Individualised multimodal cortical parcellations in UK Biobank

Logan Z. J. Williams[1,2], Matthew F. Glasser[3,4], Fidel Alfaro-Almagro[5], Anderson M. Winkler[6], Simon Dahan[1], Yourong Guo[1,2], Abdulah Fawaz[1], Mohamed A. Suliman[1], Timothy S. Coalson[4], Sean P. Fitzgibbon[5], David C. Van Essen[4], Stephen M. Smith[5] & Emma C. Robinson[1,2]

[1] Department of Biomedical Engineering, School of BIomedical Engineering and Imaging Sciences, King's College London, London, SE1 7EH UK
[2] Centre for the Developing Brain, School of Biomedical Engineering and Imaging Sciences, King's College London, London, SE1 7EH, UK
[3] Department of Radiology, Washington University Medical School, Saint Louis, 63110, Missouri, USA
[4] Department of Neuroscience, Washington University Medical School, Saint Louis, 63110, Missouri, USA
[5] Wellcome Centre for Integrative Neuroimaging, Nuffield Department of Clinical Neurosciences, University of Oxford, Oxford, OX3 9DU, UK
[6] Department of Human Genetics, University of Texas Rio Grande Valley, Brownsville, 78520, Texas, USA

Motivation

- *HCP multimodal parcellation* delineates areas based on function, architecture, connectivity and topography
- *Individualised parcellations* were generated using fully-connected neural networks

Challenges

- Individualised HCP parcellations required *lots of data* per subject, and *multimodal cortical alignment*
- It is unknown if HCP neuroimaging approach *generalises to non-HCP studies*

This work

- UK Biobank (UKB) *population demographics* and *imaging protocols* differ markedly from HCP
- We use UKB brain imaging data to evaluate the generalisability of HCP-style imaging methods

1. Multimodal alignment (MSMAll) ▶▶

- Surface registration driven by T1w/T2w ratio map, 32 RSN spatial maps, and 8 visuotopic maps
- MSMAll-aligned cortical features from UKB were highly similar to HCP
- This improved alignment did not come at the cost of biologically implausible distortions

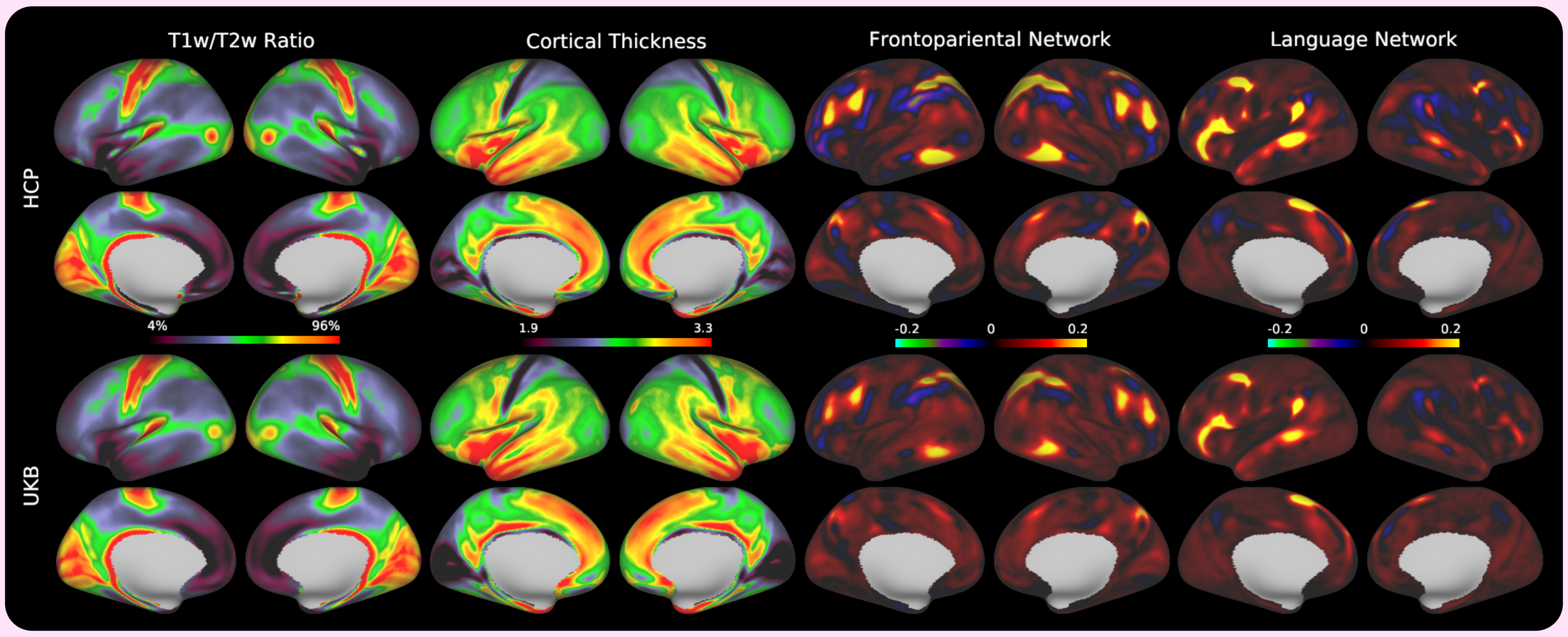

Figure 1.

