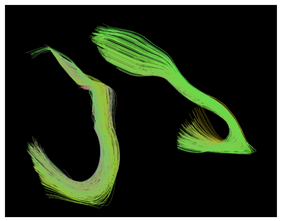

Persistent Homology Distances for Comparing Disease-Filtered Structural Connectomes

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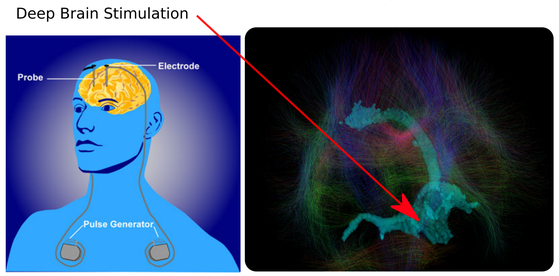
Introduction

Deep Brain Stimulation (DBS) is precisely implanted inside the brain - but the treatment-salient targets are not clear.

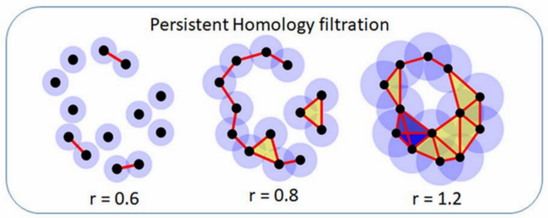
Recent efforts to map brain wiring are leading to **whole-brain connectomes** that can be used to filter fibers relevant to DBS efficacy.

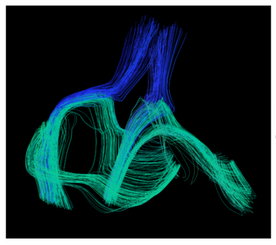
Comparing these fiber filtered disease subatlases remains difficult, particularly in the **streamlines space itself**.

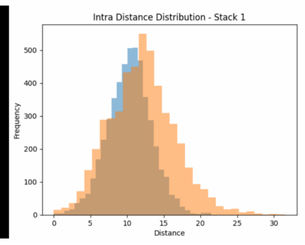


Topological Data Analysis (TDA) techniques, such as persistent homology (PH), can help us compare **disease subatlases** to each other in a way robust to small, trivial differences.

