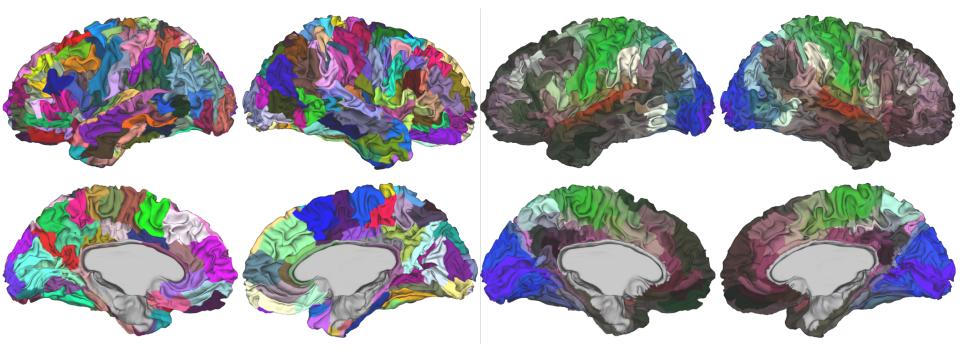
An updated MSM surface registration pipeline to bridge atlases across the BigBrain and FS / HCP worlds



Lindsay B. Lewis
BigBrain Workshop / HIBALL launch, June 26, 2020 (OHBM poster #1888)

In collaboration with:



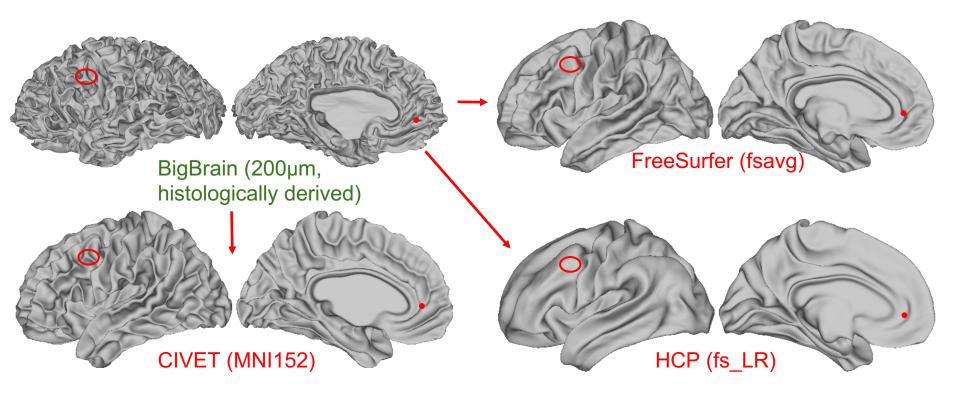


Claude Lepage Alan C. Evans

Human Connectome Project (HCP) team:
Timothy Coalson
Matt Glasser
David Van Essen

Question: where exactly does a given region on BigBrain surface correspond to on other reference average surfaces?

Goal: robust registration across pipelines and across resolutions



Several registration tools exist, but each has only been validated / parameterized within its own pipeline

☐ MSM is most flexible, most recent:



