Amyloid PET Variability due to Variation in MRI Protocol and Anatomical Segmentation

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Introduction

- Anatomical brain segmentation (atlas-based) depends on accurate imaging protocol maintenance
- Changes to the MRI acquisition protocol (e.g. voxel-size, contrast parameters) can indirectly cause anatomical region delineation differences
- If those segmentations are being used for PET Regional SUVR sampling

→ this can constitute an additional source of cross-sectional variability on regional amyloid beta PET (Ab-PET) SUVR estimates

AIM → Quantify variability of Ab-PET attributable to brain segmentation differences due to changes of the MR T1w protocol

KEYWORDS: Amyloid-PET, pre-processing, T1w-MR protocol variability

Results

- Both intra and inter-segmentation variability of Ab-PET were **not significantly different between harmonisation levels** (HZ vs NHZ datasets, Figure 2A; paired t-test, $p > 0.05$, Cohen's $d < 0.01$)
- Inter-segmentation variability: inter-quartile range 1.6-5.3% → comparable to scan-rescan levels (5-9% [Tolboom;JNM;2009])

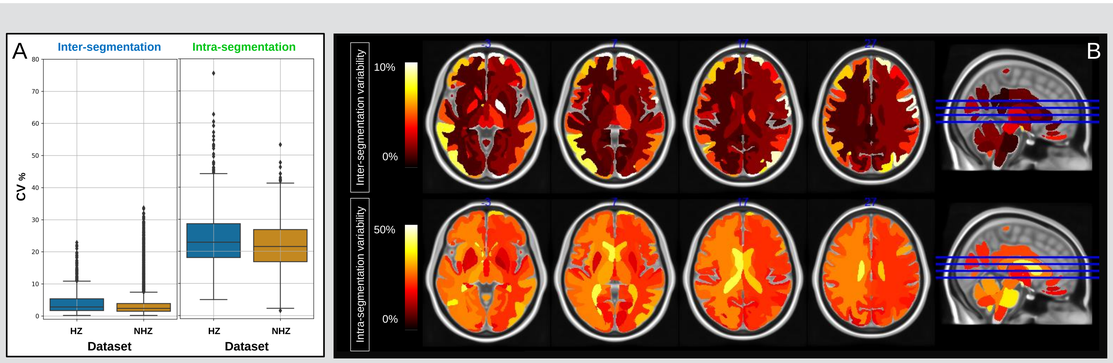

Figure 2. **(A)** Distribution of 18F-FLUT uptake variability in all regions (coefficient of variation, CV) respectively left) across segmentations (obtained from different MRI protocols); and right) within-segmentation (ROI). Distribution boxplots are separately reported for the harmonised (HZ) and non-harmonised (NHZ) protocol datasets. **(B)** Spatial distribution of CV% between segmentations (top row) or within-ROI (bottom row) for HZ datasets.

- Intra-segmentation variability (i.e. uptake variability within-ROI) one order of magnitude higher all segmentation-related variability condition (Figure 2B; paired t-test, $p < 0.05$)
- Intra-segmentation variability inter-quartile range: 18.0 - 28.6% → significantly different between harmonisation (HZ vs NHZ datasets, Figure 2A; paired t-test, $p > 0.05$) with however small effect size (Cohen's $d = 0.23$).

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Methodology

Data

1 - Single subject scanned with 18 T1w-MRI *harmonised protocols* (**HZ**) [Duchesne; JMRI; 2018]

→ Assess SUVR regional variability when **segmentations are being obtained from similar T1w images: minimal impact ?**

2 - Four subjects scanned with 8 *non-harmonised protocols* (**NHZ**) [Kempton; NeuroImage; 2011]

→ Assess SUVR regional variability when **segmentations are being obtained from different T1w images: significant impact ?**

3 - ADNI2 (http://adni.loni.ucla.edu). Amyloid-PET reconstructed images for 20 ADNI subjects randomly selected whilst being visually representative of the AD spectrum deposition patterns

Image pre-processing

T1w-MRI:
- Bias field-corrected [Tustison;IEEE-TMI;2010] + Skull-stripped [Heckemann;PLOS-ONE;2015] + Automatic whole brain parcelation was performed with LEAP [Wolz;Neuroimage;2010]
- Used to create a subject-specific T1w template (see Figure 1).

Ab-PET:
- Non-linearly warped to each subject-specific T1w template (target resolution 5 mm isotropic)

→ Define within-subject a range of uptakes to ensure segmentation-related variability not biased by uptake
- Registrations were quality assured by visual inspection.

Ab-PET variability quantification

- *Inter-segmentation*: standard deviation of regional uptake across segmentations (within-subject and for the same brain region) divided by the global average.
- *Intra-segmentation*: standard deviation of uptake distribution within ROI (average) divided by the global within-ROI average.

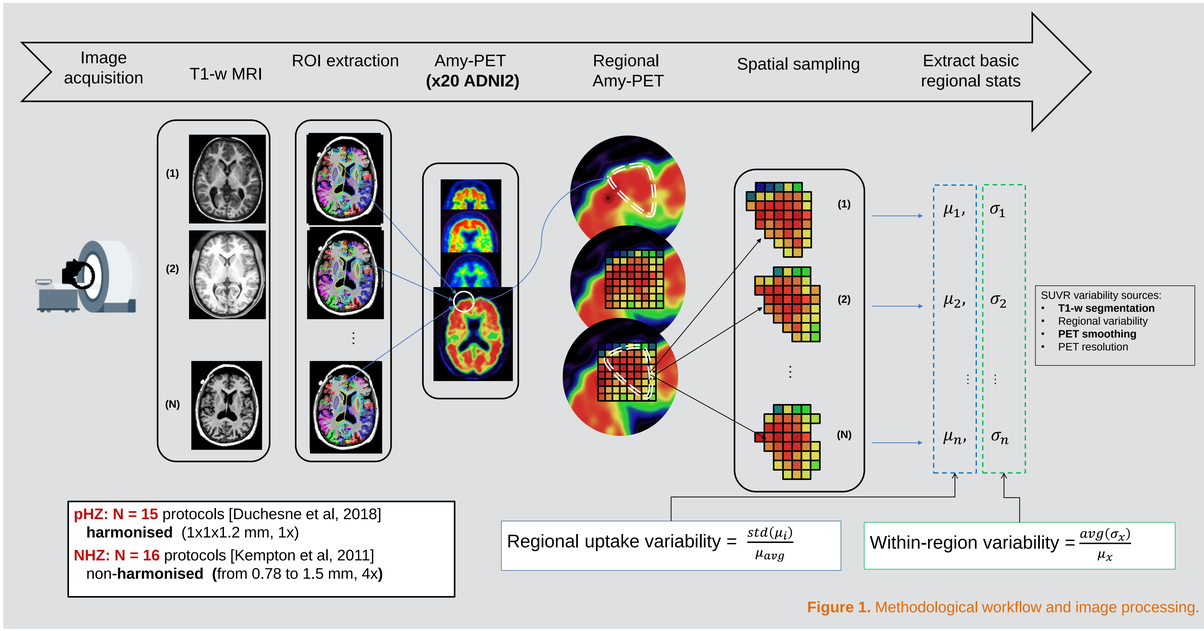

Figure 1. Methodological workflow and image processing.

Conclusions

- Variability of regional Ab-PET introduced by MRI-related segmentation differences

→ within the physiological scan-rescan range → lower than the within-ROI variability
- These results suggest the tolerability of using compliant MR data with minimal impact in Ab-PET.