

Centiloid PET SUVR analysis using the supratentorial white matter as reference region

Introduction

The Centiloid project provides a data transformation framework to standardize PET quantification for direct comparisons across different amyloid tracers. We previously reported data for the Centiloid validation of the AMYPAD PET-SUVR analysis pipeline for [18F]flutemetamol (FLUT) and [18F]florbetaben (FBB) tracers. This SUVR pipeline relies on a T1-weighted subject specific multi-atlas segmentation to identify regions for analysis. Following the work of Salvadó et al (HAI 2018), showing the improved performance of an atlas based supratentorial white matter (sWM) reference region (RR) in a longitudinal study, we have included this approach in the AMYPAD SUVR pipeline. Centiloid validation has been carried out for this novel region and compared with the default RRs.

Results

Ten conversion equations have been identified for each RR and tracer combination (Table 1) which resulted, after conversion, in the averaged Centiloid values reported in Table 2 for the HE, MCI and AD groups. The average in the AD group is 95, comparing well with the value of 100 as defined in the Centiloid scale. Variability within each group is due to the heterogeneity of the population under analysis. All 5 reference regions provide comparable average values and power to discriminate clinical groups.

	Florbetaben	Flutemetamol	AD	MCI	HE
GM Cerebellum	CL = 139.70 * FBB _{SUVR} - 174.14	CL = 104.66 * FLUT _{SUVR} - 135.00	103.9 ± 46.6	63.5 ± 57.6	9.7 ± 30.4
Whole Cerebellum	CL = 161.46 * FBB _{SUVR} - 169.35	CL = 123.85 * FLUT _{SUVR} - 136.06	102.5 ± 44.6	61.4 ± 59.1	13.2 ± 32.5
Whole Cereb + Brain Stem	CL = 168.65 * FBB _{SUVR} - 172.63	CL = 139.90 * FLUT _{SUVR} - 137.92	97.4 ± 43.5	54.7 ± 56.5	8.8 ± 30.7
Pons	CL = 243.07 * FBB _{SUVR} - 174.08	CL = 235.45 * FLUT _{SUVR} - 149.08	92.8 ± 46.4	43.3 ± 58.3	6.4 ± 29.7
White Matter	CL = 281.76 * FBB _{SUVR} - 178.95	CL = 248.96 * FLUT _{SUVR} - 151.84	95.0 ± 45.9	57.6 ± 60.7	14.9 ± 31.1