Comparison of MSMAll-aligned group average (n = 998) T1w/T2w ratio, cortical thickness and two rs-fMRI spatial maps in HCP (top row) and UKB (bottom row). Correlations between HCP and UKB were r = 0.979 for 32 rs-fMRI spatial maps (range: 0.966 - 0.990), r = 0.959 for T1w/T2w ratio, r = 0.921 (range: 0.863 - 0.948) for 8 rs-fMRI visuotopic map, and r = 0.941 for cortical thickness.

2. Task fMRI validation ▶▶

- Task fMRI used to validate MSMAll (not used to drive registration)
- Both HCP and UKB acquired Hariri faces/shapes emotion task
- UKB data reprocessed to match HCP (no volumetric smoothing)
- MSMAll improved inter-subject overlap across all unique task contrasts for UKB

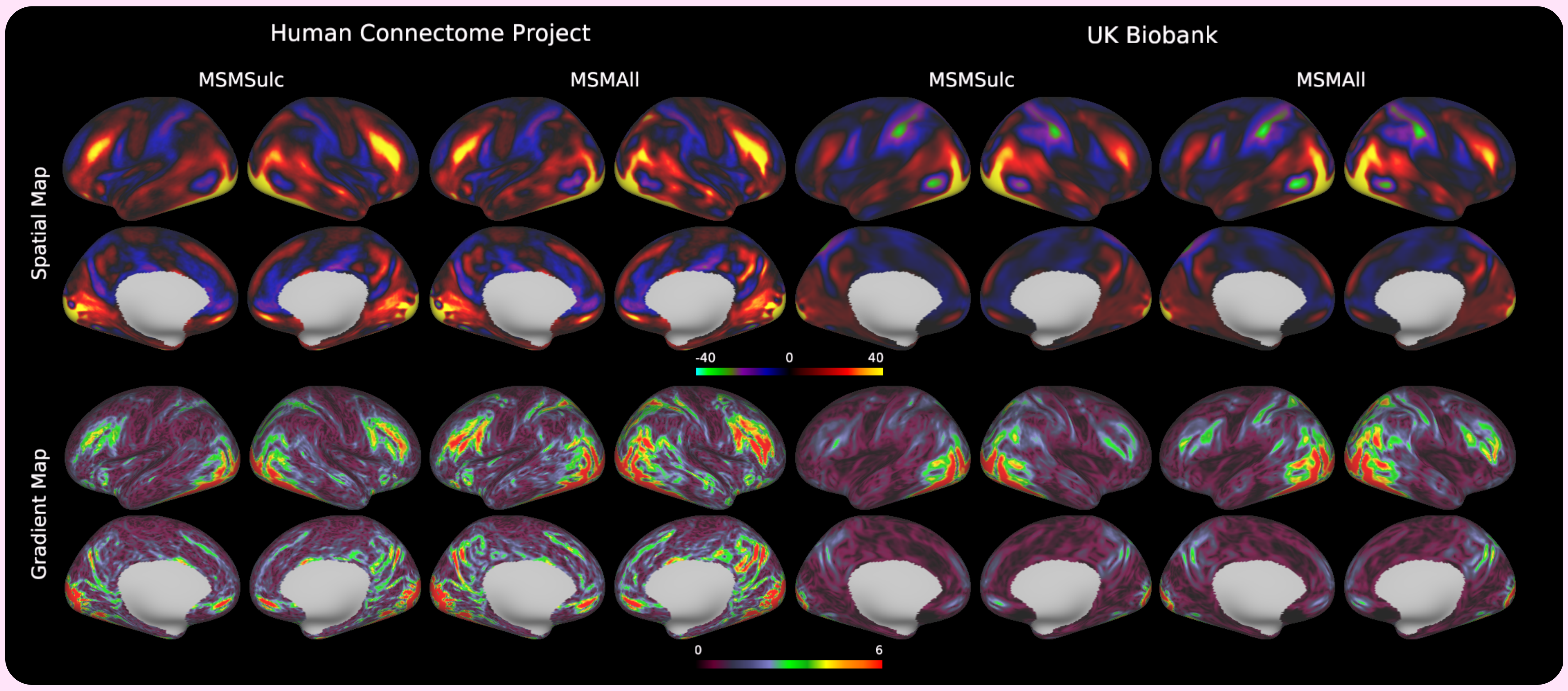

Figure 2.

Comparison of group average (n = 798) 'Faces - Shapes' Emotion contrast for MSMSulc and MSMAll aligned data in HCP (left) and UKB (right). The spatial gradient maps in the bottom row represent how sharply activity changes over the cortical surface. Improved alignment is represented as clusters of activation with higher spatial gradients.

