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Advances in MSM surface registration to bridge data across the BigBrain and FS/HCP ecosystems

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Introduction

Structural MRI-derived population average cortical surfaces such as FreeSurfer's (FS) fsaverage 'fsavg' (Fischl 2012) and Human Connectome Project's (HCP) fs_LR (Van Essen et al., 2012) serve as reference frameworks for multimodal data integration.

The cortical surface extracted from the high-resolution 3D-reconstructed histological BigBrain model (Amunts et al., 2013, Lewis et al., 2014, Wagstyl et al., 2018) is also a notable reference space for increasing amounts of data.

Accurate surface registration between BigBrain and MRI-derived average surfaces is critical, not only for a wide range of functional applications, but also for comparison and cross-validation of the pipelines, themselves.

However, the BigBrain surface presents several challenges to existing registration tools designed for use with MRI and validated within a particular software ecosystem .

Recently, we introduced the first surface registration pipeline linking these reference surfaces (Lewis et al., 2019, 2020) via HCP's Multimodal Surface Matching (MSM) tool (Robinson et al., 2014, 2018). In 2021, our registration was included in BigBrainWarp (Paquola et al., 2021).

In the present work, we incorporate new tool developments in both the MNI and FS ecosystems to optimize our pre-processing, leading to improved alignment of folding-based landmarks, as well as reductions in maximum distortion.

Methods

Preprocessing:

1. input: CIVET-tessellated BigBrain white surface (2021 update: 163k vertices per hemisphere, medial cut excluding hippocampus)
2. volumetric transform from histological to HCP 'dedrift'space
3. use FS tool mris_remesh (new in v7.1) to re-tessellate white surface to 800,000 vertices per hemisphere
4. inflate FS-tessellated white surface to sphere with modified FS inflation tools
5. MNI tool surf_surf_interpolate (new output map function) to obtain vertex correspondence between 2 versions of white surface (original CIVET-tessellated 163k and FS re-tessellated 800k)
6. 'borrow'FS sphere at 163k using obtained vertex correspondence

MSM BigBrain to fsavg (then concatenate to fs_LR via HCP registration fsavg-to-fs_LR):

- Stage 1: Affine rotation. 2 landmarks: single vertex near anterior and posterior border of medial cut
- Multiscale approach (discrete / non-linear processing). Stage 2: Sulcal depth (global scale); Stage 3: Curvature (finer features)

–trans flag used across all stages (accounts for distortions from all previous stages)

- sampling grid and datagrid were 1 level higher than default

Analysis:

18 landmarks were manually defined on both BigBrain and fsavg. Geodesic distance (error) between the resampled and original landmarks was used to assess accuracy of the registration process.

Results

Our modified MSM pipeline yields improvements in alignment of folding-based landmarks relative to standard MSM and our previous versions (reduction of mean and maximum error, and elimination of outliers; Fig 1), as well as reductions in maximum distortion values.

Conclusions

Future work aims to compare BigBrain with atlases in fsavg or fs_LR space. Such comparisons [e.g., BigBrain cytoarchitecturally-defined areas to multi-modally defined areas from the HCP-MMP1.0 (Glasser et al., 2016)] will be critical for validating that the modified folding-based registration shown here achieves accurate alignment of cortical areas (as HCP-data MSMSulc registration was optimized for brain areal alignment based only on cortical folds when multi-modal information is not available).

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