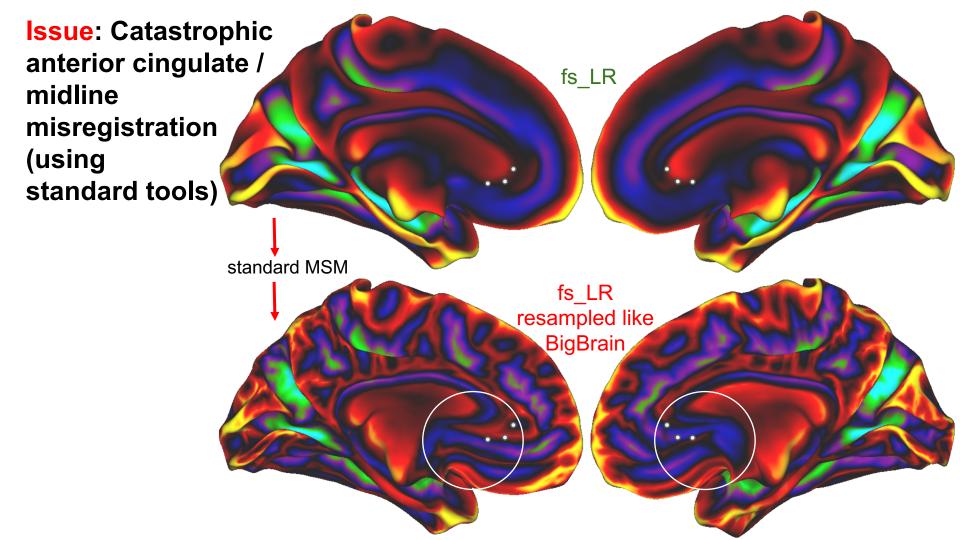
Neurolmage

Volume 167, 15 February 2018, Pages 453-465

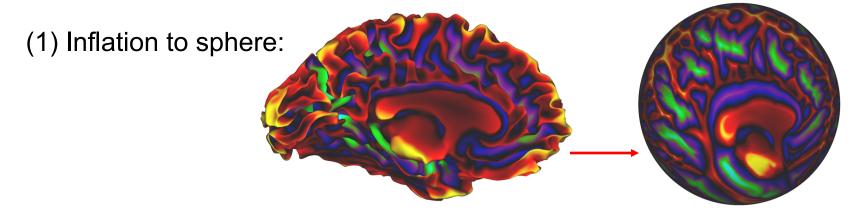


Multimodal surface matching with higher-order smoothness constraints

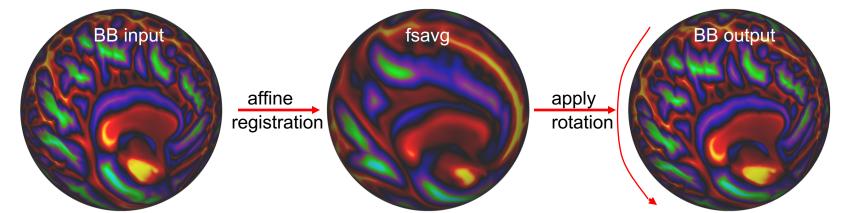
Emma C. Robinson a, g, h A M, Kara Garcia b, 1, Matthew F. Glasser e, d, 1, Zhengdao Chen e, Timothy S. Coalson e, Antonios Makropoulos a, Jelena Bozek f, Robert Wright h, Andreas Schuh a, Matthew Webster i, Jana Hutter g, Anthony Price g, Lucilio Cordero Grande g, Emer Hughes g, Nora Tusor g, Philip V. Bayly c, David C. Van Essen e, Stephen M. Smith i ... Daniel Rueckert a



Solution: Optimize pre-processing at 2 points:



(2) Affine rotation of sphere:



(1) Inflation to sphere: Re-tessellate BigBrain white surface with

OpenFlipper and 'borrow' its inflated sphere

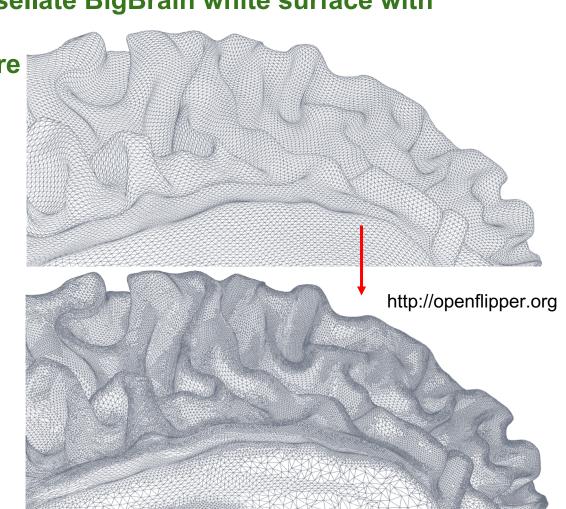
CIVET tessellation (200µm):

