Robustness of a fully automated brain segmentation tool for multiple MRI protocols: test for clinical applications

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The target audience of this study is neuroimaging scientists and clinicians, particularly radiologists and neurologists.

PURPOSE: Although quantitative analysis tools of brain MRI data have advanced substantially in the past decade, they have not being widely translated to the clinical diagnosis. One of the reasons is their sensitivity to imaging protocols, which requests data acquired with a highly consistent protocol. In this study, we examined the robustness of a state-of-the-art multiple-atlas brain segmentation tool. This tool identifies 286 brain structures automatically without pre-processing such as skull stripping. We analyzed 72 healthy brains, with various image protocols, from Alzheimer's Disease Neuroimaging Initiative (ADNI) database (adni.loni.usc.edu). The impact of the protocol was then evaluated with respect to biological effects such as aging.

Manufacturer - Tesla	Sample size	Age (years)	Resolution (mm)
Philips - 1.5	12	75-90	1.2x0.94x0.94
Philips - 3.0	12	66-91	1.2x1x1
Siemens - 1.5	12	65-96	1.2x1.25x1.25
Siemens - 3.0	12	56-86	1.2x1.x1
GE - 1.5	12	76-94	1.2x0.94x0.94
GE - 3.0	12	64-88	1.2x1.02x1.02

METHODS: 72 high-resolution T1-weighted sagittal scans (MPRAGE) of healthy individuals from the ADNI were used, which include three manufacturers and two field strengths as shown in Table 1. All images were parcellated by a cloud-based fully automated process (https://mricloud.org/) based on large diffeomorphic deformation metric mapping[1] and a multi-atlas likelihood fusion algorithm[2]. 286 structures were defined with a five-level ontological hierarchy relationship[3]. Differences in protocols and age effect were tested by ANOVA and Pearson regression, respectively, and reviewed by bootstrapping (1000 folds). The p-values were corrected for multiple comparisons with Bonferroni, at $p<0.05$.

RESULTS: Only two structures (rectus gyrus and inferior temporal) showed volumes significantly affected by the protocols (Fig. 1). Significant age effects were observed in various brain regions regardless of the heterogeneity of the protocols (Fig. 2). The age effects explained 10.4% of the total data variation while the protocol explained 1.5%, and the error, 1%.

Fig. 1: Differences among protocols

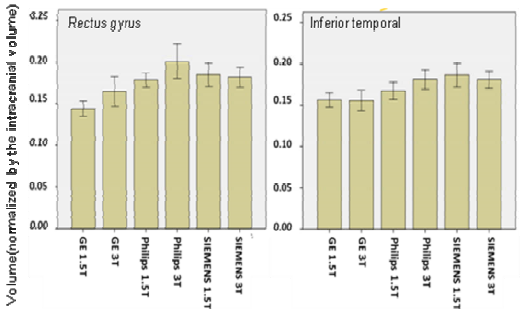
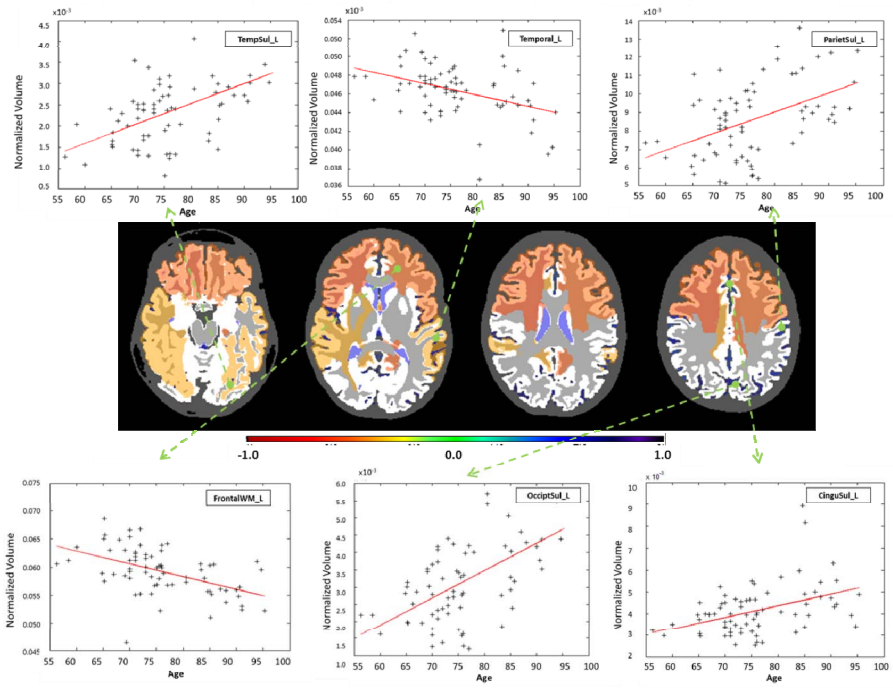


Fig. 2: Examples of significant correlations between regional normalized volumes (y axis) and age (x axis). The colors code the strength of the correlation (Pearson r); red/yellow are regions that shrink overtime (negative r) and purple / blue are regions that expand overtime. Gray / white are regions that did not show significant trends, at this level of granularity. Sul=sulcus, WM=white matter.



DISCUSSION and CONCLUSION: The results indicate that, regardless of the large amount of protocol differences, the multi-atlas tool was highly robust to detect age (biological) effect. Only two regions were significantly affected by the protocol variation, while the age effect was clearly delineated in the ventricles and in multiple structures in the parenchyma. This robustness is a key to apply automated quantification tools of brain MRI data in clinical diagnosis.

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2. Tang, X.Y., et al., Bayesian Parameter Estimation and Segmentation in the Multi-Atlas Random Orbit Model,"*Plos One*," **8**(6) (2013).
3. Djamanakova, A., et al., Tools for multiple granularity analysis of brain MRI data for individualized image analysis,"*Neuroimage*," **101**, 168-76 (2014).

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