M430: A whole-brain multimodal discrimination of Parkinson's Disease, Multiple System Atrophy and Controls

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Background and Aim

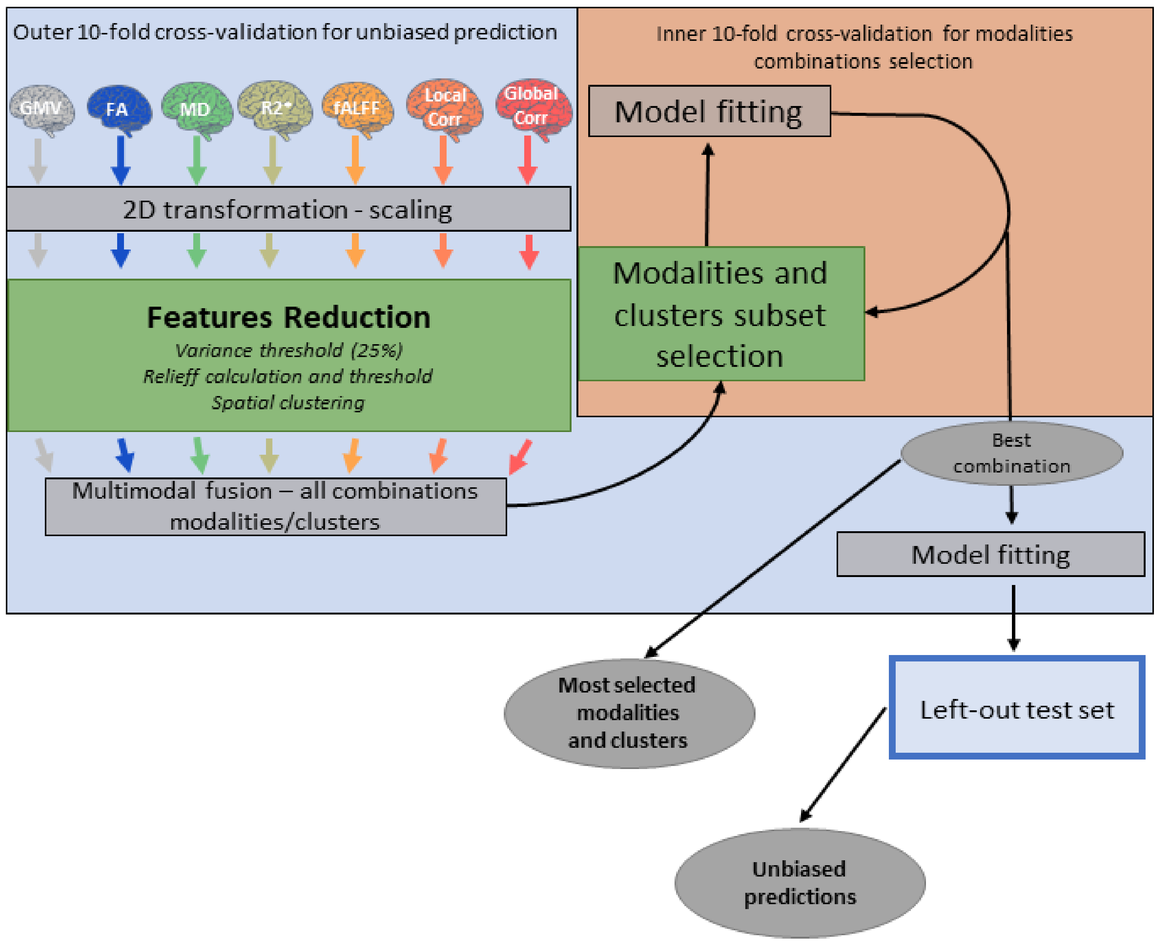
Parkinson's Disease (PD) and Multiple System Atrophy (MSA) share many symptoms, albeit having very different prognosis. Studies combining all MRI indexes relevant for these disorders (i.e. grey matter volume, fractional anisotropy, mean diffusivity, iron deposition, brain activity at rest and brain connectivity) with a completely data-driven voxelwise analysis for discrimination are lacking. In this study, we used such a complete MRI protocol and adapted a fully-data driven pipeline to discriminate between these populations and a healthy controls (HC) group.

Materials & Methods[1]

