Parcellating the internal and external globus pallidus using diffusion based clustering

Patrick Beukema[1,3] and Timothy Verstynen[2,3]
[1]Center for Neuroscience, University of Pittsburgh [2]Dept. of Psychology, Carnegie Mellon University
[3]Center for the Neural Basis of Cognition, Carnegie Mellon University

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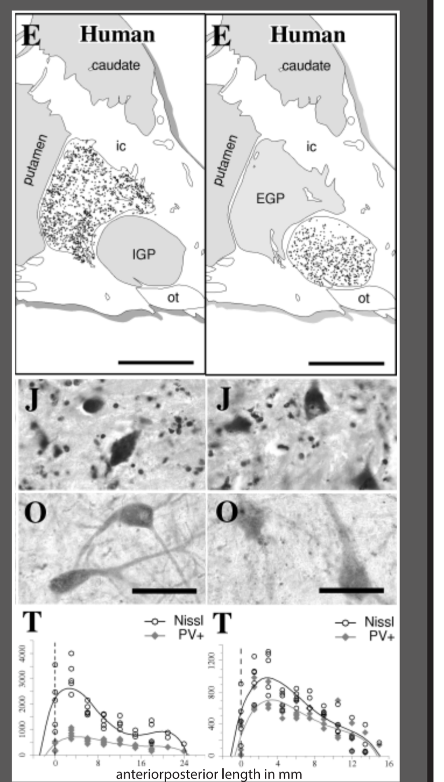
Background

- The boundary between the the external and internal segments of the globus pallidus are difficult to distinguish with automatic routines.

- Previous anatomical studies have found differences in cellular density and morphology in these two segments (Hardman et al., 2002).

- Segmentation of sub-cortical structures based on diffusion tensor magnetic resonance imaging has been successfully applied to resolve thalamic nuclei (Wiegell et al., 2003).



Hardman et al, 2002

Goal

Are there reliable differences in the diffusion signal of the inner and external segments of the globus pallidus to segment these independent regions?

Methods

Data

CMU 60

60 subjects (29 male) were recruited from the local Pittsburgh community and the Army Research Laboratory in Aberdeen Maryland. All subjects were neurologically healthy, with no history of either head trauma or neurological or psychiatric illness. Subject ages ranged from 18 to 45 years of age at the time of scanning, with a mean age of 26 years (+/- 6 standard deviation). Six subjects were left handed (3 males, 3 females).

HCP 80

80 subjects (36 male) were scanned on a customized Siemens 3T "Connectome Skyra" housed at Washington University in St. Louis, using a standard 32-channel Siemens receive head coil and a "body" transmission coil designed by Siemens specifically for the smaller space available using the special gradients of the WU-Minn and MGH-UCLA.

Acquisition

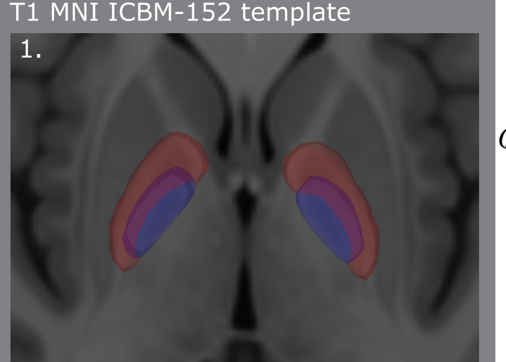
Parameter	HCP 80	CMU 60
Scanner	Seimens 3 T Skyra System	Siemens Verio 3T
Coil	32-channel	32-channel
Sequence	Spin-echo EPI	Spin-echo EPI
TR	5520 ms	9916 ms
TE	89.5 ms	157 ms
Q-space sampling	3shell: 1000, 2000, and 3000 s/mm^2	Grid: Maximum 5000 s/mm^2

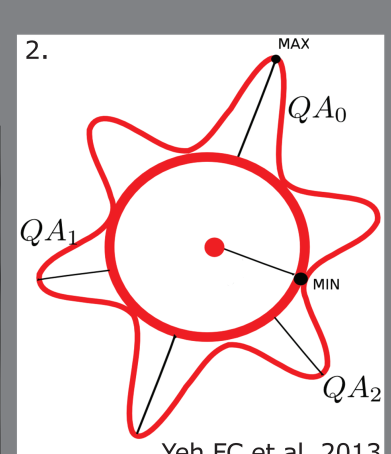
Reconstruction

All images were processed using a q-space diffeomorphic reconstruction method described previously (Yeh & Tseng, 2011). Briefly, this approach uses a non-linear coregistration approach (ICBM-152 space template regularization, 16 non-linear iterations) that registers the voxel-coordinate into MNI space while also maintaining distortion of the q-space vector during the normalization process. From here diffusion orientation distribution functions (dODFs) are reconstructed to a spatial resolution of 1x1x1 mm.