Equalized triangle area, subdivisions of the icosahedron

OpenFlipper 'adaptive remeshing':

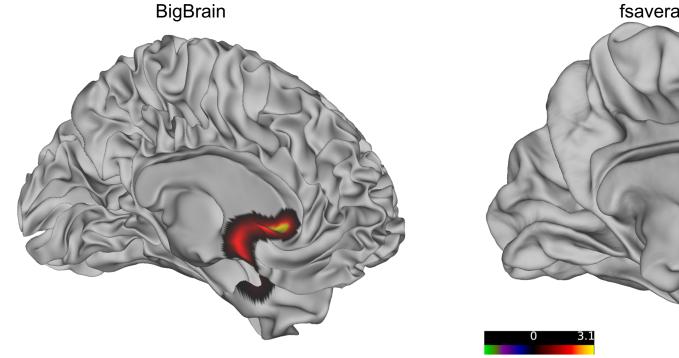
Greater vertex density at regions with greater curvature

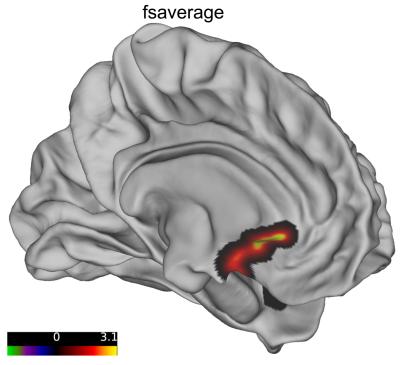
(inflates to sphere more flexibly)



(2) Affine rotation: use y/z coordinates along midline border as 'anchor'

'Anchor quadrant': Mask y coordinates for positive values only (anterior) and by negative z values (inferior), then blur 2mm





MSM multiscale (coarse-to-fine) approach

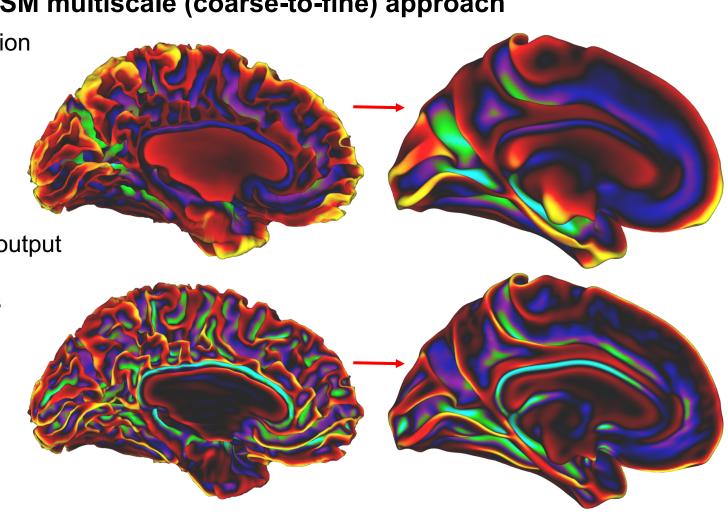
Stage #1: Affine rotation ('anchor quadrant')

Stage #2: MSMsulc (non-linear / discrete, sulcal depth maps)

