# SCAN-RESCAN AND FIELD-STRENGTH REPRODUCIBILITY OF BRAIN VOLUMETRY AND WHITE MATTER LESIONS DETERMINED USING QYSCORE®, A REGULATORY-APPROVED AUTOMATED SOFTWARE PLATFORM

<sup>1</sup>Center for Neurological Imaging, Department of Radiology, Brigham and Women's Hospital, Harvard Medical School, Boston, MA <sup>2</sup>Laboratory for Neuroimaging Research, Department of Neurology, Brigham and Women's Hospital, Harvard Medical School, Boston, MA <sup>3</sup>Department of Neurology, Brigham and Women's Hospital, Harvard Medical School, Boston, MA <sup>4</sup>Qynapse, Paris, France <sup>5</sup>Qynapse, Boston, MA <sup>4</sup>Qynapse, Paris, France <sup>5</sup>Qynapse, Boston, MA <sup>4</sup>Qynapse, Boston, MA <sup>4</sup>Qynapse, Paris, France <sup>5</sup>Qynapse, Boston, MA <sup>4</sup>Qynapse, Boston, Boston, MA <sup>4</sup>Qynapse, Boston, Bosto

## BACKGROUND

- For any biomarker, an understanding of its intrinsic measurement variability is critical in order to ascertain its **sensitivity** to detect biological change.
- In the case of measurements derived from MRI scans, two important sources of variability are **differences in subject positioning within the scanner** and associated calibration adjustments, and the scanner field strength (1.5T or 3T) and associated hardware and physics differences.
- **QyScore**<sup>®</sup> is a commercially-available, automated brain image analysis platform that is CE-marked and FDA-cleared as a medical device.

### OBJECTIVES

- 1. To evaluate the scan-rescan variability associated with automated measurements of brain volumes at both 1.5T and 3T
- 2. To evaluate the scan-rescan variability in white matter lesion volume and count at 3T
- 3. To evaluate differences in **brain volume** estimates on the **same individuals** scanned at 1.5T and 3T

