

MS Journal Appendix for MRI methodology

Hardware	
Field strength	3.0 Tesla
Manufacturer	Philips
Model	Achieva X-series with Quasar Dual gradients
Coil type (e.g. head, surface)	Combines brain and cervical cord coil
Number of coil channels	12: 8 head, 4 neck

Acquisition sequence	
Type (e.g. FLAIR, DIR, DTI, fMRI)	Brain: MPRAGE, proton density, T2, FLAIR
Acquisition time	60 minutes
Orientation	MPRAGE & FLAIR: Sagittal; Proton density & T2: Axial
Alignment (e.g. anterior commissure/poster commissure line)	Subcallosal line
Voxel size	MPRAGE and FLAIR: 1 mm ³ ; Proton density and T2: 1 mm ²
TR (msec)	MPRAGE: ~8.19; proton density: ~2000; T2: ~3000; FLAIR: ~8000
TE	MPRAGE: ~3.75; proton density: ~25; T2: ~80; FLAIR: ~331.6
T1	MPRAGE/proton density/T2: --- FLAIR: 2,400
Flip angle	MPRAGE: 8; proton density, T2, and FLAIR: 90
NEX	MPRAGE, T2, and FLAIR: 1; proton density: 2
Field of view	MPRAGE & FLAIR: voxels; proton density & T2: in plane resolution
Matrix size	MPRAGE & FLAIR: 1 mm ³ ; Proton density & T2: 1 mm ²
Parallel imaging	Yes No

Acquisition sequence	
If used, parallel imaging method: (e.g. SENSE, GRAPPA)	FLAIR and MPRAGE: SENSE
Cardiac gating	Yes No
If used, cardiac gating method: (e.g. PPU or ECG)	
Contrast enhancement	Yes No
If used, provide name of contrast agent, dose and timing of scan post-contrast administration	No contrast was used
Other parameters:	

Image analysis methods and outputs	
Lesions	
Type (e.g. Gd-enhancing, T2-hyperintense, T1-hypointense)	Enlarged Perivascular Space (ePVS) Score
Analysis method	Visual, ordinal ePVS rating scale on conventional MRI that has been described previously. ¹
Analysis software	NA
Output measure (e.g. count or volume [ml])	ePVS ratings were performed on the basal ganglia, centrum semiovale, and midbrain. Basal ganglia and centrum semiovale PVS were rated 0 (none), 1 (1-10), 2 (11-20), 3 (21-40) and 4 (>40), and midbrain PVS were rated 0 (none visible) or 1 (visible).
Tissue volumes	
Type (e.g. whole brain, grey matter, white matter, spinal cord)	Cerebral T2 Hyperintense Lesion Volume
Analysis method	<p>A processing pipeline created and run within MIPAV's Java Image Science Toolkit (JIST) environment² is used to preprocess each subject's MPRAGE and FLAIR scans and run Lesion TOADS. Preprocessing includes MPRAGE brain extraction via SPECTRE (Simple Paradigm for Extra-Cranial Tissue REmoval)³, co-registration of the series, FLAIR masking, rigid registration of both series to the Montreal Neurological Institute (MNI) 152 T1 1mm brain atlas, and removal of 10 slices from the inferior aspect of each study to reduce field of view.</p> <p>LesionTOADS provides tissue classification and MS lesion segmentation. MIPAV tools are used to overlay a binary lesion mask on to the multichannel MR brain images for manual editing by an experienced MS lesion tracer to correct any false positive designations or omissions.</p> <p>In cases where the segmentation is deemed by the reviewer to have been overestimated by LesionTOADS, default settings are modified with respect to Maximum Grey Matter and Ventricle Distance, LesionTOADS is run again, and the new settings documented for use in follow up scan processing.</p>