(--trans initiates with output from previous stage,

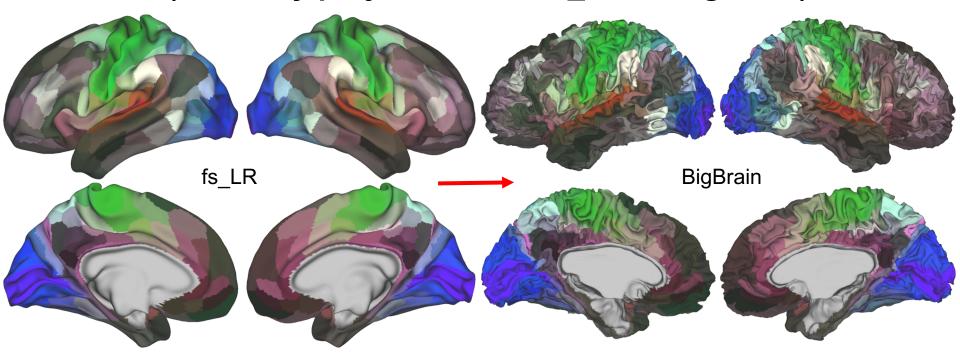
accounts for previous distortion)

Stage #3: MSMcurv (non-linear / discrete, curvature maps)

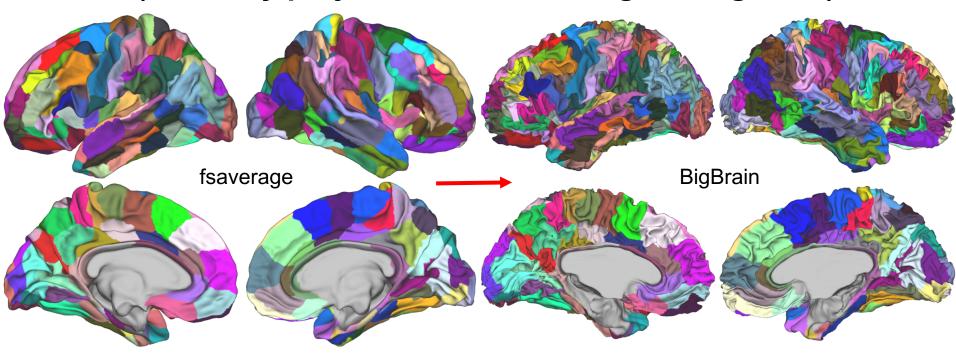


Output visualization: Atlases

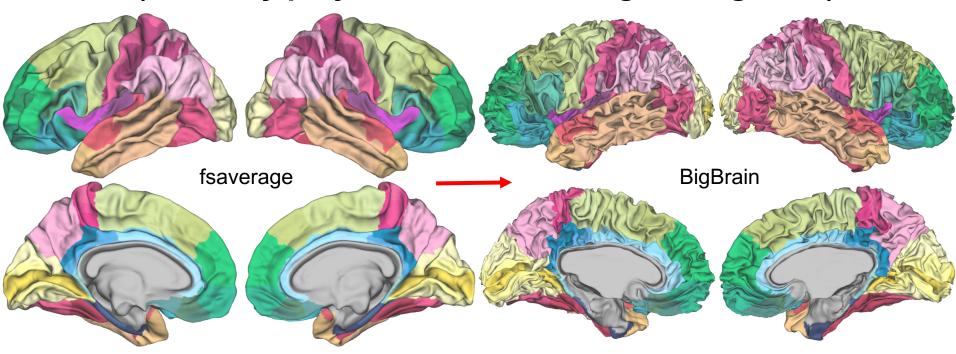
HCP MMP-1.0 atlas (Glasser et al. 2016) (inversely projected from fs_LR to BigBrain)



Brainnetome atlas (Fan et al. 2016) (inversely projected from fsaverage to BigBrain)