Pipeline

1. Manual segmentation of the GPe and GPi drawn on the high resolution T1 MNI ICBM-152 template



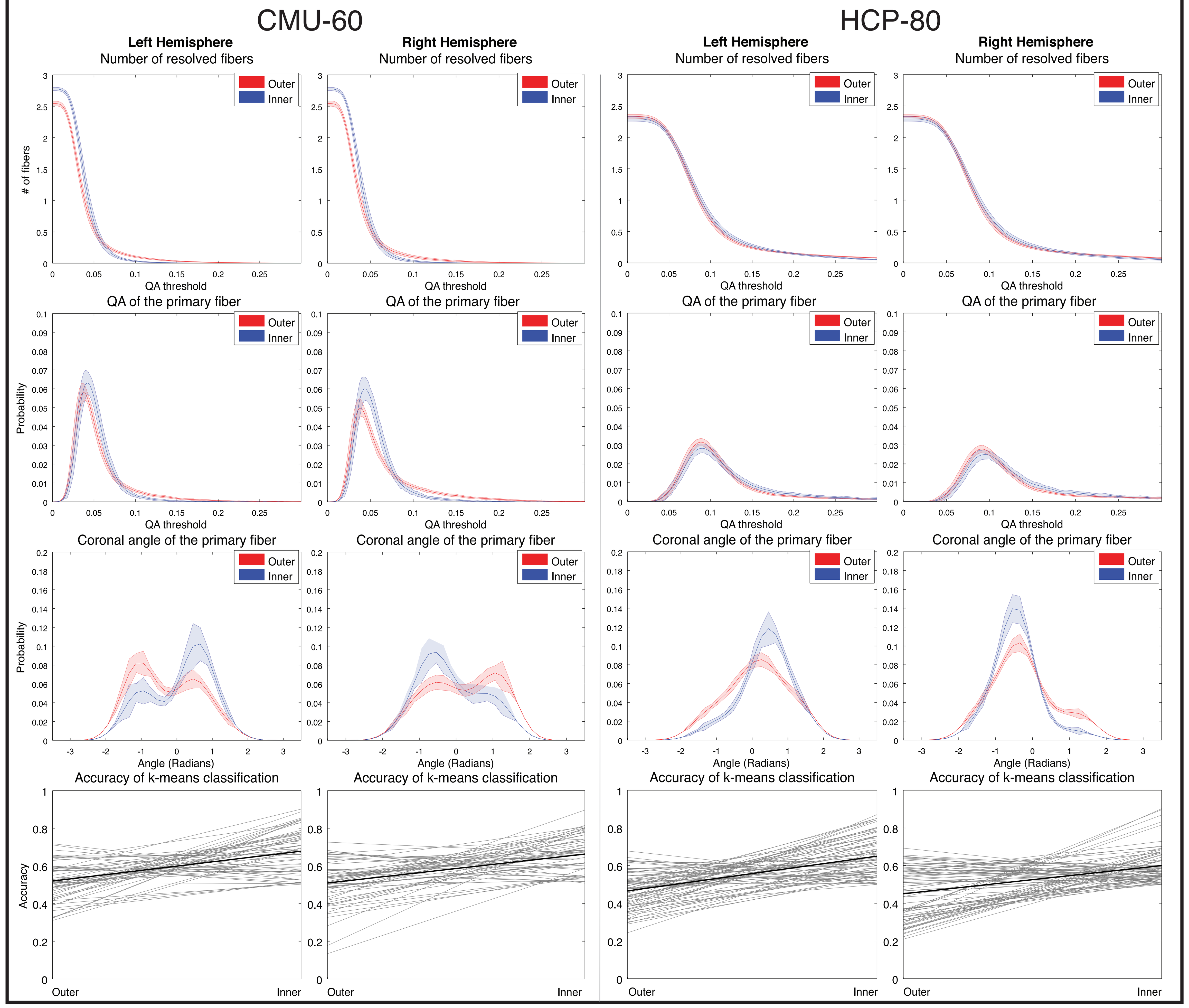


Yeh FC et al. 2013

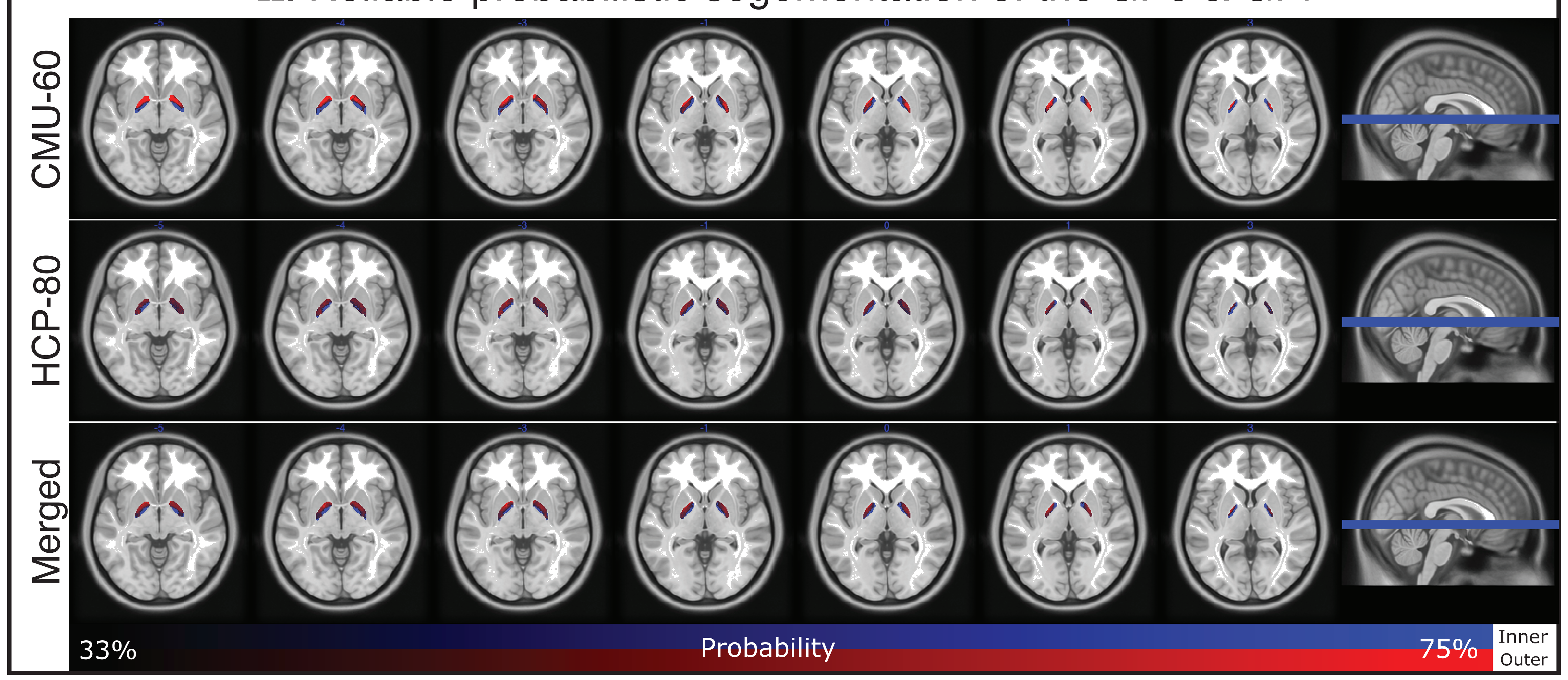
2. Spin distribution function showing number of resolved fibers, quantitative anisotropy (QA) value, and angle used to generate graphs in panel I.
$QA = Z_0(\psi(\hat{a}) - iso(\psi))$

3. Probablistic maps (Panel II) were generated by averaging the segmentations of the inner and outer segments across subjects in the CMU 60 and DSI 80 subjects pools and combined datasets (Merged), thresholded between [33%, 75%].

