Atlas-free Brain Tissue Segmentation Using a Single T1-weighted MRI Acquisition

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Introduction

Many studies investigating the aging brain or disease-induced brain alterations rely on accurate and reproducible brain tissue segmentation. Being a preliminary processing step prior to the segmentation, reliable skull-stripping – the removal of non-brain tissue – is also crucial for all later image assessment. Typically, segmentation algorithms rely on an atlas i.e. pre-segmented template data. Brain morphology, however, differs considerably depending on age, sex and race. In addition, diseased brains may deviate significantly from the atlas information typically gained from healthy volunteers. The imposed prior atlas information can thus lead to degradation of segmentation results. The recently introduced MP2RAGE sequence provides a bias-free T1 contrast with heavily reduced T2*- and PD-weighting compared to the standard MP-RAGE [1]. To this end, it acquires two image volumes at different inversion times in one acquisition, combining them to a "uniform", i.e. homogenous image. In this work, we exploit the advantageous contrast properties of the MP2RAGE and combine it with a Dixon (i.e. fat-water separation) approach. The information gained by the additional fat image of the head considerably improves the skull-stripping outcome [2]. In conjunction with the pure T1 contrast of the MP2RAGE uniform image, we achieve robust skull-stripping and brain tissue segmentation without the use of an atlas.

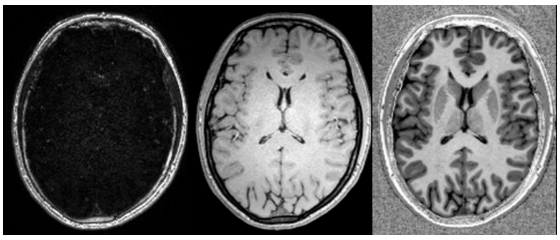

Fig. 1 – Exemplary image slices of the input to the segmentation algorithm. From left to right: cFAT, cINV2, cUNI

Material and Methods

Four healthy volunteers (25±4yo) were scanned at 3T (MAGNETOM Trio and Skyra, Siemens Healthcare, Germany) using a double-echo MP2RAGE sequence with the following parameters: TI1/TI2/TR= 700/2500/5000 ms, TE1/TE2=2.44/6.06 ms, GRAPPA R=3, TA=8:52 min. Per echo time, three image volumes were thus obtained (at the 1st and 2nd inversion time 'INV1' and 'INV2', and the homogeneous pure-T1w image 'UNI'). In each session, a scan and a rescan were conducted in addition to a standard MP-RAGE (TI/TR=900/2200 ms, GRAPPA R=2, TA=5:12 min). To fit the two echo readouts without changing the recommended MP2RAGE protocol, the readout bandwidth had to be increased. The resulting SNR loss is mostly recovered by the later combination of the echo images. After employing a homodyne phase filter, the well-known 2-point Dixon image decomposition was performed [3], yielding fat images from both INV1 and INV2. These two image volumes were combined by calculating their root mean square (RMS) as proposed in [4]. Also, the two echoes of INV2 and UNI were combined like this. The final three combined image volumes cFAT, cINV2 and cUNI ('c' for combined) were used as an input for a multi-channel segmentation algorithm. Notably, cINV2 was included to provide uniform background intensity since the MP2RAGE cUNI contrast suffers from background noise enhancement (see Fig. 1 right). Segmentation in seven tissues classes (GM, WM, fluid, dura mater, muscle, fat, and air) was implemented using a Markov random field model via graph cuts [5]. The Markov model enforced topological constraints by penalising anatomically impossible links between brain tissues and non-brain classes, thus rendering the segmentation more robust to image noise. Total intracranial volume extraction was then achieved by means of standard mathematical morphology operations which removed non-brain voxels classified as fluid (opening, largest connected component extraction and hole-filling). The segmentation took 5 min per volume on a standard PC. Finally, grey matter volumes were calculated from all scans.

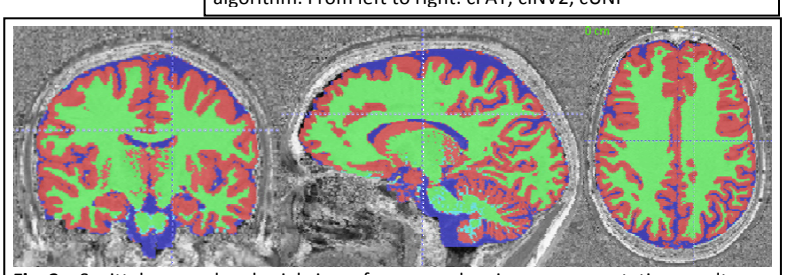

Fig. 2 – Sagittal, coronal and axial view of an exemplary image segmentation result.

Results and Discussion

The presented results indicate that an MP2RAGE-Dixon acquisition contains enough information to perform reliable brain tissue segmentation without the use of an atlas. The additional fat image supports the segmentation by providing robust information about non-brain tissue. Notably, no image registration is necessary, since all image volumes are acquired simultaneously, preventing the introduction of further partial volume effects. Quantitative comparison of atlas-free MP2RAGE and atlas-based MP-RAGE segmentations showed similar outcomes. Confirming this, the segmentations resulted in very reproducible grey matter volumes (Fig. 3, differences <1%) and only little differences to the MP-RAGE values except for one subject (Fig. 3, green). It should be noted that the atlas-based segmentation is shown here to illustrate the range of the expected values; it also suffers from limitations in brain/non-brain tissue interface regions of similar intensities; it thus cannot be considered as a hard reference. In conclusion, the presented work shows a high potential to ameliorate automatic brain segmentation results by drawing a maximum of image information from a single acquisition.

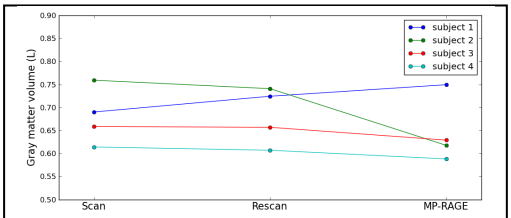

Fig. 3 – Grey matter volumes of all subjects for the MP2RAGE-Dixon scans, rescans and the MP-RAGEs.

References

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