Concentration maps improve detection of gray matter alteration in cerebellum and deep gray matter structures

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Target audience: MR engineers, clinicians interested in MS and partial-volume estimation.

Introduction: Grey-matter (GM) tissue segmentation in brain MRI is challenged by the presence of more than one tissue type in a voxel, an effect known as partial volume. This problem is particularly evident in regions where grey and white matter are intermingled (i.e. the lateral part of the central nuclei, CN) or where clinically compatible spatial resolution is not sufficient to disentangle GM from white-matter structures (i.e. the cerebellar folia). This study proposes to use brain tissue concentration maps to improve GM segmentation and the quantitative analysis in the CN and in the cerebellum.

Methods: Brain MRI was acquired at 3T (MAGNETOM Trio TIM, Siemens AG, Erlangen, Germany) in 26 relapsing remitting multiple sclerosis (RRMS) patients and 8 healthy controls (HC). The MRI protocol included: high-resolution 3D MPRAGE (TR/TI = 2300/900 ms) and a prototype MP2RAGE (TR/TI1/TI2 = 5000/700/2500 ms). Both protocols had a matched voxel size of 1x1x1.2 mm³ and FOV of 256x240x160mm³. Quantitative T1 maps (Figure 1.B) were derived from the MP2RAGE volumes [1]. The MPRAGE images were linearly registered to the T1 maps using ELASTIX [2]. Binary brain masks (CN and cerebellum) were obtained using an automated morphometry package [4] (Figure 1.C). Brain tissue concentrations (Figure 1.D-F) were estimated using the non-biased MP2RAGE volume [1] (Figure 1.A) with a new iterative prototype algorithm based on a Bayesian maximum a-posteriori framework [3]. Comparison of concentration maps and binary brain masks was performed both qualitatively and quantitatively by (i) estimating visually the segmentation quality in the CN of HC compared with known histology [5] and (ii) by comparing average T1 relaxation time differences in CN (thalamus, caudate, putamen, pallidum) and cerebellum GM between MS patients and HC. For (ii) we performed a two-sample permutation t-tests corrected for family-wise error rate on T1 GM in the following regions of interest (ROIs): thalamus, caudate, putamen, pallidum and cerebellum. Mean T1 values in all ROIs were calculated: 1) considering only voxels with estimated GM concentration larger than 90%; 2) including all voxels from the brain masks (Figure 1.C).

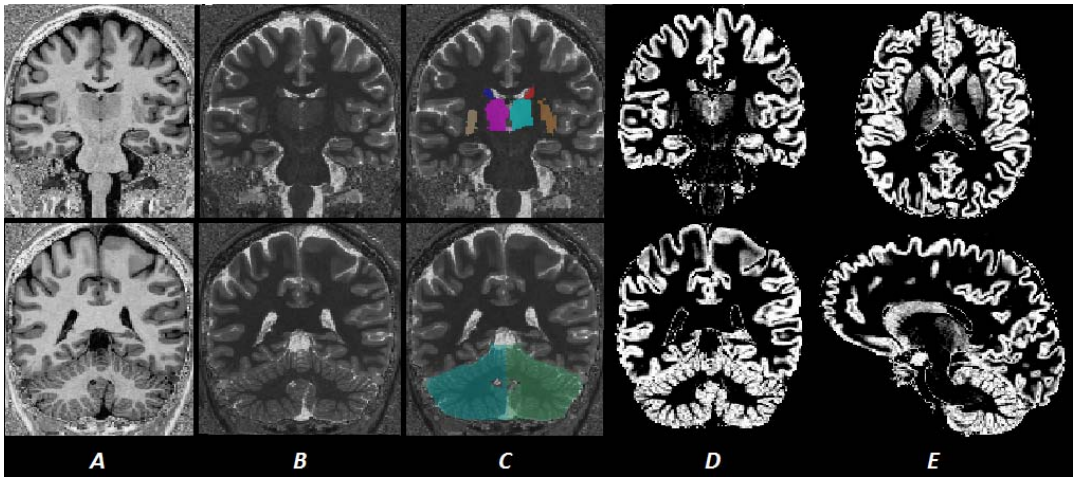
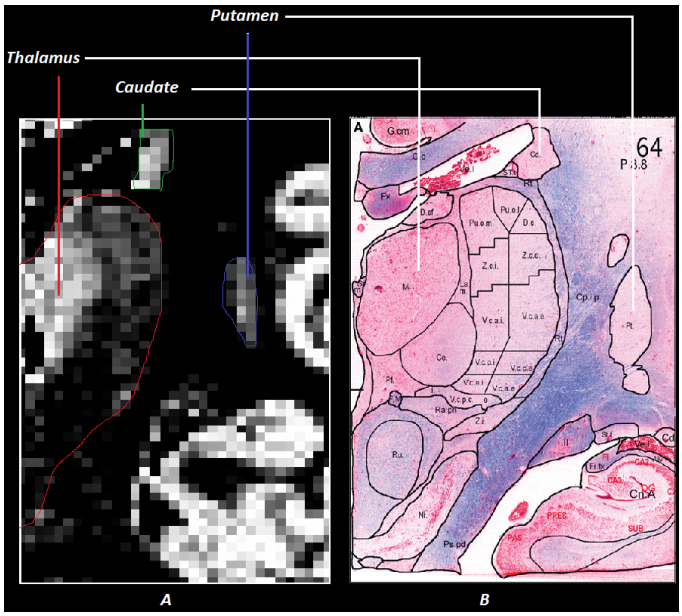


***Figure 1**. Representative coronal slice of non-biased MP2RAGE (A) T1 map(B), brain masks of CN (first row) and cerebellum (second row) (C) and GM concentration maps (D). Axial and sagittal view of CN and cerebellum (E).*



Results: Qualitative analysis showed good estimation of GM concentration in thalamus, caudate and pallidum when compared to histological data (Figure 2). High-intensity regions in the GM concentration maps (white voxels) correspond in fact to areas of high cellularity (GM) in the histological image of the CN (medial thalamic nucleus-M, and caudate-Cd). Quantitative analysis using concentration maps showed significant T1 differences between RRMS patients and HC in the GM of cerebellum (p=0.006), thalamus (p=0.004), caudate (p=0.004), putamen (p=0.008) and pallidum (p=0.056). Analysis using tissue binary brain masks showed less significant differences in CGMN: thalamus (p=0.016), caudate (p=0.02), putamen (p=0.059), pallidum (p=0.2), and in the cerebellum (p=0.06).

***Figure2.** Structures of thalamus, caudate and putamen (delineated in red, green and blue in the GM concentration map) evidenced by histology (B) appears in the GM concentration map (A). Coronal histological section from [5]: Luxol Fast Blue staining (blue-violet) was used to evidence myelin presence and Nissl staining (pink-red) to reveal neurons and glia.*

Conclusion & discussion: This qualitative analysis showed good results between our GM concentration maps and histological data in HC. In addition, quantitative analysis showed that GM analysis using concentration maps has higher sensitivity than binary brain masks to detect T1 differences between MS patients and HC in the CN and cerebellum. This novel analysis could hence open the possibility to better detect subtle pathological changes caused by MS, notably in the GM.

***References:** [1] Marques JP et al;, NeuroImage 2010; [2] Klein S. et al, IEEE 2010; [3] Roche A, MICCAI 2014; [4] Schmitter et al. , 2014, NeuroImage : Clinical; [5] Sadikot Abbas F. et al., Front. Syst. Neurosci., 06 September 2011.*