### MATERIALS & METHODS

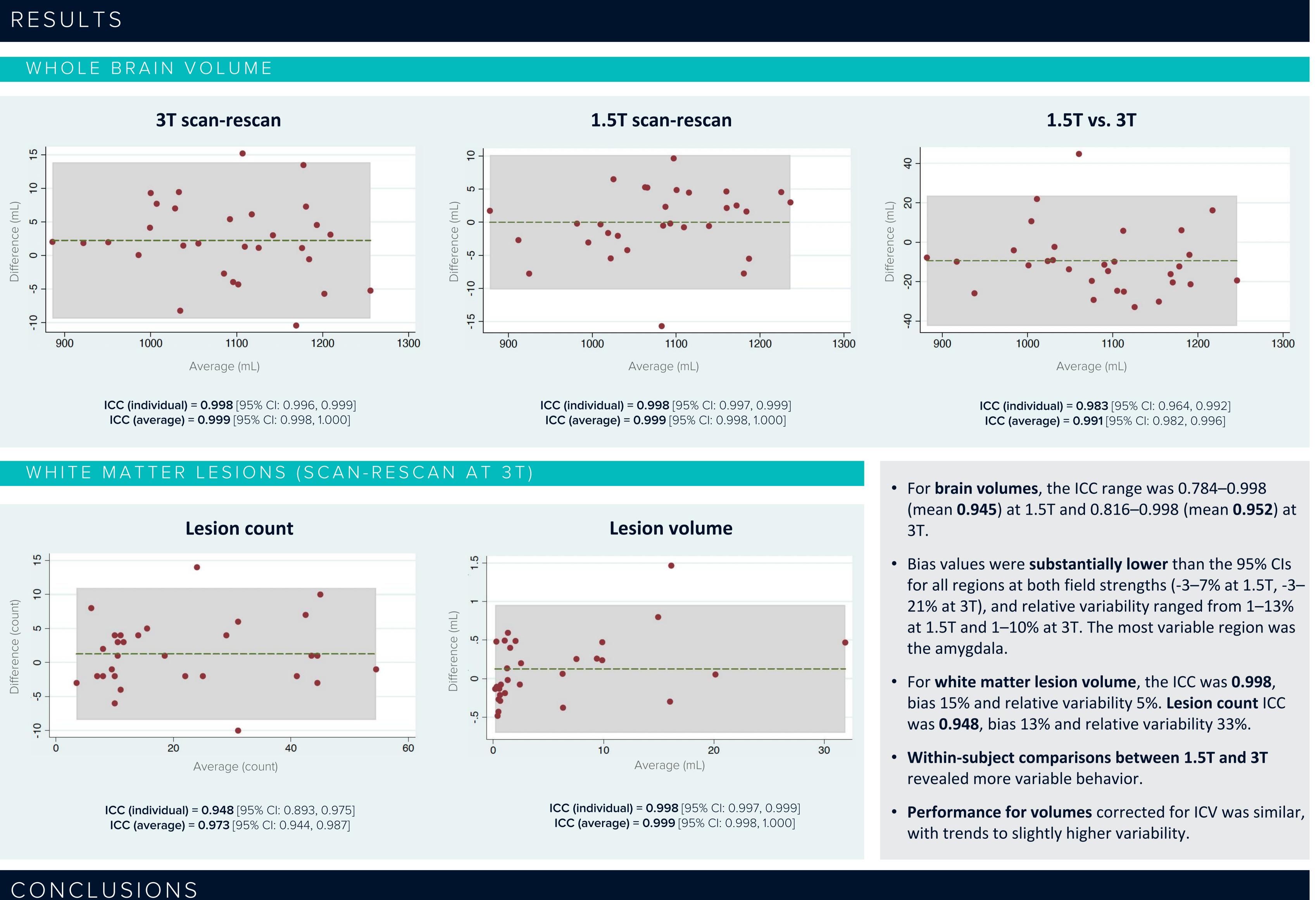
### IMAGING DATA

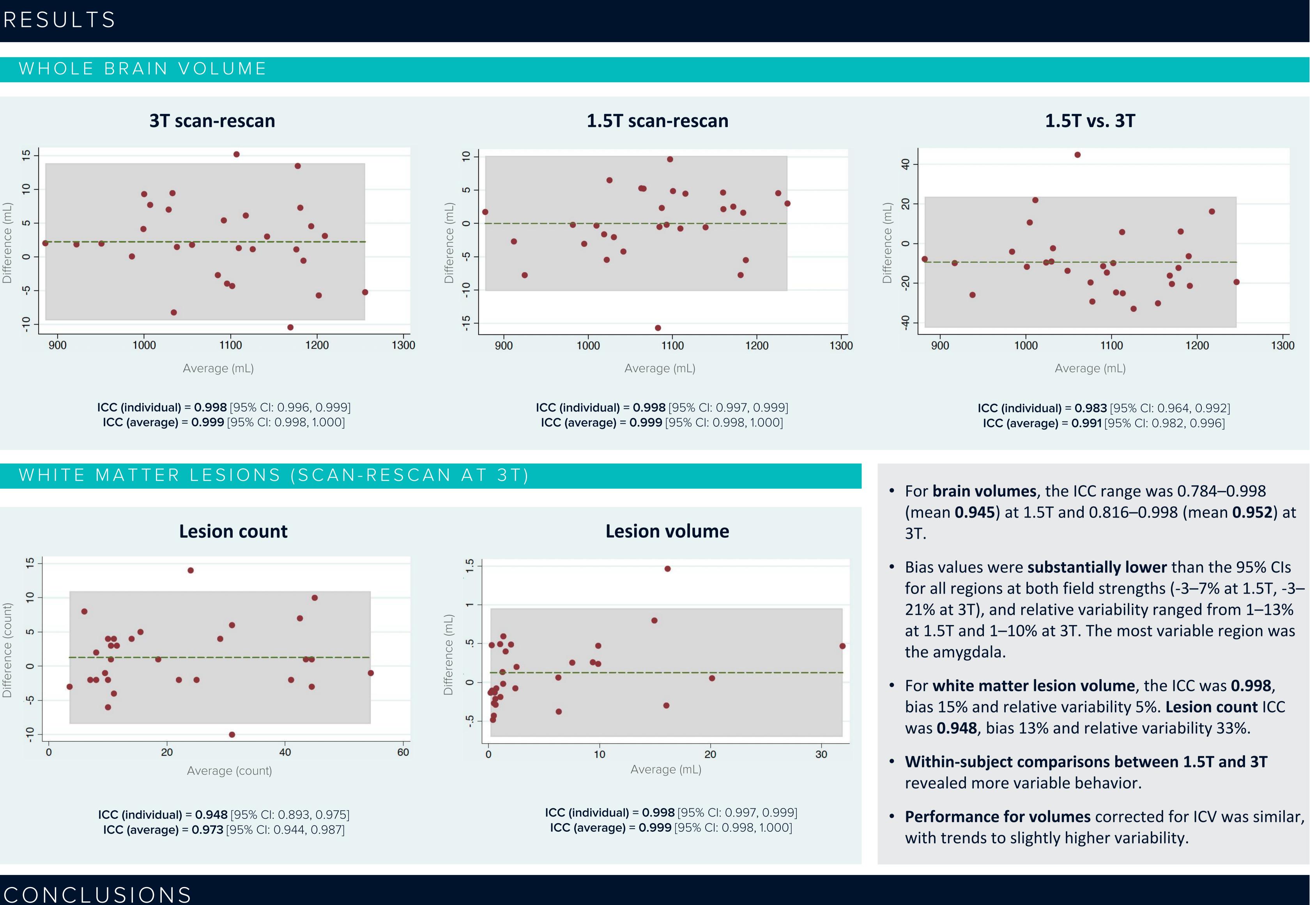
- A total of **30 subjects** (15 HC and 15 MS) were each scanned four times: twice on a 1.5T scanner (GE Signa Excite) and twice on a 3T scanner (Siemens Magnetom Skyra).
- Each of the paired **1.5T and 3T** scans took place on the same day, with the subjects taken out of the scanner in between.
- The 1.5T and 3T scan pairs were acquired between **0 and 47 (mean 2, median 0) days** apart. A 3DT1 sequence was acquired at both field strengths, and a 2D FLAIR sequence at 3T only.
- These scans were analyzed using **QyScore® v1.7**.
- Outcome measures were whole brain, grey matter, white matter, hippocampus and amygdala volumes from the 3DT1 scans, and the count and total volume of white matter lesions from the FLAIR scans.
- Volumes were corrected by **intracranial volume** (ICV).

### STATISTICS

• **Reproducibility** was assessed using intraclass correlation (ICC), as well as Bland-Altman analysis, including bias (mean difference divided by the 95% CI of the difference) and relative variability measures (95% CI divided by the grand average value of the measurand).

# A. Morales-Pinzón<sup>1</sup>, M. Wallack<sup>1</sup>, M. Cavallari<sup>1</sup>, E. Cavedo<sup>4</sup>, E. Gordon<sup>4</sup>, C. Longo dos Santos<sup>4</sup>, S. Khalil<sup>3</sup>, M. Palotai<sup>1</sup>, R. Bakshi<sup>3</sup>, A.J. Schwarz<sup>5</sup>, C.R.G. Guttmann<sup>1</sup>





• The QyScore<sup>®</sup> analysis **yielded highly reproducible** within-subject measurements, with the amygdala (smallest region) being most variable. • This study provides limits of detectability for the use of these algorithms to detect change due to disease progression or therapeutic intervention.