

# The Mayo Clinic Adult Lifespan Template (MCALT): Better Quantification across the Lifespan

Christopher G. Schwarz<sup>1</sup>, Jeffrey L. Gunter<sup>12</sup>, Chadwick P. Ward<sup>1</sup>, Prashanthi Vemuri<sup>1</sup>, Matthew L. Senjem<sup>12</sup>, Heather J. Wiste<sup>3</sup>, Ronald C. Petersen<sup>4</sup>, David S. Knopman<sup>4</sup>, Clifford R. Jack Jr.<sup>1</sup>

<sup>1</sup>Department of Radiology <sup>2</sup>Department of Information Technology <sup>3</sup>Department of Health Sciences Research <sup>4</sup>Department of Neurology

Mayo Clinic, Rochester, MN, USA

## Background

Most MRI standard templates such as MNI152 are generated from scans of younger individuals. Because templates that match the population of interest provide better quantitative MRI analysis, the goal of this work was to construct and make publicly available a template for the analysis needs of aging and Alzheimer's Disease (AD) population studies.

## Subject Characteristics

This template was constructed from T1-weighted scans of 202 Mayo Clinic subjects from the Mayo Clinic Study of Aging (MCSA) and Alzheimer's Disease Research Center (ADRC) including:

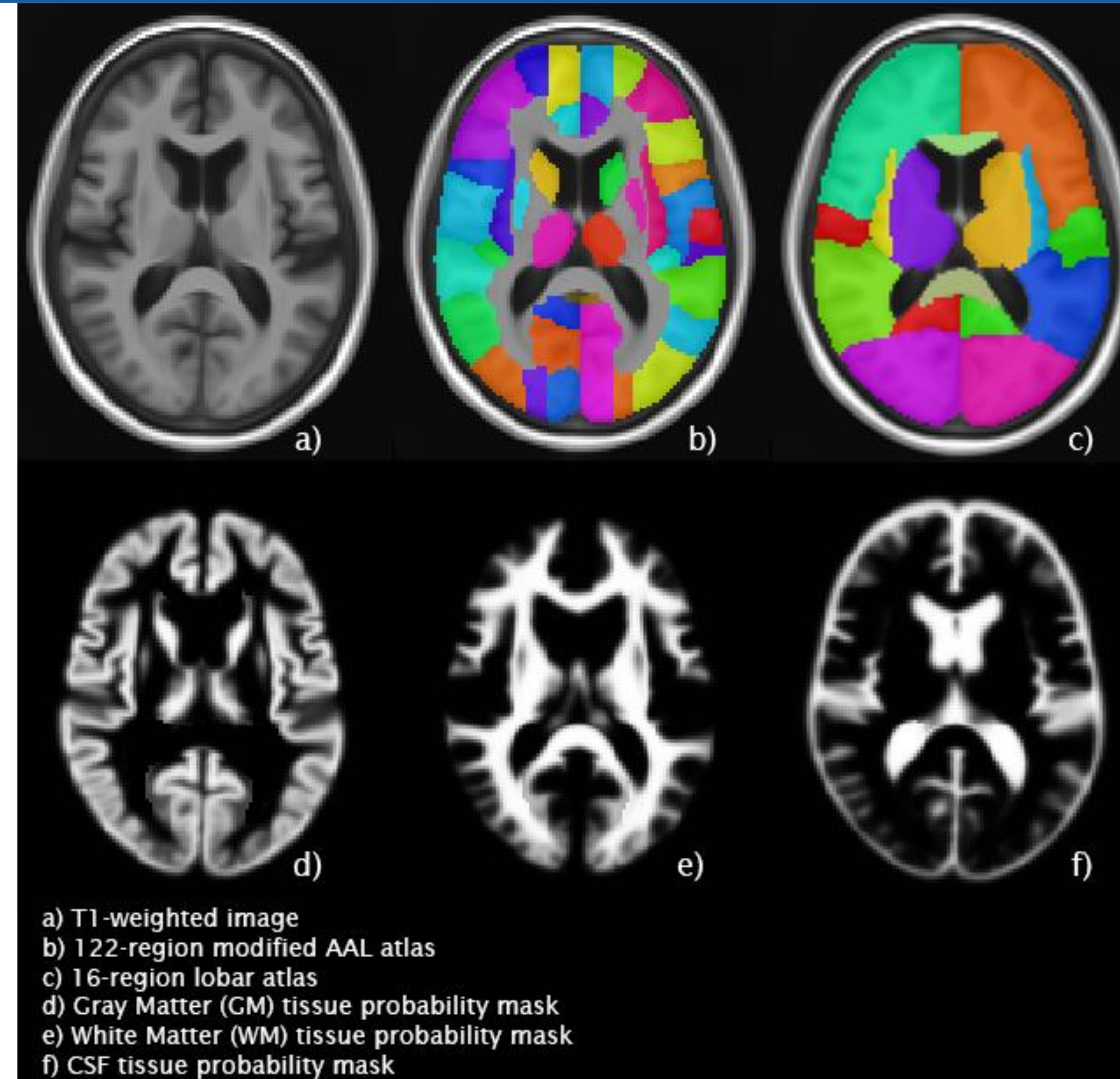
- 39 young clinically unimpaired subjects aged 30-49 (10 men + 10 women from 30-39, 10 men + 9 women from 40-49)
- 80 randomly selected MCSA clinically unimpaired subjects aged 51-89 (10 men + 10 women from each age decade)
- 83 MCSA or ADRC subjects with probable Alzheimer's Disease dementia aged 51-92, 61% male

