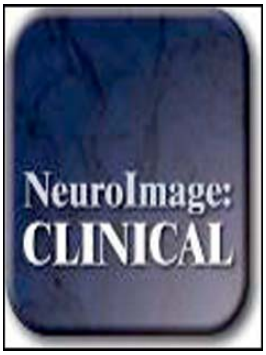

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A Test-Retest Study on Parkinson's PPMI Dataset Yields Statistically Significant White Matter Fascicles

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Abstract

In this work, we propose a diffusion MRI protocol for mining Parkinson's disease diffusion MRI datasets and recover robust disease-specific biomarkers. Using advanced high angular resolution diffusion imaging (HARDI) crossing fiber modeling and tractography robust to partial volume effects, we automatically dissected 50 white matter (WM) fascicles. These fascicles connect deep nuclei (thalamus, putamen, pallidum) to different cortical functional areas (associative, motor, sensorimotor, limbic), basal forebrain and substantia nigra. Then, among these 50 candidate WM fascicles, only the ones that passed a test-retest reproducibility procedure qualified for further tractometry analysis. Leveraging the unique 2-timepoints test-retest Parkinson's Progression Markers Initiative (PPMI) dataset of over 600 subjects, we found statistically significant differences in tract profiles along the subcortico-cortical pathways between Parkinson's disease patients and healthy controls. In particular, significant increases in FA, apparent fiber density, tract-density and generalized FA were detected in some locations of the nigro-subthalamo-putaminal-thalamo-cortical pathway. This connection is one of the major motor circuits balancing the coordination of motor output. Detailed and quantifiable knowledge on WM fascicles in these areas is thus essential to improve the quality and outcome of Deep Brain Stimulation, and to target new WM locations for investigation.

Keywords: test-retest, Parkinson, white matter, diffusion, MRI, tractography, tractometry

1. Introduction

The number of studies relying on tractography statistics has grown at a steady pace. While some are exploratory and use a single population dataset [1, 2], most compare healthy to non-healthy populations by either trying to find significant group differences [3, 4, 5, 6, 7, 8] or trying