Structural variation in human auditory cortex gyrification revealed by data-driven curvature-based clustering

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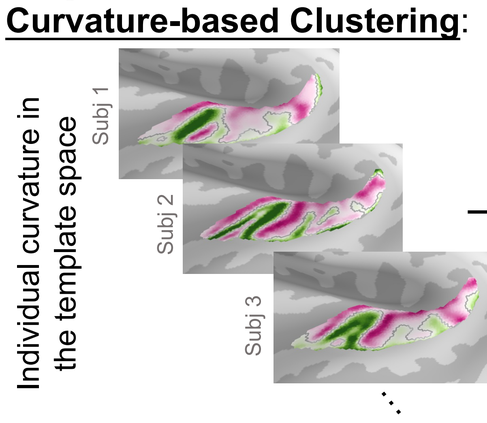
Summary

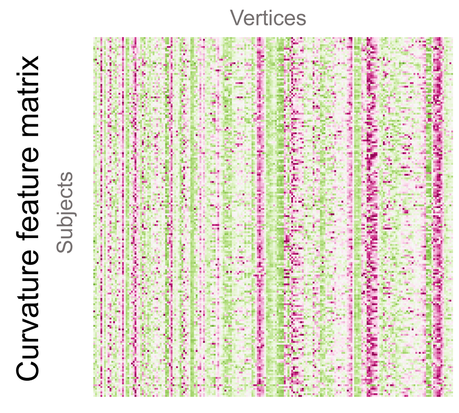
Heschl's gyrus (HG) has traditionally been described as having three distinct gyrification patterns[3]. Gyrification of planum temporale (PT), lying posterior to HG, is also highly variable but less well characterized[5]. Delineation of these folding patterns is typically based on manual inspection of brain volumes or surfaces. Here, we used an unsupervised data-driven clustering approach to characterize folding patterns of HG and PT. In contrast to the three classic categories, this approach suggested that superior temporal morphology was best characterized by five distinct gyrification patterns. We found distinct variations of the single HG morphotype and observed a previously undescribed curvature pattern consisting of a wider HG with a notch at the anterolateral end. These morphological variations are paralleled in the cortical microstructure variation.

Methods

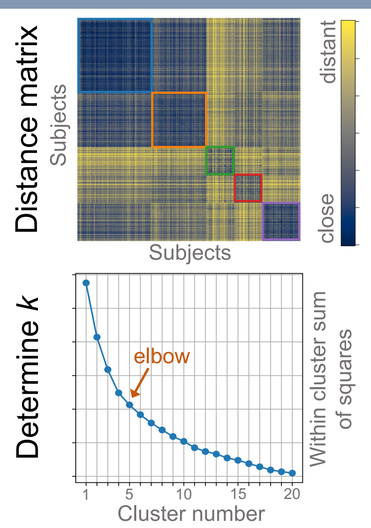
Participants: N = 1,065 adult participants with preprocessed structural images from Human Connectome Project Young Adults

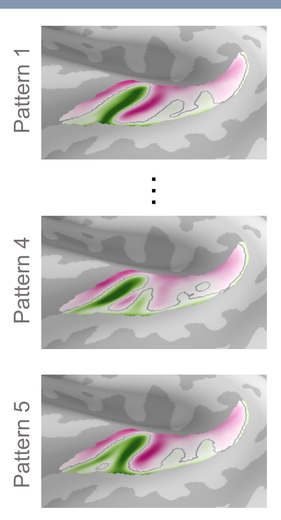
Curvature-based Clustering:





