Methods to Improve SPM12 Tissue Segmentations of Older Adult Brains

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Background

SPM12's default settings and priors for tissue segmentation were designed using healthy, younger adult brains.

The signal intensity of white matter (WM) voxels is modelled using a single Gaussian (does not model pathologic WM), and the nonlinear registration parameters may be too stringent for highly atrophic brains.

Here we present modifications to SPM12 that optimize for older and atrophic brains, and we compare the resulting segmentations against standard methods.

Methods

To compare the standard and modified pipelines, we transformed the MCALT_ADIR122 atlas to each subject's MRI using each pipeline's normalization approach. We then summed the segmented gray matter (GM) tissue class probabilities in each region and normalized them by the total intracranial volume as computed by each pipeline. Then, we tested the ability of these regional GM volumes to discriminate between T1-weighted scans of amyloid-PET-negative cognitively unimpaired (CU; n=108) and age/sex-matched amyloid-PET-positive impaired (MCI/AD; n=108) subjects from the Mayo Clinic Study of Aging.

Methods

We modified SPM12 in four ways:

1. Replaced SPM's nonlinear normalization with ANTs for transforming atlas regions to subject space
2. Replaced tissue priors with those from the Mayo Clinic Adult Lifespan Template (MCALT)
3. Allowed increased deformation during segmentation
4. Used two Gaussians to model WM signal intensity

We found that directly fitting two WM Gaussians occasionally failed in subjects with severe atrophy. To fix this, we adopted an approach where segmentation is first performed using one WM Gaussian, and then a second Gaussian is added. The second mean is initialized to a fraction of the existing WM mean and its width is copied from the existing WM Gaussian. Segmentation is continued from these modified parameters.

Results

AUROC values for the top-10 discriminative regions are plotted for the standard SPM12 pipeline and for our modified SPM12 pipeline (Figure 1). Using our proposed modifications substantially increased classification accuracy for hippocampal volume (a commonly-used AD biomarker) and also improved other biologically-plausible regions.

Conclusions

Gray matter volumes measured using our modified SPM12 pipeline had greater power to classify AD subjects from CU, compared to the standard SPM12 pipeline. Source code and atlases to produce SPM12 segmentations using our modified approach are now available publically at:

https://www.nitrc.org/projects/mcalt/

Figure 1

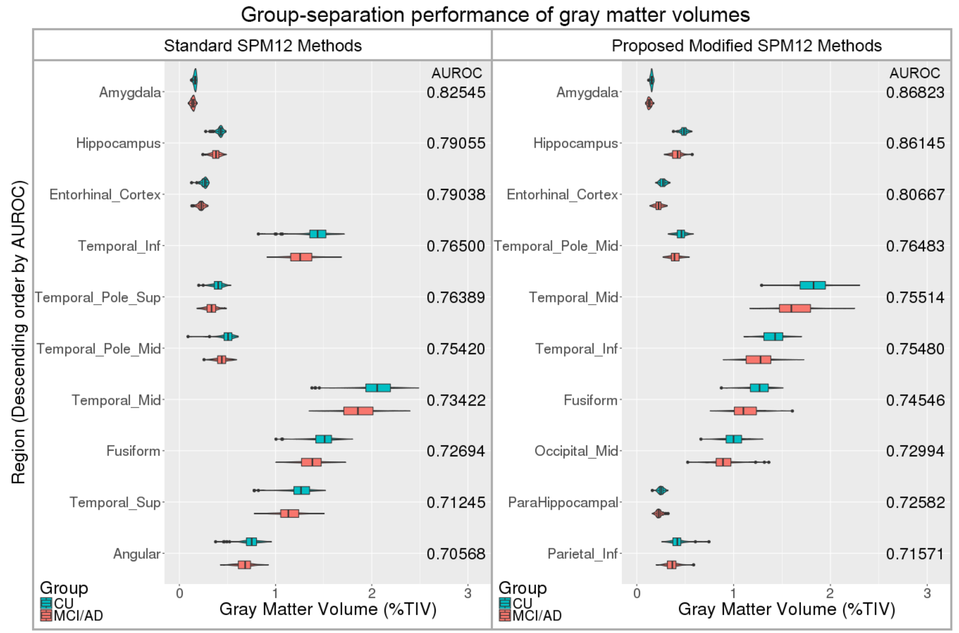

Figure 1: Box and violin plots for gray matter volumes computed using each method. The top 10 regions are presented (descending order) according to their group-wise separation ability as measured by area under the receiver operating characteristic curve (AUROC), plotted on the right side of each row. Volumes were each normalized by total intracranial volume (TIV) to correct for differences in head size.