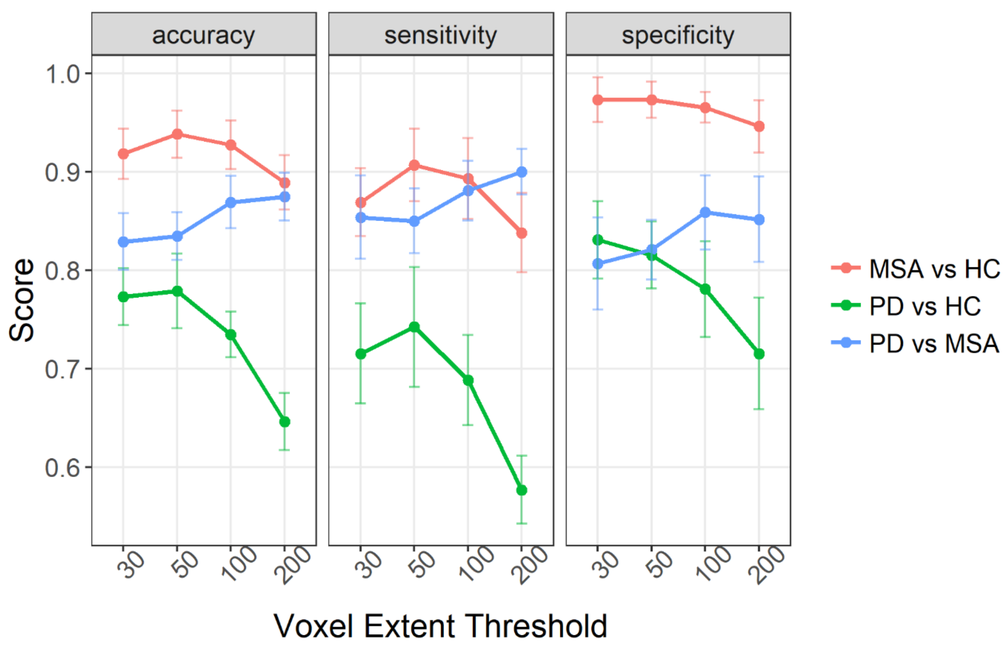
- 26 PD patients (12 males, 63.8 ± 6.3 years old, disease duration = 7.4 ± 4.5 years)
- 29 MSA patients (13 males, 64 ± 7.5 years old, disease duration = 5.7 ± 2.3 years)
- 26 HC (13 M, 63 ± 8.5 years)
- Grey Matter Volume (GMV) was calculated using CAT12[2]
- Fractional Anisotropy (FA) and Mean Diffusivity (MD) were calculated using standard FSL pipeline[3]
- R2* was calculated using in-house script[4]
- Functional indexes were calculating using Conn[5]
- Performance was calculated using a repeated 10-fold cross-validation
- All images were resampled at 3mm isotropic.
- The process was repeated for different cluster extent thresholds and using both smoothed (8mm FWHM) and non-smoothed data.
- Results are presented for smoothed data

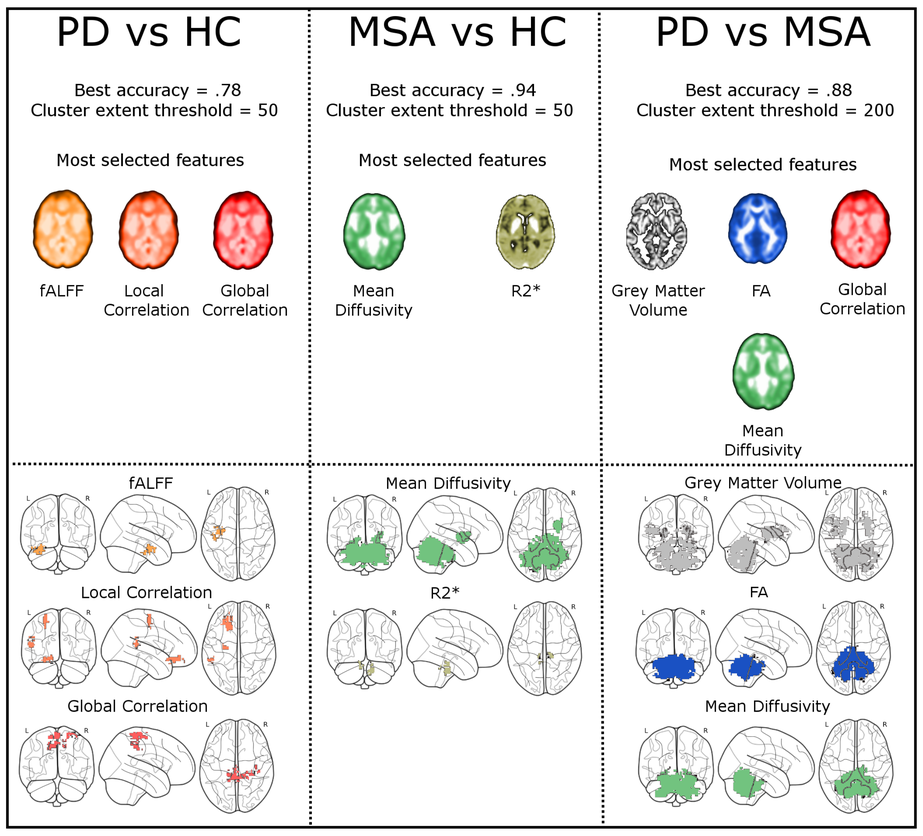
: indexes
: processing steps, fitting and end-points
: features reduction/selection steps
: internal cross-validation to find the best combination of indexes

The 3 groups were comparable in terms of age, sex, T1 quality and in-scanner movement during DWI and rs-fMRI acquisition



Results





Discussion

- There is a striking difference in the indexes selected for the different discrimination tasks
- The performance of our pipeline for discriminating between PD and HC is in line or better than some previously published studies[6,7,8], but lower than some others[9,10]
- The performance of the classifiers between MSA and HC and MSA and PD is better than previously published studies[6,7]
- For all discrimination tasks, the selected indexes and the associated regions are in line with the known pathophysiology of PD and MSA and with previous imaging studies[11,12,13,14,15,16]
- There is a systematic effect of the cluster extent threshold on the performance of the pipeline: future works should focus on this issue and possibly choose this hyper-parameter in a data-driven manner
- Although the effect of smoothing was not extreme (data not shown) unsmoothed data led to different performance (higher for MSA vs HC and PD vs MSA but lower for PD vs MSA). The best smoothing kernel should be chosen wisely (and possibly in a data driven fashion)
- This pipeline can be easily extended by including different modalities as SPECT imaging (DATscan) or PET imaging acquired using marker of neuroinflammation[17,18].
- We are planning to expand our pipeline to non-imaging modalities (e.g. biological samples, cognitive testing, clinical data). The clustering step of the pipeline should be adapted for non-imaging features.
- Future studies including bigger samples are needed to confirm our results and the performance of this pipeline.

References

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