K-Means





Family Analysis

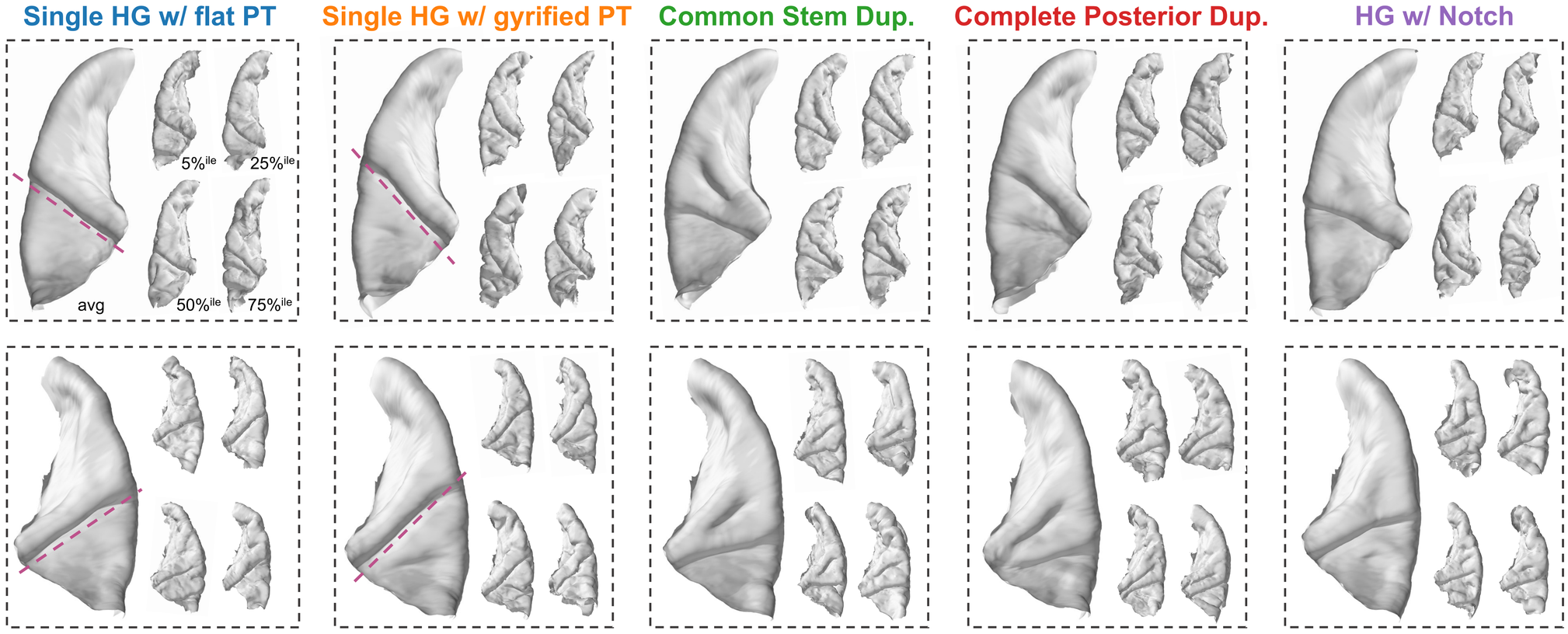
Same cluster fraction (SCF):

$$\frac{\#\ of\ pairs\ in\ the\ same\ cluster}{\#\ of\ total\ pairs}$$

Bootstrap null distribution:
Random cross-family pairs

make_average_subj to reconstruct template brains for each pattern; *mri_label2label* and *mris_anatomical_stats* to measure anatomical features in native space

Distinct and Novel Curvature Patterns Revealed by Data-driven Clustering



Example Subjects: Rank subjects based on their overall similarity to other subjects within the cluster, and select subjects at the 5th (top left), 25th (top right), 50th (bottom left), and 75th (bottom right) percentiles

Family Analysis

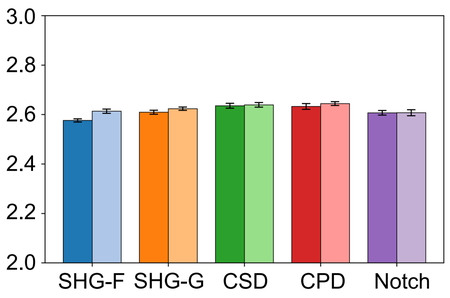
	Pairs	SCF	One-side *p*
MZ	147	0.30	0.034
DZ	80	0.35	0.012
FS	678	0.27	0.010
HS	44	0.16	0.908

	Pairs	SCF
M-D	12	0.25
M-S	4	0.75
M-DS	20	0.05
F-D	6	0
F-S	0	NA
F-DS	2	0

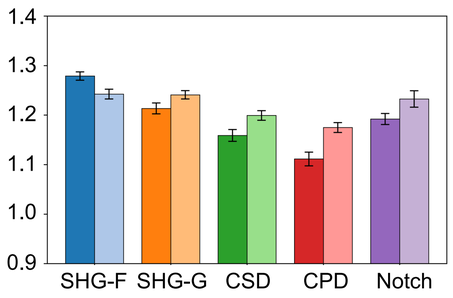
MZ = monozygotic; DZ = dizygotic; FS = full sibling; HS = half sibling (same mother or same father)

M-D = mother-daughter; M-S = mother-son; M-DS = mother-mixed (daughter and son); F-D = father-daughter; F-S = father-son; F-DS = father-mixed

Mean thickness



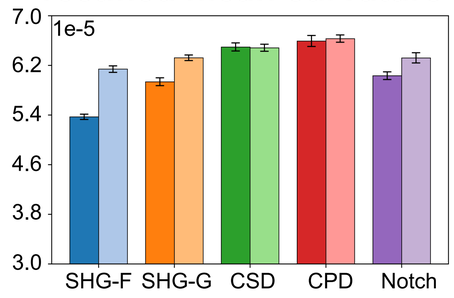
Scaled surface area



Surface area was computed in the native space and scaled by LH/RH fsaverage ROI area