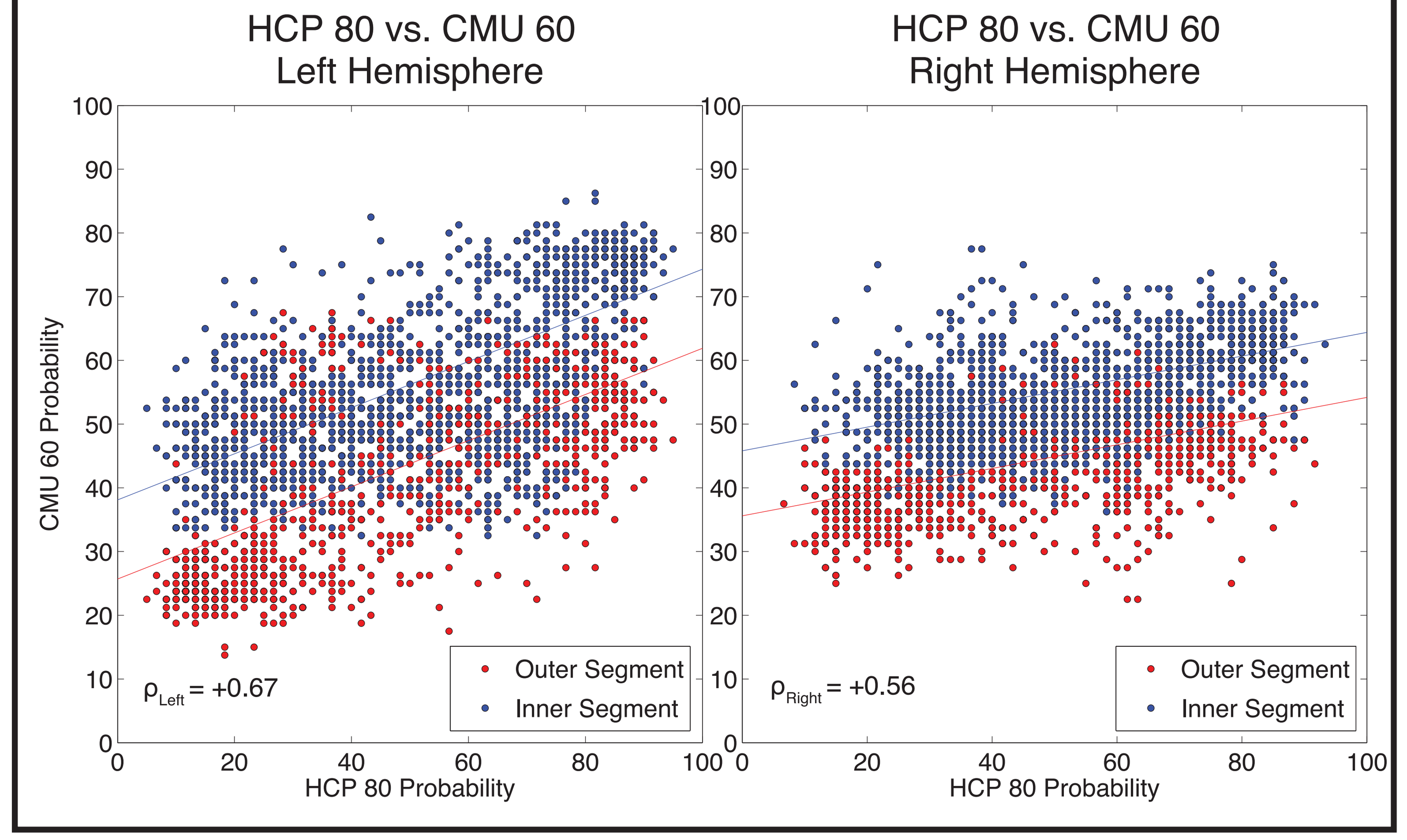
I. The number of fibers, quantitative anisotropy, and fiber angle distributions differ betwen the inner and outer segments.



II. Reliable probabilistic segementation of the GPe & GPi



III. Voxelwise probabilities are highly reliable and consistent across data sets.



Summary

- We observed significant differences in the structure of the spin distribution functions between the outer and inner segments of the pallidum, reflecting differences in the cellular composition of the pallidal nuclei.

- The diffusion signal in the GPi and the GPe exhibit reliable enough differences to distinguish these two nuclei using automatic clustering in two different datasets.

- The probabilistic maps are highly consistent across diffusion weighted imaging data sets that are acquired at different scanners and using different imaging sequences.

References

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