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BACKGROUND

Standardized amyloid PET quantification using the Centiloid scale is essential for Alzheimer's disease research and therapeutic trials. Implementations require expensive MATLAB licenses and high-performance local hardware, creating significant barriers to accessibility and multi-center harmonization.

METHOD

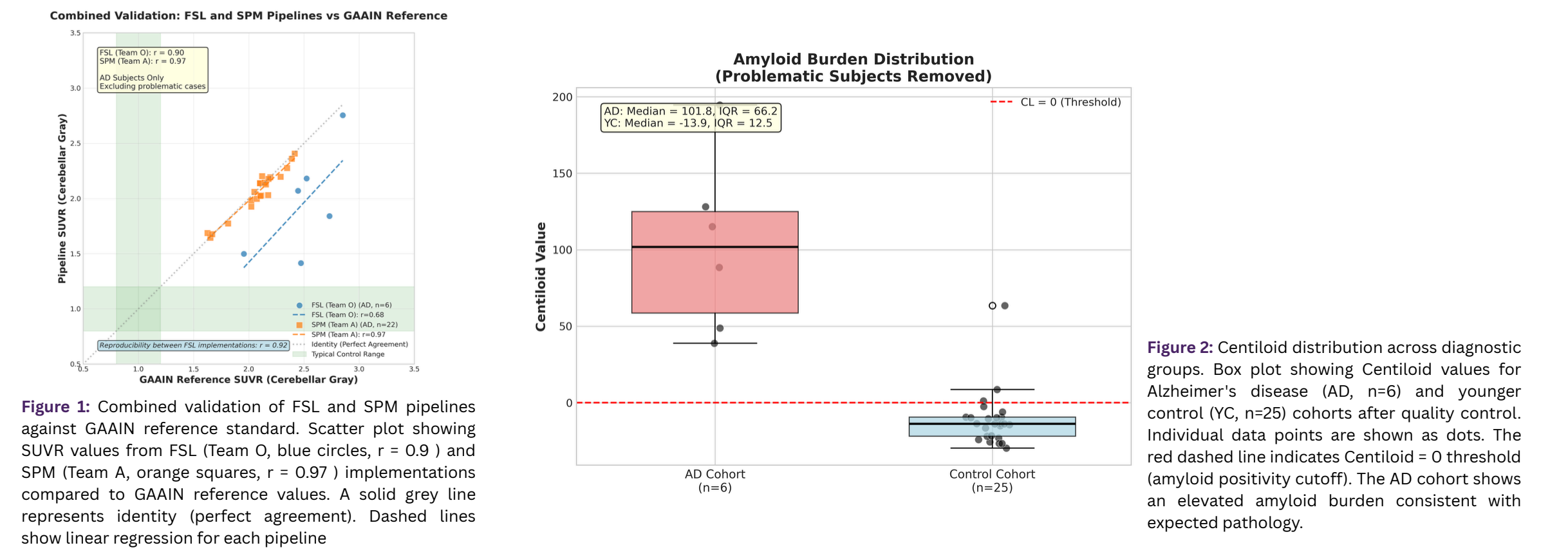
To address this, we developed a combined, cloud-based pipeline integrating SPM12 preprocessing (via free MATLAB Runtime) with FSL6 quantification, containerized within the Neurodesk platform. This work was performed as part of the 2025 CONNExIN (Comprehensive Neuroimaging Analysis Experience In resource-constrained Settings) Program. Two CONNExIN trainee teams independently implemented complementary approaches: Team O developed the FSL quantification pipeline, while Team A implemented SPM preprocessing with FSL quantification and replicated the FSL pipeline. Using the GAAIN reference dataset (25 AD: AD01-AD25, 25 YC: YC101-YC125), we analyzed 50-70 minute 11C-PiB frames. SPM preprocessing included motion correction, PET-MRI registration, and spatial normalization. FSL quantification used binary masks with automated intensity normalization (threshold: 1.0-4.0 SUV). SUVR was calculated as cortical mean / reference mean. Subjects with data quality issues (n=4 AD) were excluded. Validation included correlation with GAAIN SUVRs and an inter-pipeline reproducibility assessment between independently implemented SPM and FSL quantification arms. Protocol is available on <https://dx.doi.org/10.17504/protocols.io.8epv55jydv1b/v1>

CONCLUSION

We present a validated, cloud-based Centiloid pipeline that eliminates cost and hardware barriers. Developed under the CONNExIN program, this tool makes standardized amyloid PET quantification - a key molecular biomarker - accessible for resource-constrained settings, facilitating multi-center research and trial work in Alzheimer's disease.

RESULTS

Automated quality control identified and corrected intensity scaling issues in 32% (8/25) of AD participants, with 4 subjects excluded from final analysis due to persistent data quality issues (Figure 1). In the validated dataset, our pipeline showed strong agreement with GAAIN reference values (FSL: r=0.90; SPM: r=0.97; Figure 2), yielding SUVRs (AD cohort: 1.96±0.49, control cohort: 0.98±0.16, n=25; Figure 3). Team A's SPM implementation demonstrated excellent accuracy against GAAIN references (r=0.97), while reproducibility between independently implemented FSL pipelines was high (r=0.92, relative difference=+12.2%), with agreement against GAAIN showing minimal bias (Table 1). The cloud implementation enabled processing without local hardware or MATLAB license costs.



Analysis Pipeline	AD SUVR in arbitrary values Mean ± SD	Mean SUVR Error compared to Reference	Relative Difference with FSL Validation
GAAIN Reference Standard	2.31 ± 0.28 (25 AD patients)	-	-
FSL Validation (Team O)	1.96 ± 0.49 (n=6 AD patients)	-0.25	-
FSL Replication (Team A)	2.30 ± 0.26 (n=21 AD patients)	-0.11	+12.2%*
SPM Validation (Team A)	2.05 ± 0.21 (n=22 AD patients)	-0.03	+4.6%

Table 1: Pipeline validation and reproducibility results. Team A's SPM implementation showed the highest accuracy (error=-0.03 SUVR), while reproducibility between FSL implementations was excellent (r=0.92, relative difference=+12.2%).

*Reproducibility of FSL between Team O vs. Team A (n=20): r = 0.92, relative difference = +12.2%

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