TABLE 1

TABLE 2

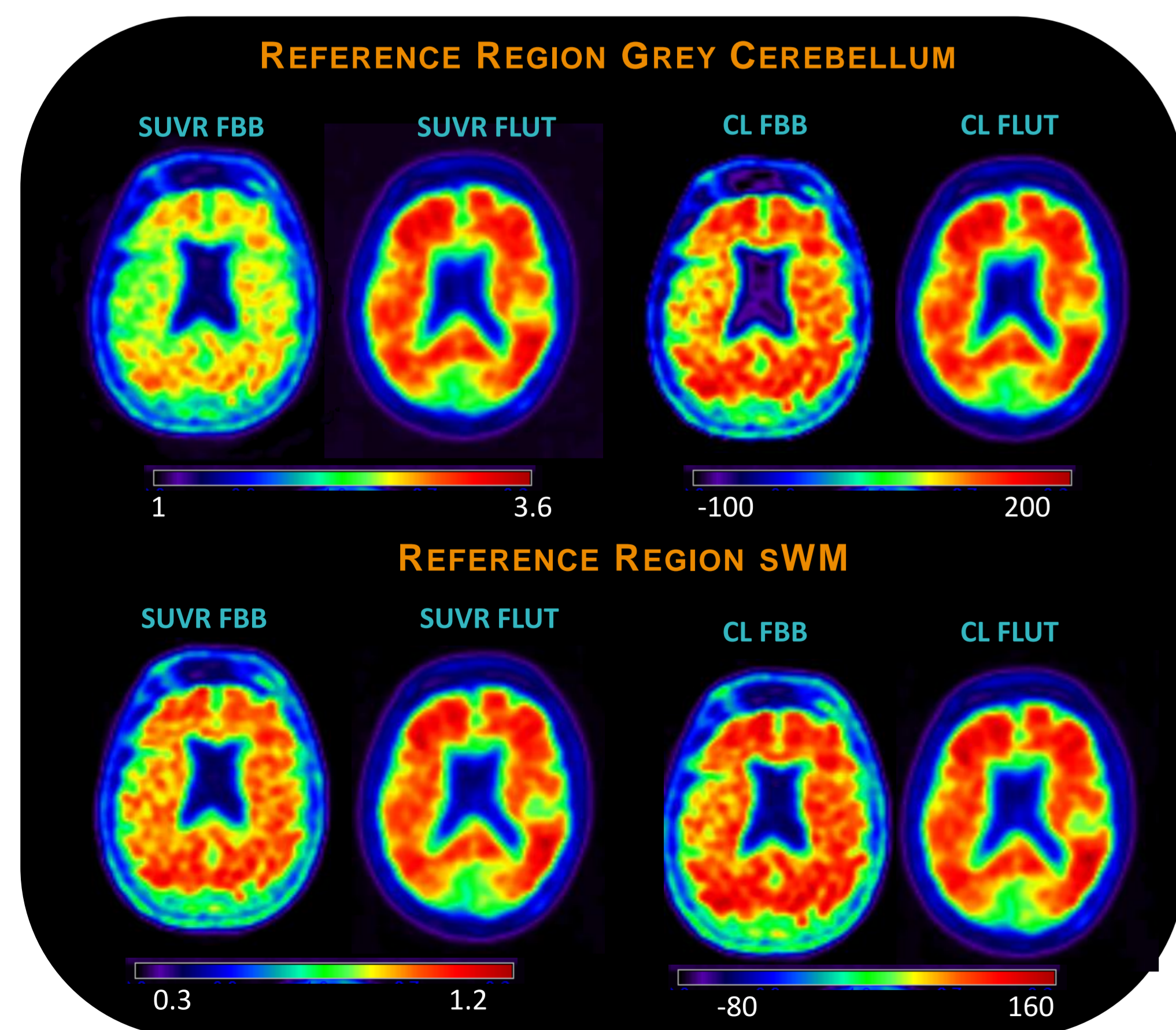


FIGURE 2) REFERENCE REGION QUALITATIVE COMPARISON - TWO AD SUBJECTS WITH AVERAGE CENTILOID ~100

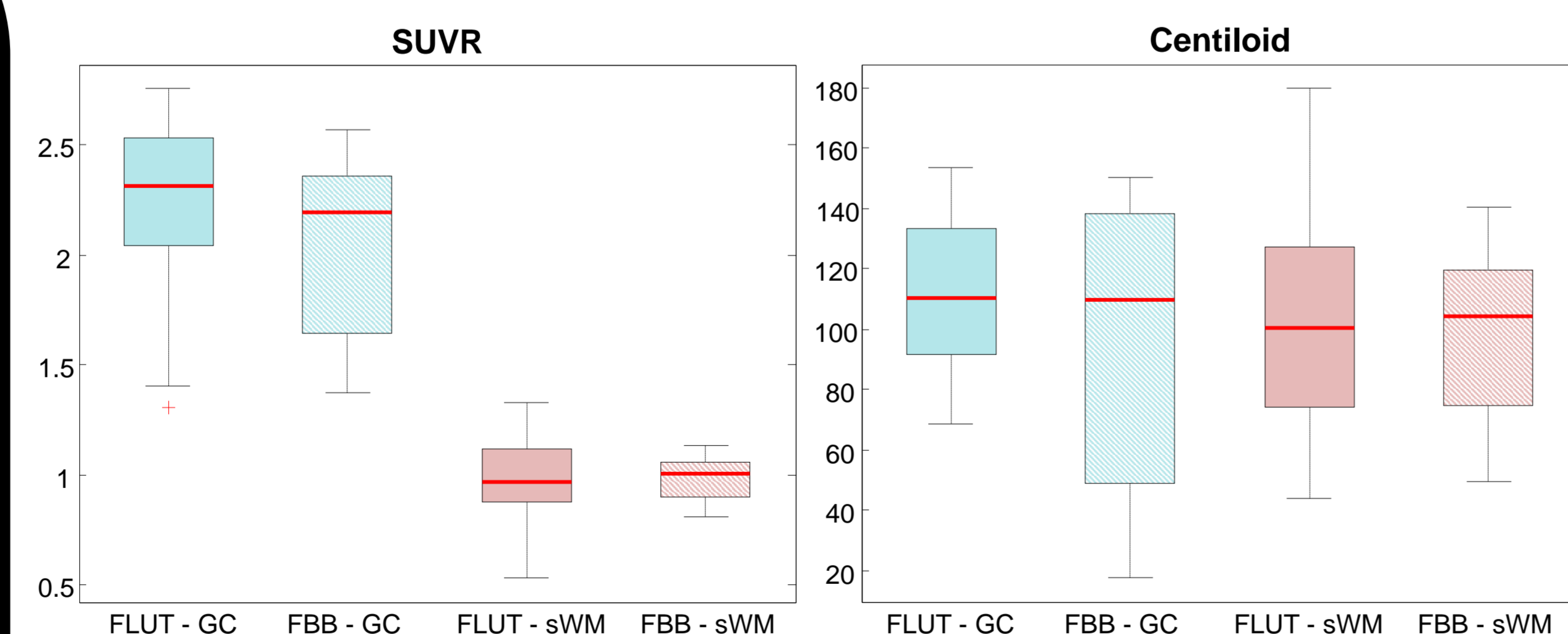


FIGURE 3) REFERENCE REGION QUANTITATIVE COMPARISON IN THE AD POPULATION

Methodology

The AMYPAD SUVR analysis pipeline, which operates in subject native space, has been modified to allow use of any additional atlas in standard space. Three different databases have been analysed to validate the use of the sWM mask as RR for Centiloid conversion.