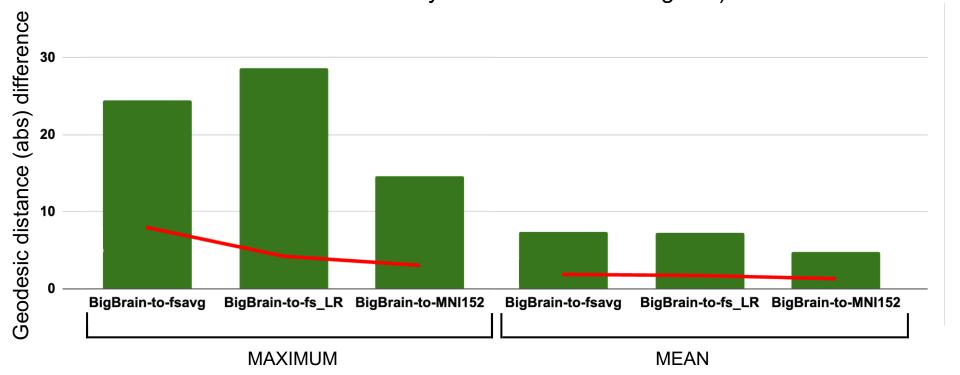


Von Economo atlas (Scholtens et al. 2018) (inversely projected from fsaverage to BigBrain)

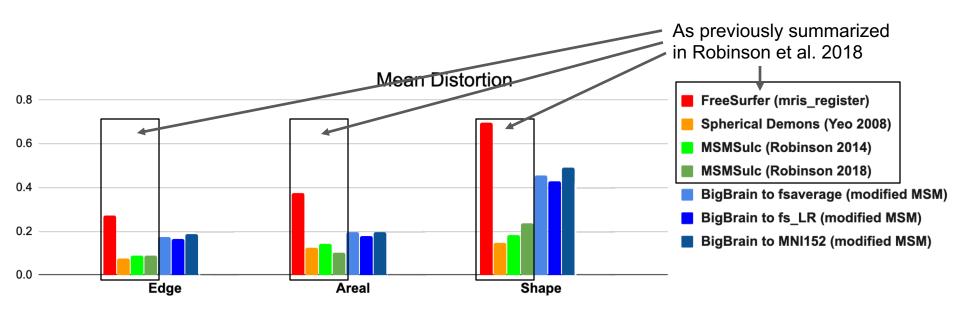


Landmarks analysis

'Accuracy benefit' > 'accuracy cost' in geodesic distance (improvements in regions that were badly misaligned are greater in extent than small accuracy sacrifices in other regions)



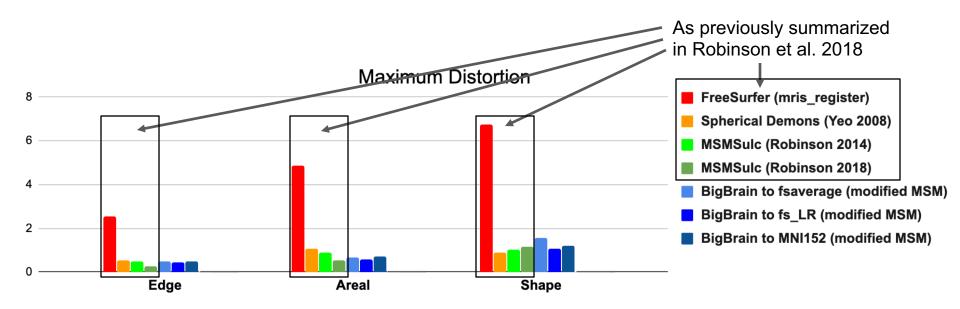
Mean distortion: slightly higher than MSM HCP, much lower than FS



FreeSurfer (*mris_register*) on HCP data (previously reported) = red MSM on HCP data (previously reported) = greens

BigBrain vs. reference surfs = blues

Maximum distortion: comparably (low) as MSM HCP, much lower than FS



FreeSurfer (*mris_register*) on HCP data (previously reported) = red MSM on HCP data (previously reported) = greens

BigBrain vs. reference surfs = blues

Conclusions

- ☐ BigBrain can now serve as an unprecedented cross-validation tool
- ☐ From FS/HCP to BigBrain: Macroscopic parcellation boundaries derived from *in vivo* imaging can be directly compared to cytoarchitectural properties
- ☐ From BigBrain to FS/HCP: Conversely, BigBrain's histological landmarks or cortical layers (Wagstyl et al. 2020) may be transposed back to fs LR and fsaverage

Thank you!

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