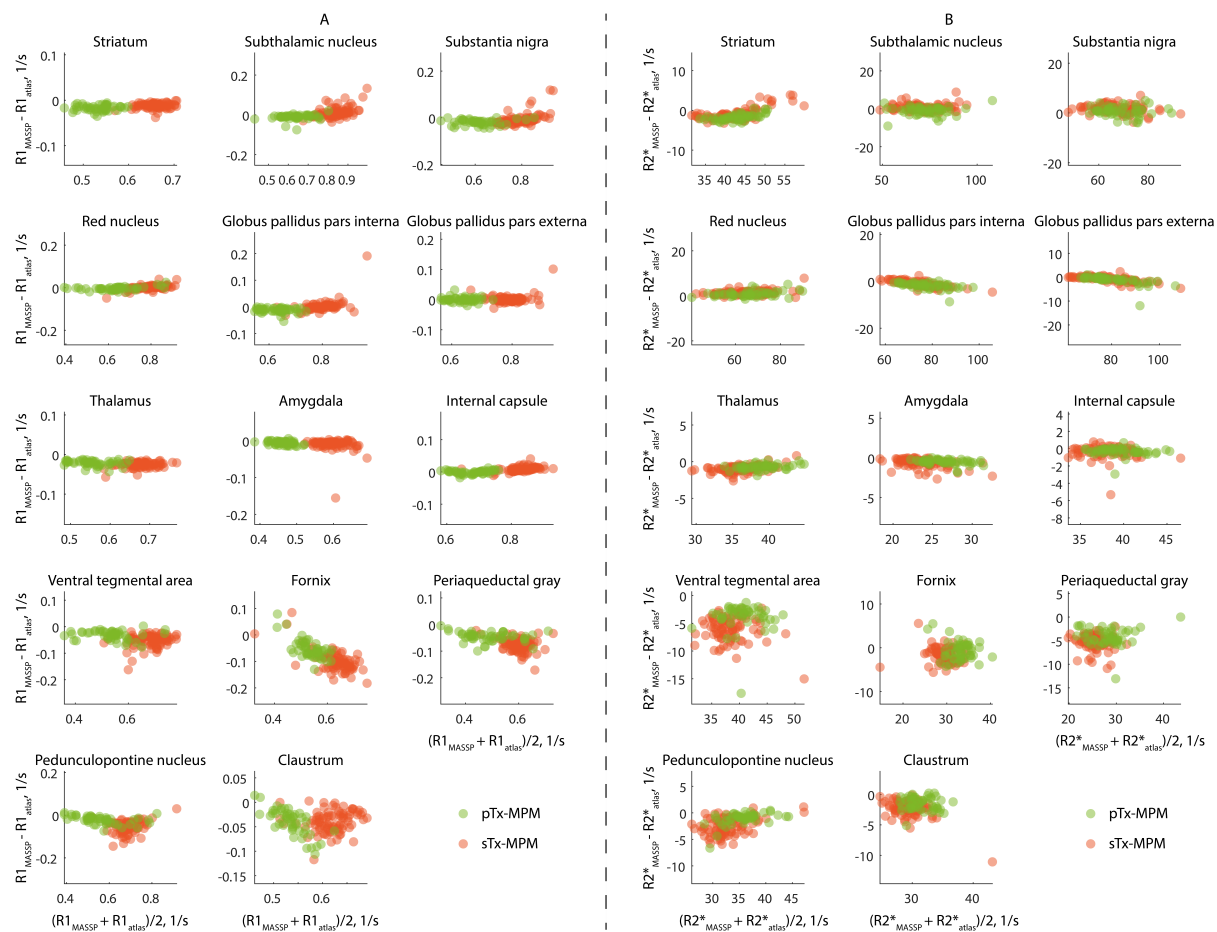


Figure 4. Bland-Altman plots indicate the nuclei exhibiting dependence of median R1 (A), and R2* (B) values on the segmentation approach