“A whole-brain multimodal discrimination of Parkinsons dDiseas, Multiple System Atrophy and Controls”.

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Background and aims: Parkinson's Disease (PD) multiple system atrophy (MSA) are two parkinsonian syndromes that share many symptoms, albeit having different prognosis. Although previous studies have proposed multimodal MRI protocols combined with multivariate analysis to discriminate between these two populations and healthy controls, studies combining all MRI indexes relevant for these disorders (i.e. grey matter, fractional anisotropy, mean diffusivity, iron deposition, brain activity at rest and connectivity) with a completely data-driven voxelwise analysis for discrimination are still lacking.
Methods: In this study, we used such a complete MRI protocol and adapted a fully-data driven analysis pipeline to discriminate between these populations and a healthy controls (HC) group. The pipeline combined several feature selection and reduction steps to obtain interpretable models
with a low number of discriminant features that can shed light onto the brain pathology of PD and MSA.
Results: Using this pipeline, we could discriminate between PD and HC (best accuracy =.78), MSA and HC (best accuracy =.94) and PD and MSA (best accuracy =.88).Moreover, we showed that indexes derived from restingstate fMRI alone could discriminate between PD and HC, while mean diffusivity in the cerebellum and the putamen alone could discriminate between MSA and HC. On the other hand, a more diverse set of indexes derived by multiple modalities was needed to discriminate between the two disorders.
Conclusion: We showed that our pipeline was able to discriminate between distinct pathological populations while delivering sparse model that could be used to better understand the neural underpinning of the pathologies.