3. Multimodal parcellation ▶▶

- Optimised fully-connected neural network generated individualised parcellation for 998 HCP subjects
- Individualised HCP labels used to generate parcellations for UKB
- Group average UKB and HCP parcellations very similar
- Average areal detection rates were 99% for both studies
- Parcellations capture subject-specific topography

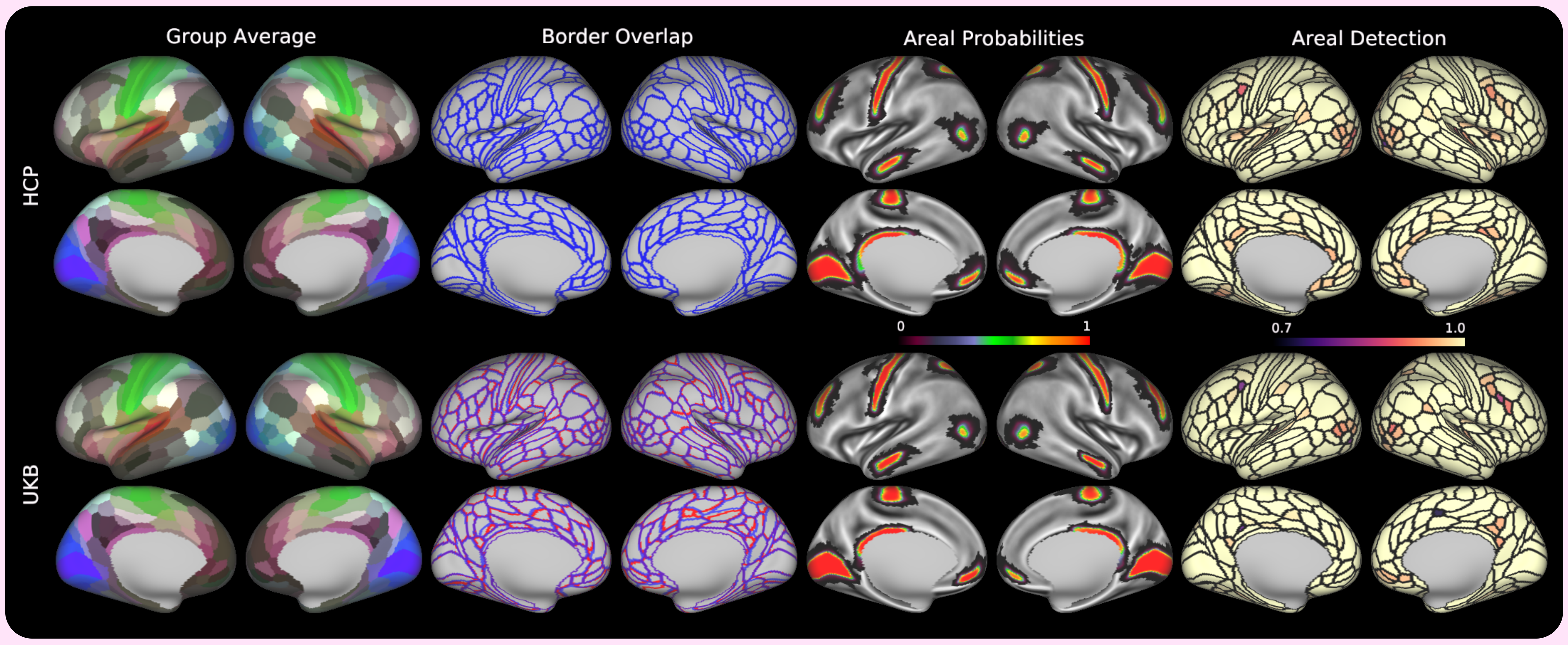

Figure 3.

Comparison of group average (n = 998) multimodal parcellation, border overlap, areal probabilities and areal detection for HCP (top row) and UKB (bottom row). Border overlap between HCP 998 (blue) and UKB 998 (red) is represented as purple. Areal probabilities represent the overlap of single subject areas at each vertex. Areal detecton represents the fraction of total subjects having a given area.

References

1. Glasser et al. (2016). *A multimodal parcellation of human cerebral cortex*
2. Robinson et al. (2014). *MSM: a new flexible framework for Multimodal Surface Matching*
3. Robinson et al. (2018). *Multimodal surface matching with higher-order smoothness constraints*
4. Coalson et al. (2018). *The impact of traditional neuroimaging methods on the spatial localization of cortical areas*
5. Fischl et al. (2008). *Cortical folding patterns and predicting cytoarchitecture*
6. Miller et al. (2016). *Multimodal population brain imaging in the UK Biobank prospective epidemiological study*
7. Glasser et al. (2013). *The Minimal Preprocessing Pipelines for the Human Connectome Project*
8. Alfaro-Almagro et al. (2018). *Image processing and Quality Control for the first 10,000 brain imaging datasets from UK Biobank*