On the performance of manually or automatically segmented DATSCAN-SPECT for biomarker extraction in PD

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Introduction

- Current clinical standard for Parkinson's Disease (PD) requires the assessment of degeneration of dopaminergic neurons in brain's striatum region.
- In-vivo, this assessment can be done by imaging the dopamine transporter (DaT) activity by means of single photon emission computerized tomography (SPECT) after the injection of Iodine-123 fluoropropyl (123I-FP-CIT).
- Visual read can be complemented by quantitative binding assessment for objective striatal markers derived from the tracer biodistribution.
- We assessed the impact of the regional delineation methodology (see Figure 1) used to extract such biomarkers on their classification performances in a mixed controls/PD cohort.

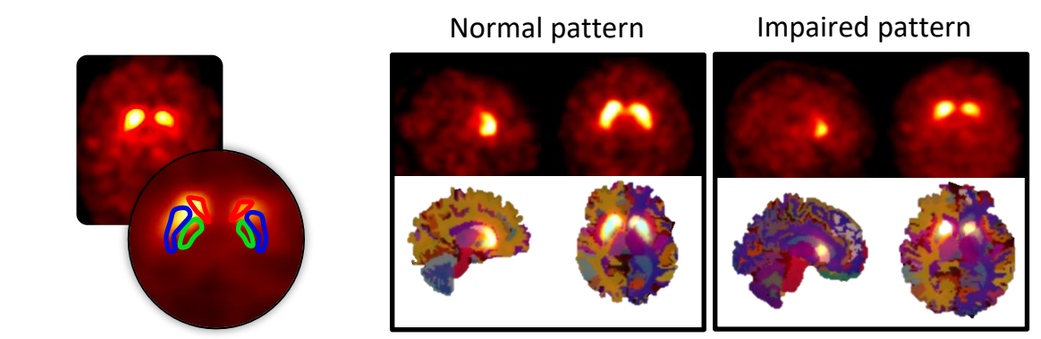
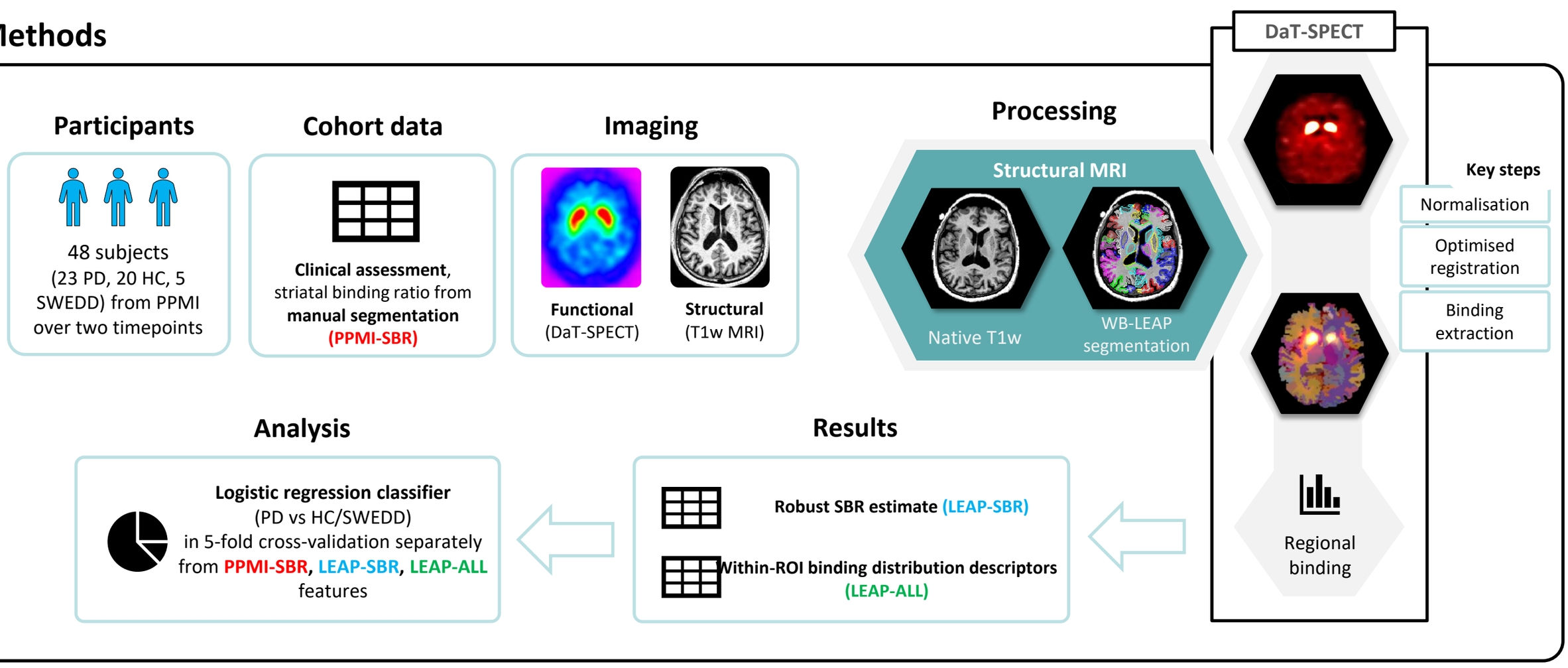


Figure 1. Approaches for striatal binding ratio (SBR) by delineation method.

