A convolutional neural network-based framework for imaging biomarkers in multiple sclerosis: white matter hyperintensity and brain region volumes



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Introduction

- White matter (WM) lesions are a hallmark of multiple sclerosis (MS) and reflect the inflammatory activity.
- Automatic detection of WM hyperintensities (WMH) from magnetic resonance imaging (MRI) T2-fluid attenuated inversion recovery (FLAIR) scans can support MS diagnosis and help to monitor treatment effectiveness in clinical trials.
- Brain volumetric measures can be used to study the neurodegenerative component of MS, to predict disability progression, and to evaluate potential anti-inflammatory, remyelinating or neuroprotective therapies.¹⁻³
- IXICO's IXIQ.Ai is a framework for MRI segmentation workflows.⁴⁻⁶

Methods

- CNNs trained to segment WMH from 3D FLAIR scans and brain regions, incl. whole-brain (WB) and thalamus, from 3D T1W scans
- Jacobian integration used to estimate WB volume change
- Dataset for WMH workflow validation: a publicly available MS dataset⁷ with 3D FLAIR scans, manual segmentations by seven expert raters, and a rater majority voting consensus Datasets for brain region workflow validation: ADNI (https://adni.loni.usc.edu/), OASIS (https://www.oasis-brains.org/), Huntington's disease (two, internal), multiple system atrophy (internal), healthy controls aged 75-86 and 19-25 (https://braindevelopment.org/ixi-dataset/)

Objectives/Aims

To validate convolutional neural networks (CNNs) for:

- segmentation of WMH from 1. **3D FLAIR scans**
- 2. segmentation of MS-relevant brain regions from 3D T1weighted (T1W) scans
- volumetric analysis 3.









Baseline



WMH seg

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- WMH ground truth = majority voting consensus
- Brain region ground truth = semi-automated segmentations (with manual edits)
- Accuracy/robustness from dice score coefficient (DSC), visual assessment, volume correlation/volume error, group separation
- Test-retest performance (ADNI BTB and OASIS datasets)

Figure 1: IXIQ.Ai workflows for A) pre-processing for cross-sectional and longitudinal analyses, B) region segmentation, and C) Jacobian Integration for volume change analysis



Figure 2: Boxplots showing the distribution of DSCs: IXIQ.Ai WMH workflow (prediction), each individual expert rater (raters 1-77) and other WMH segmentation methods compared to the WMH ground truth (consensus). (antspy, https://github.com/ANTsX/ANTs/wiki; BIANCA, https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/BIANCA/Userguide - lesion probability maps thresholded at 0.8/0.9/0.95; nic_MSlesion, https://github.com/sergivalverde/nicMSlesions)

The WMH workflow's ground-truth overlap (mean ± SD DSC = 0.65 ± 0.17) was comparable to the individual raters' and higher than for other automated methods (antspy 0.51 ± 0.19; bianca 0.9) 0.35±0.19; nic_MSlesion 0.52±0.23) (also see Figure 2). Its average volume correlation with the ground truth (r = 0.96) was higher than for the other methods (antspy r = 0.85; bianca_0.9 r = 0.69; nic MSlesion r = 0.87) and its average volume error (AVE) relative to the ground truth (mean ± SD AVE, mL = 3.1 ± 3.3) was the lowest (antspy 6.5 ± 9.1 ; bianca $0.9 \times 8.3 \pm 11.0$; nic Mslesion 5.1 ± 6.9).

Region Segmentation: WB and Thalamus



Volume Change: WB

	--				CN vs MCI				
1	•					Freesurfer	BSI	ANTs+J	IXIQ.Ai
ionth Volume Change [%]					p-value	0.004	5e-7	0.007	8e-6
	٠				CLES	0.67	0.81	0.67	0.78
				III III	Median (SD) group difference [%]	1.02 (0.16)	1.06 (0.02)	0.27 (0.01)	0.43 (0.01)
					CN vs AD				
						Freesurfer	BSI	ANTs+J	IXIQ.Ai
					p-value	0.005	1e-7	6e-8	2e-10
					CLES	0.67	0.83	0.84	0.89
	.	T		•	Median (SD) group difference [%]	1.16 (0.11)	1.12 (0.03)	0.46 (0.01)	0.73 (0.01)
	1				MCI vs AD				
^{−6}	•					Freesurfer	BSI	ANTs+J	IXIQ.Ai
-8	•		=	CN (n=45) MCI (n=45) AD (n=45)	p-value	0.86	0.41	0.009	0.001
					CLES	0.48	0.55	0.66	0.70
	٠				Median (SD) group difference [%]	0.13 (0.18)	0.05 (0.03)	0.18 (0.01)	0.30 (0.01)
	Freesurfer	BSI	ANTs+Jacobian	AI					

The IXIQ.Ai segmentations (CNN) had high ground-truth overlaps (mean DSC>97). Visual QC found consistently high segmentation quality (see Figure 4): 98% of the whole-brain and 100% of the thalamus segmentations passed QC.

Figure 4: Examples of WB and thalamus segmentations from IXIQ.Ai brain region workflow (CNN) that passed QC without manual edits.

Figure 5: WB volume change (negative change = loss) estimated by IXIQ.Ai (CNN + Jacobian), compared to FreeSurfer⁸, BSI⁹, and ANTS (https://github.com/ANTsX/ANTs/wiki) + Jacobian. p-value: Mann-Whitney U-test. CLES: Common Language Effect Size.

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The IXIQ.Ai volume change method (CNN + Jacobian), applied to the WB, detected significant group differences in changes over 12 months, with similar or higher CLES and similar or lower SD of group differences (%) than other methods (Figure 5).

The WB and thalamus volume differences were normally distributed and the distributions zero-centred.

Conclusions

- The WMH workflow shows higher overlap and volume correlation with the ground truth than comparable automated methods.
- The brain region workflow produces high-quality and reliable whole-brain and thalamus regions for volumetric analysis.
- The IXIQ.Ai framework provides a scalable and robust automatic solution for volumetric analysis of brain WMH and regions of interest in MS.

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