## Methods

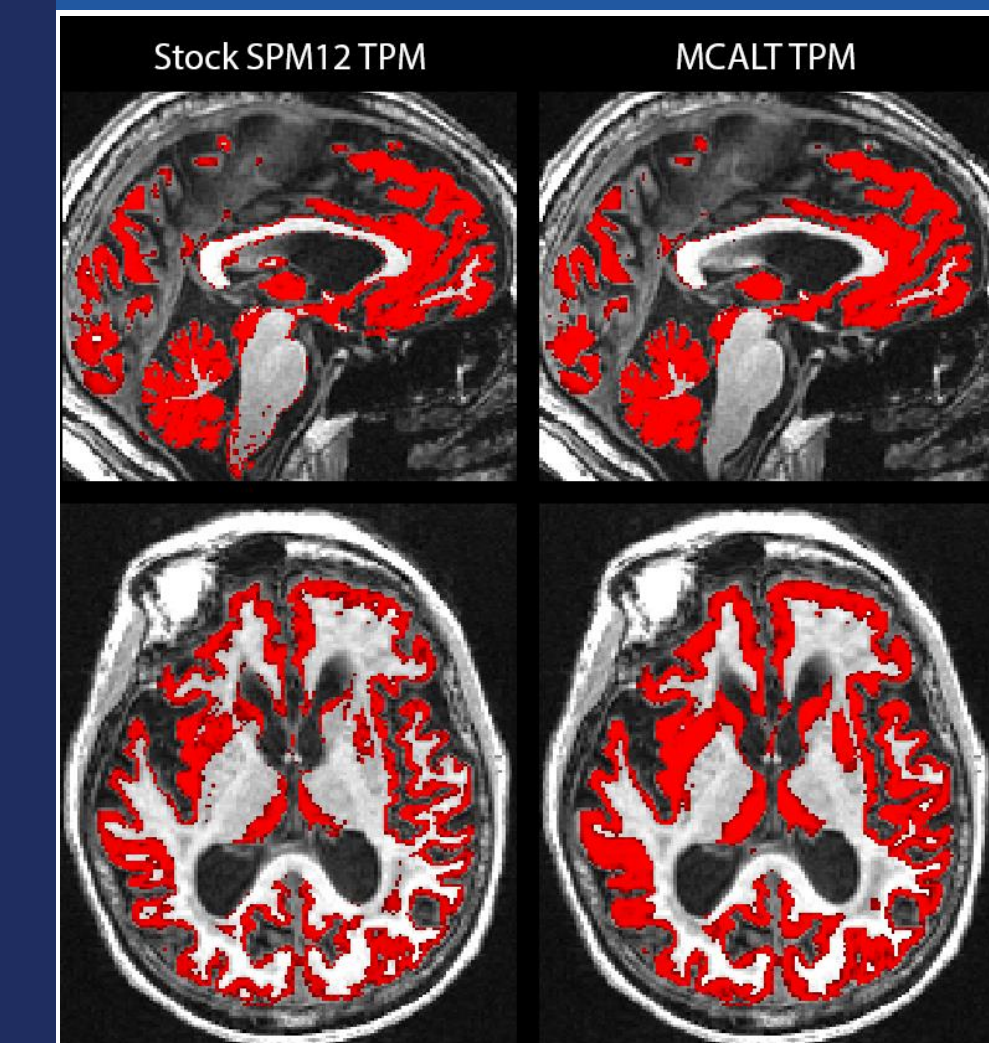
Input images were acquired at Mayo Clinic, Rochester, MN, USA using two 3T GE scanners (models 750, Signa Excite) with ADNI-1 MP-RAGE protocols and corrected for gradient distortion in 3D and non-uniformity using N3 and SPM5. SPM12b was used to segment these preprocessed images with stock priors/settings, and these segmentations were validated by image analysts. SPM12b DARTEL groupwise registration was used to produce new tissue priors and deformations in the new template space. A T1-weighted template was produced by intensity-normalizing each scan to equalize the mean intensity value of white matter, using the DARTEL warps to transform them to the common space, and voxel-wise averaging across subjects. Tissue priors were edited manually to reduce erroneous GM prior probability at WM/CSF borders, in the brainstem, and in the neck/face, and to create a more-defined fornix region in the WM priors. An in-house modified AAL gray matter atlas was transformed to the template using ANTs nonlinear registration and manually edited to create accurate boundaries. A 16-region lobar atlas was also drawn manually.

We visually compared SPM12 segmentations of older adult brains segmented using MCALT tissue priors with those from using SPM's included default tissue priors (TPM.nii).

## Figure 1: Atlas and Tissue Priors



## Figure 2: Example SPM12 Segmentations



Compared to those using the SPM12 default tissue priors, SPM12 gray matter segmentations using the MCALT priors showed: reduced false GM in the brainstem, WMH, and WM/CSF boundaries; more-complete cortical segmentation; and improved definition of deep GM nuclei.

## Conclusions

- We created a template/atlas suitable for studies with a wide range of ages and disease states throughout the adult lifespan ages 30+.
- This template, tissue priors, and related atlases have been made publicly available for non-commercial use at: <http://www.nitrc.org/projects/mcalt/>
- Although the MCALT was designed for use with SPM12, it is not specific to SPM12 and could potentially be used with other software.