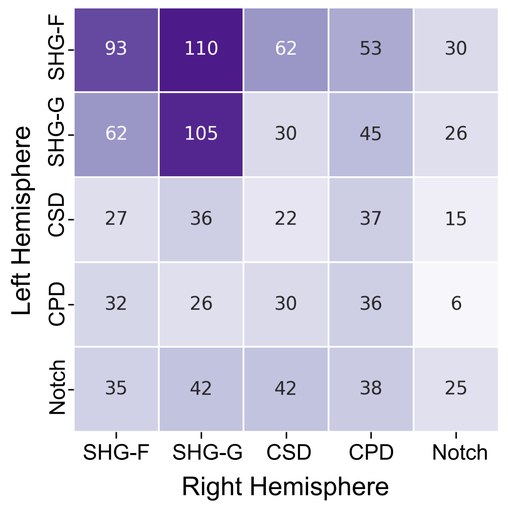
LH RH

Area weighted integrated rectified mean curvature

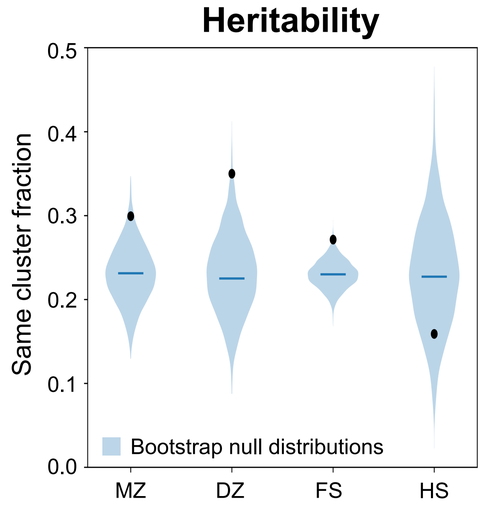


$$\frac{1}{Total\ Area}\sum(|curvature| \cdot Area)$$

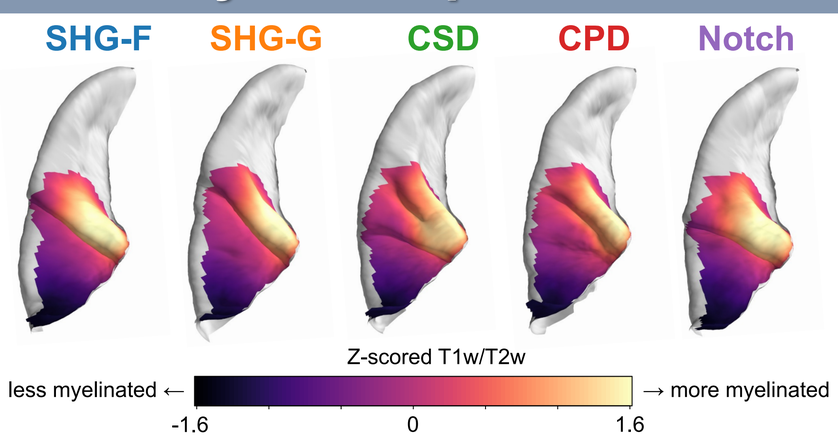
Distributions

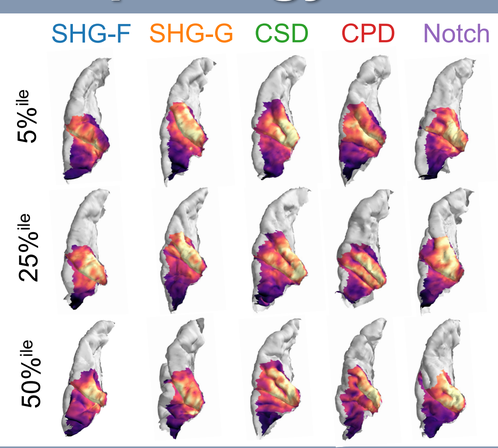


Heritability



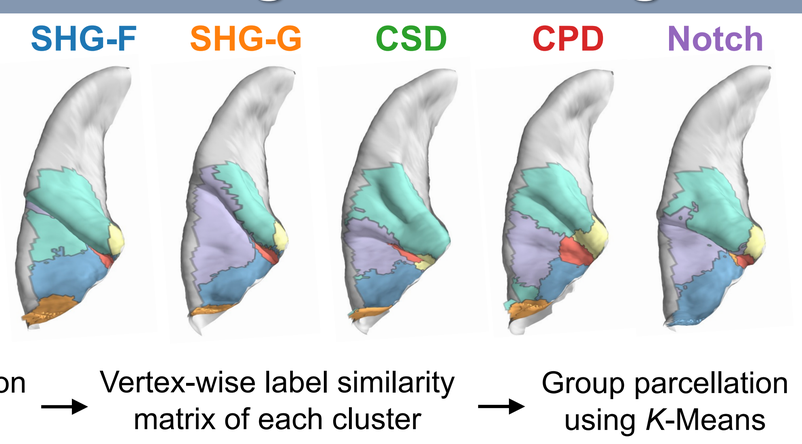
Myelin Maps Parallel the Morphology





Patterns of Resting State Subregions

Time series projected to surface → Pearson's r & Fisher's z for each pair of vertices in the ROI → Individual parcellation using *K*-Means → Vertex-wise label similarity matrix of each cluster → Group parcellation using *K*-Means



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References: [1] Akiki & Abdallah, (2019), *Sci. Rep*. [2] Kepinska et al., (2024), *Biorxiv*. [3] Marie et al., (2015), *Brain Struct Funct*. [4] Shimony et al., (2016), *NeuroImage*. [5] Tzourio-Mazoyer & Mazoyer, (2017), *Brain Struct Funct*.