PH and Distributions



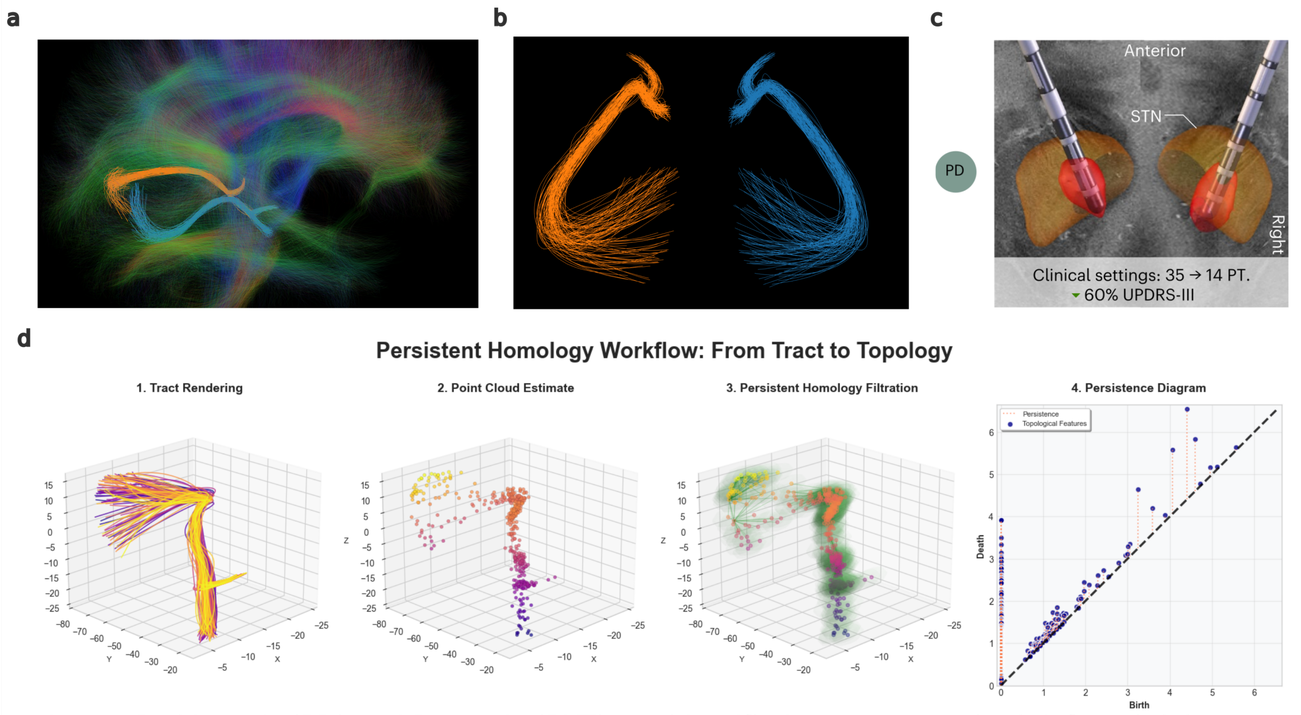




> Via DBS FiberFiltering, we identify disease-specific tracts that, when stimulated with DBS, are associated with improved symptom relief.

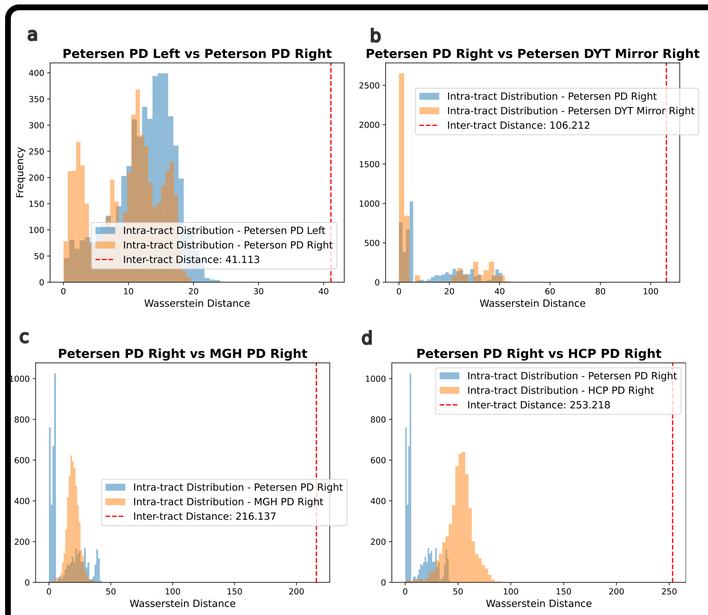
> We build Persistence Diagrams for tracts (sets of streamlines) by subsampling (N-1) streamlines N times.

> Wasserstein Distances are calculated on the resulting distributions



.> Across Parkinson's (PD) and Dystonia (DYT), we identified tracts across both left and right hemispheres associated with improved DBS outcome. Asymmetries in these subatlases were strong, and in most cases only one hemisphere contributed.

> PH and Barcodes were calculated (via GUDHI library Vietoris-Rips) via statistical subsampling of all streamlines in a tract. Distributions were then calculated between barcodes, and these distances were compared across tracts.



> Distributions with variance reflect those with streamlines that are relatively unlike the others. Their exclusion changes the PH substantially, making it "further" in 2-Wasserstein than others.

> Inter-hemispheric comparison of Left and Right with Parkinson's shows relatively small distances.

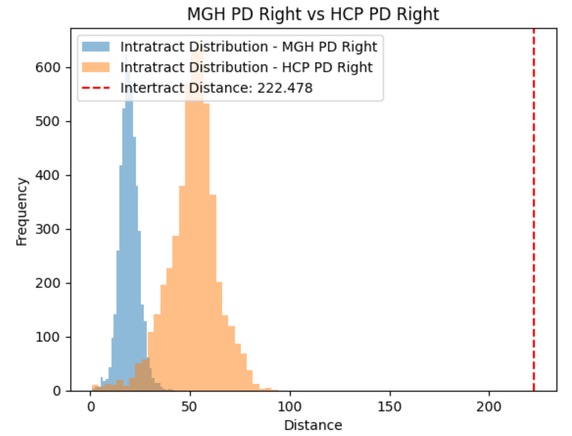
> Comparison between diseases within a given hemisphere yields larger distances.

> Comparisons between connectomes (Petersen and MGH, and Petersen and HCP) yield the largest distances.

> Petersen, a constructed connectome, exhibits a distinct distribution from the dMRI based connectomes.

Comparing Connectomes

Distributions Differ Between Connectomes



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> Across all comparisons we observe a consistent ordering of topological separations: hemisphere < disease < connectome.

diffome

https://github.com/virati/diffome

Python Library for Comparing Connectomes

> Open source Python Library for visualizing, filtering, and comparing disease-specific subatlases.

> General utility in analysing structural and function connectomes (WIP)

> Integration with AutoLie and SINDy for dynamics-specific subatlas comparison and preliminary controller design (WIP) [3]