Methods



Results

- The model trained with different feature set achieved performances reported in Table 1.
- Improvement in performances by using binding descriptors (**LEAP-ALL**) in addition to SBR-only (**LEAP-SBR**) consistent with [Prashanth et al., 2017] and offer balanced error types (see Figure 2).
- The simple feature set (intensity-based only) defined did not reach, if not loosely (within the standard deviation) the performances of classification based on SBR from manual delineations (**PPMI-SBR**).

Feature set	Accuracy	Precision
PPMI-SBR	0.96 ± 0.05	0.95 ± 0.06
LEAP-SBR	0.82 ± 0.11	0.84 ± 0.10
LEAP-ALL	0.88 ± 0.10	0.91 ± 0.07

Table 1. Classifier results from different feature sets. Results are reported as average cross folds ± the standard deviation across folds.

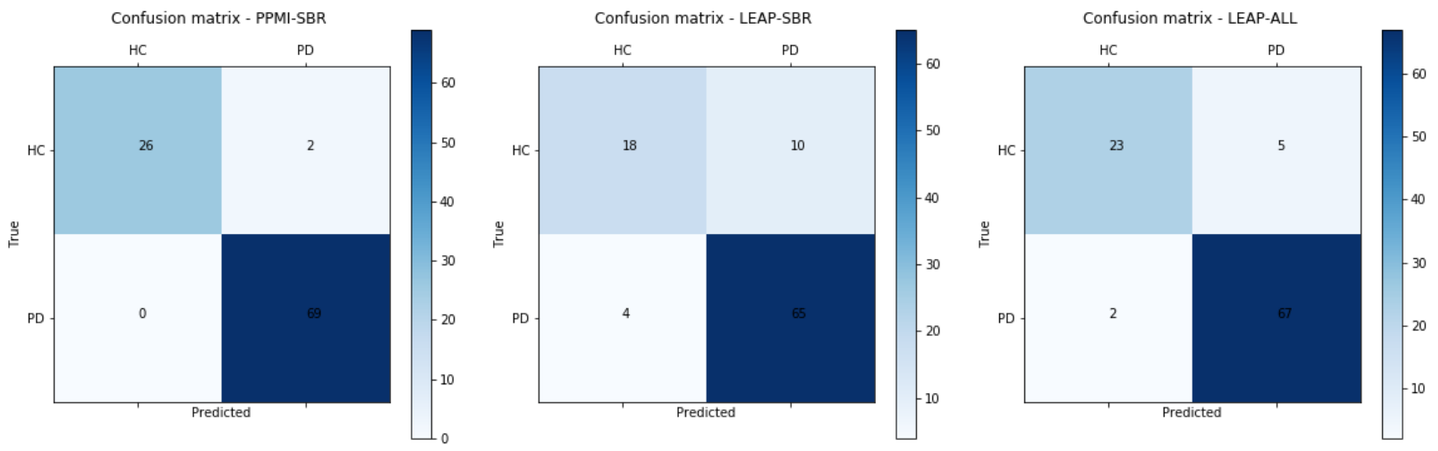


Figure 2. Confusion matrices across dataset from **PPMI-SBR** (left box), **LEAP-SBR** (central box) or **LEAP-ALL** (left box) features. Intensity scales by number of datasets.

Conclusions

This study shows results of a fully automatic quantitative analysis of DaT-SPECT based on MRI data for accurate within-subject anatomical striatal delineations.
Imaging biomarkers from automatic SPECT processing provided classification performances close to PPMI measures on early-PD subjects.
The proposed processing, however, requires no manual intervention for a repeatable biomarker extraction suitable for large clinical studies whose comparison is shown in Table 2.

Method	Sensitivity	Human time	Endpoint reproducibility	Resources required	Extensibility of analysis
Manual (PPMI)	High (variable)	Medium-high	Variable	Trained radiologist, manual segmentation software	Limited
Automatic (IXICO)	Medium/high	Low	High	Processing facility	High

Table 2. Head to head comparison of DaT-SPECT analysis approaches by criteria.