Estimation of total intracranial volume – a comparison of methods

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Summary
Total intracranial volume is a useful measure of inter-subject variability in pre-morbid brain volume, which has been recommended for inclusion in region of interest and voxel-based morphometric studies of dementia [1]. TIV can be estimated from structural MRI using time-consuming manual tracing or using automated methods. We show that recent improvements to the Statistical Parametric Mapping (SPM) software’s unified segmentation method allow highly accurate and unbiased estimates to be obtained rapidly and without interaction.

Introduction
Regional cortical and subcortical grey matter (GM) and white matter (WM) volumes correlate with total brain volume, which in turn is correlated with total intracranial volume (TIV). In studies of neurodegenerative diseases, total brain volume typically decreases over time, while TIV remains constant as cerebrospinal fluid (CSF) expands to fill the vacated space. Controlling for TIV in statistical analyses can help to adjust for sampling imbalances in head-size, and explain some of the variability in regional measurements without removing atrophic effects, thus increasing power to detect group differences or structural correlates. Time-consuming manual estimation of TIV is unsuitable for large studies such as the Alzheimer’s Disease Neuroimaging Initiative (ADNI), motivating use of automatic methods. However, inaccurate automatic methods might exhibit disease-related biases with the potential to confound analyses (for instance if the TIV measure was influenced by atrophy), implying that careful evaluation is necessary.

Methods
We compare estimates of TIV using 55 subjects (37 male, 59.9 +/− 11.4 years of age), including 22 with Alzheimer’s disease and 16 with frontotemporal lobar degeneration, imaged twice (479 +/− 289 days apart). Manual tracing estimates performed with the MIDAS software [2] are compared to eight automatic methods: FreeSurfer versions 4.5 and 5 [3]; Statistical Parametric Mapping version 5, summing either native or modulated warped segmentations; SPM version 8 equivalents, which use the improved tissue prior probability maps shown in Figure 1 [4]; and Jacobian integration using either SPM8 unified segmentation or Dartel [5].

Results
Considering baseline TIV, SPM5 segmentations are highly variable and upwardly biased with respect to manual measures, while those from SPM8 are dramatically improved; FreeSurfer results lie between these (see Figure 2). The Dartel Jacobian integration method has the strongest correlation and least mean difference with respect to manual measures (see Table 1). Consideration of longitudinal changes reveals small but significant reductions in the manual measures, and in the closely correlated Dartel results (see Figure 3). The modulated warped SPM8 segmentations appear to exhibit the best balance of accuracy and stability over time.

References

Acknowledgments: NCF is supported by a UK Medical Research Council Senior Clinical Fellowship. This work was undertaken at UCLH/ULC who received a proportion of funding from the Department of Health’s NIHR Biomedical Research Centre funding scheme. The DRC is an Alzheimer’s Research UK Co-ordinating Centre and has received equipment funded by Alzheimer’s Research UK.