Image analysis methods and outputs	
Analysis software	Lesion TOpology-preserving Anatomical Segmentation (LesionTOADS). ⁴ Lesion TOADS is part of a program plug-in ⁵ developed for Medical Image Processing And Visualization software (MIPAV).
Output measure (e.g. absolute tissue volume in ml, tissue volume as a fraction of intracranial volume, percentage change in tissue volumes)	Absolute tissue volume in cubic cm
Type (e.g. whole brain, grey matter, white matter, spinal cord)	Whole brain volume
Analysis method	<p>White matter lesions interfere with grey and white matter tissue volume measures and therefore must be addressed prior to processing in cases where the software employed doesn't automatically segment lesion as a separate tissue class. To accomplish this, a copy of the edited T2 Hyperintense Lesion mask is overlaid on the T1 weighted MPRAGE image and edited again by an experienced MS lesion tracer to also include T1 hypointense lesions meeting criteria (T1-hypointense/T2-hyperintense or T2-normal intensity).</p> <p>The edited T1/T2 defined binary mask is then utilized in pre-processing the T1 MPRAGE series. FSL's lesion_filling tool⁶ part of FSL⁷ uses the mask to fill lesion voxels on the T1 series with intensities similar to neighboring normal appearing tissue voxels to fill in white matter hyperintensities that could otherwise be erroneously labeled as gray matter.</p> <p>T1-weighted MPRAGE images are utilized to determine whole brain volume, normalized for subject head size, using SIENAX,⁸ part of FSL.⁷</p> <p>SIENAX is run with options selected for improved removal of non-brain tissue and also to provide separate estimated volumes of grey matter, white matter, peripheral grey matter, and ventricular CSF.⁹</p>
Analysis software	SIENAX, ⁸ part of FSL ⁷

Image analysis methods and outputs

Output measure

(e.g. absolute tissue volume in ml, tissue volume as a fraction of intracranial volume, percentage change in tissue volumes)

Absolute tissue volume in cubic cm

Type

(e.g. whole brain, grey matter, white matter, spinal cord)

Cortical thickness

Image analysis methods and outputs

Analysis method	<p>This processing includes removal of non-brain tissue using a hybrid watershed/surface deformation procedure,¹⁰ automated Talairach transformation, tessellation of the gray matter white matter boundary, automated topology correction,^{11, 12} and surface deformation following intensity gradients to optimally place the gray/white and gray/cerebrospinal fluid borders at the location where the greatest shift in intensity defines the transition to the other tissue class.¹³⁻¹⁵ Once the cortical models are complete, a number of deformable procedures can be performed for in further data processing and analysis including surface inflation, registration to a spherical atlas which utilized individual cortical folding patterns to match cortical geometry across subjects,¹³ parcellation of the cerebral cortex into units based on gyral and sulcal structure,^{16, 17} and creation of a variety of surface based data including maps of curvature and sulcal depth. This method uses both intensity and continuity information from the entire three dimensional MR volume in segmentation and deformation procedures to produce representations of cortical thickness, calculated as the closest distance from the gray/white boundary to the gray/CSF boundary at each vertex on the tessellated surface.¹⁵ The maps are created using spatial intensity gradients across tissue classes and are therefore not simply reliant on absolute signal intensity. The maps produced are not restricted to the voxel resolution of the original data thus are capable of detecting submillimeter differences between groups. Procedures for the measurement of cortical thickness have been validated against histological analysis¹⁸ and manual measurements.^{19, 20} Freesurfer morphometric procedures have been demonstrated to show good test-retest reliability across scanner manufacturers and across field strengths.^{21, 22}</p>
Analysis software	Freesurfer image analysis suite, which is documented and freely available for download online (http://surfer.nmr.mgh.harvard.edu/).

Image analysis methods and outputs	
Output measure (e.g. absolute tissue volume in ml, tissue volume as a fraction of intracranial volume, percentage change in tissue volumes)	Tissue thickness in mm
Tissue measures (e.g. MTR, DTI, T1-RT, T2-RT, T2*, T2', ¹H-MRS, perfusion, Na)	
Type (e.g. whole brain, grey matter, white matter, spinal cord, normal-appearing grey matter or white matter)	NA
Analysis method	NA
Analysis software	NA
Output measure	NA
Other MRI measures (e.g. functional MRI)	
Type (e.g. whole brain, grey matter, white matter, spinal cord, normal-appearing grey matter or white matter)	NA
Analysis method	NA
Analysis software	NA
Output measure	NA

Other analysis details:

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