Data comprise:

- *GAAIN*: PIB images (YC=35, AD=45)
- *Piramal*: PIB and FBB images (YC=10, HE=5, MCI=9, FTD=2, AD=7)
- *GE*: PIB and FLUT images (YC=24, HE=10, MCI=20, AD=20).

Based on previous validation work of standard RRs (grey cerebellum, whole cerebellum, pons, whole cerebellum+brain stem) the Centiloid conversion equation for the new RR has been computed and compared with previous findings.

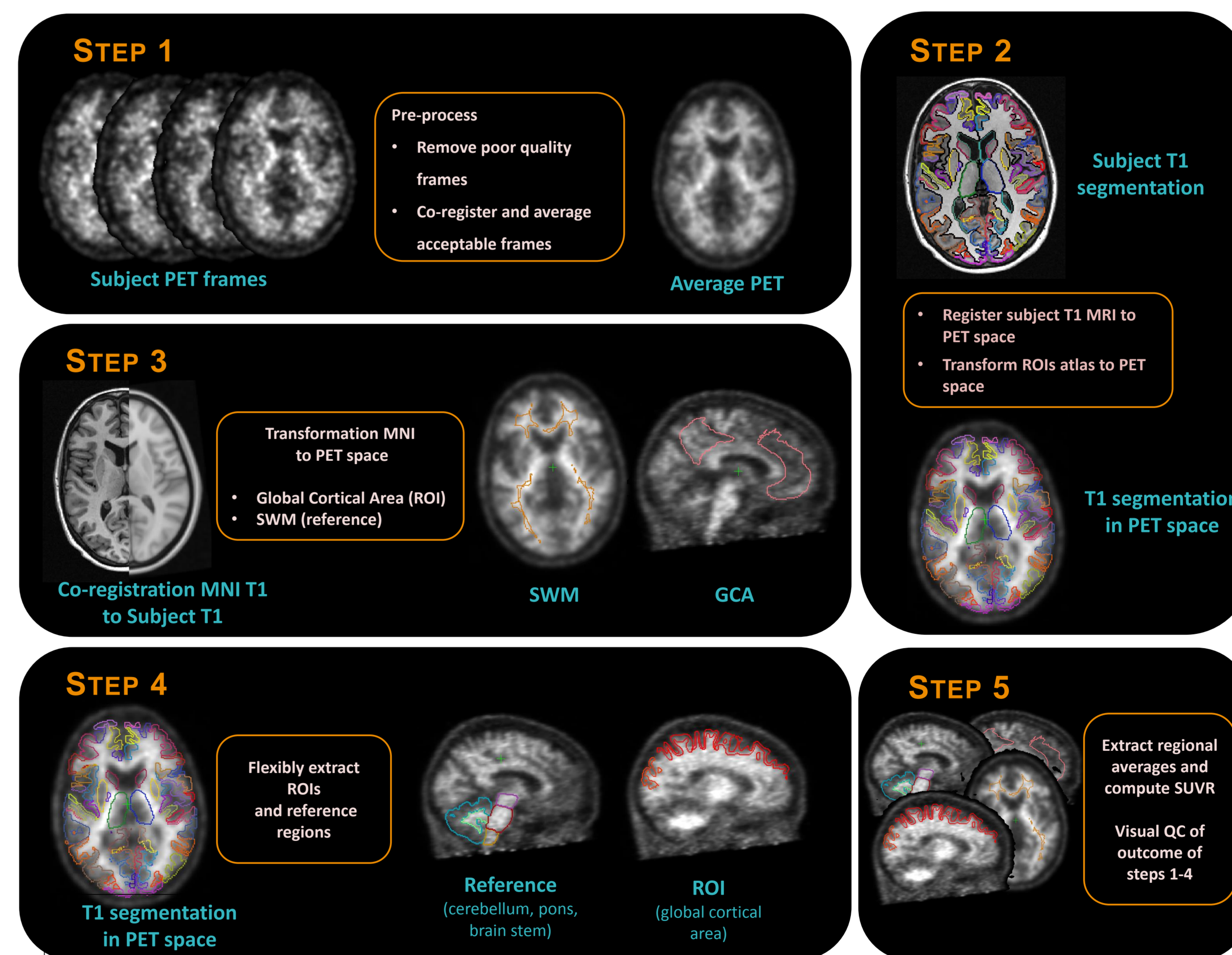


FIGURE 1) SUVR ANALYSIS PIPELINE

Conclusions

The AMYPAD Centiloid analysis has been validated with 5 reference regions. A preliminary analysis reports comparable average values but relatively high variability in the non-AD group (CV>200%). Literature reports increased interest in using sWM as it is considered to reduce variability in the longitudinal progression of amyloid retention. The inclusion of sWM in the AMYPAD Centiloid analysis will allow for a robust longitudinal comparison with more popular reference regions.