Multi-Modal Parcellation of the Frontal Lobe

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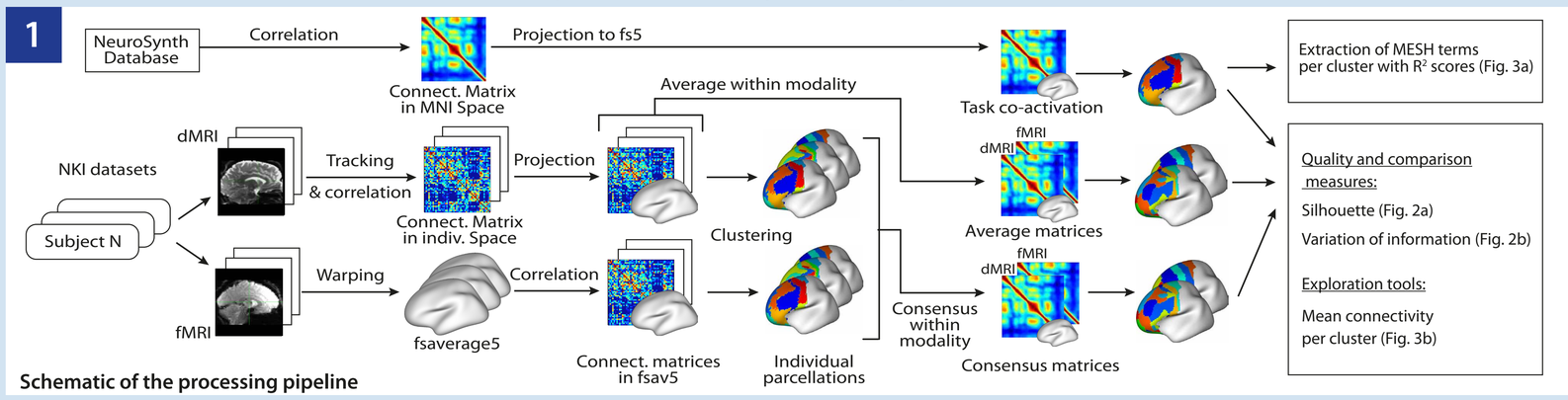
Introduction

The frontal lobe poses substantial challenges for establishing meaningful subdivisions. Nonetheless, the availability of several non-invasive large-scale datasets offers the possibility for multimodal description of the convergence of parcels. Structural connectivity, measured in-vivo in humans through diffusion-MRI (dMRI), characterizes the potential for information exchange between different regions, while functional (fMRI) connectivity, measured by correlated changes in the intrinsic BOLD activity has been demonstrated to be highly consistent with task coactivation literature. These modalities are related and partially complementary but not completely overlapping. While they have shown positive correlations [1] some recent studies have come to challenge long-held assumptions about the nature of brain connectivity [2]. Contrasting the information obtained from these three modalities is therefore an important step towards characterizing and deepening the understanding of brain organization within complex regions. Here we compare maps obtained within the frontal lobe from both dMRI tractography similarity matrices and correlation of fMRI time series from the NKI Enhanced Rockland Sample [3], as well as the coactivation maps derived from the NeuroSynth database [4].

Methods

- fMRI and dMRI (50 subjects) data from the NKI E. R. sample: structural (MPRAGE, TR=1900ms, 1mm voxel); three resting-state scans (BOLD EPI: TR=2500ms, 3mm voxel, 5' duration; TR=1400ms, 2mm voxel, 10' min; TR=645ns, 3mm voxel, 10') and diffusion (TR=2400ms, TE=85ms, Multi-band accel.=4, 137 directions, 2mm voxel, b=1500 s/mm^2, 5' duration).
- Resting-state fMRI datasets were aligned, bandpass-filtered, and motion-corrected with Nipype-mediated pipelines [5]. MNI-registered, non-smoothed rs-fMRI data was sampled to FreeSurfer's fsaverage5 surface template. r-values were Fisher's z-transformed and averaged across runs. Post-processing methods were adopted from Kelly et al [6].
- MRtrix was used to obtain spherical deconvolution based tractography from each voxel in the WM/GM interface to the whole WM as target area, then the similarity between all pairs of tracts was computed as non-centered correlation [7]. The resulting matrix was also projected to the fsaverage5 surface.
- Task-based fMRI meta-analytic data from NeuroSynth was used for the co-activation meta-analysis. Co-activation maps were extracted based on the correlation between the presence of activation at that vertex, and every other vertex of the brain [8] (https://github.com/r03ert0/cmtool).
- The individual matrices from all three modalities were clustered into distinct regions using k-means and spectral clustering algorithms from scikit-learn toolbox [9], as well as averaged matrices across subjects. Individual partitions for each cluster number solution were compiled across subjects using a consensus measure and then reclustered.

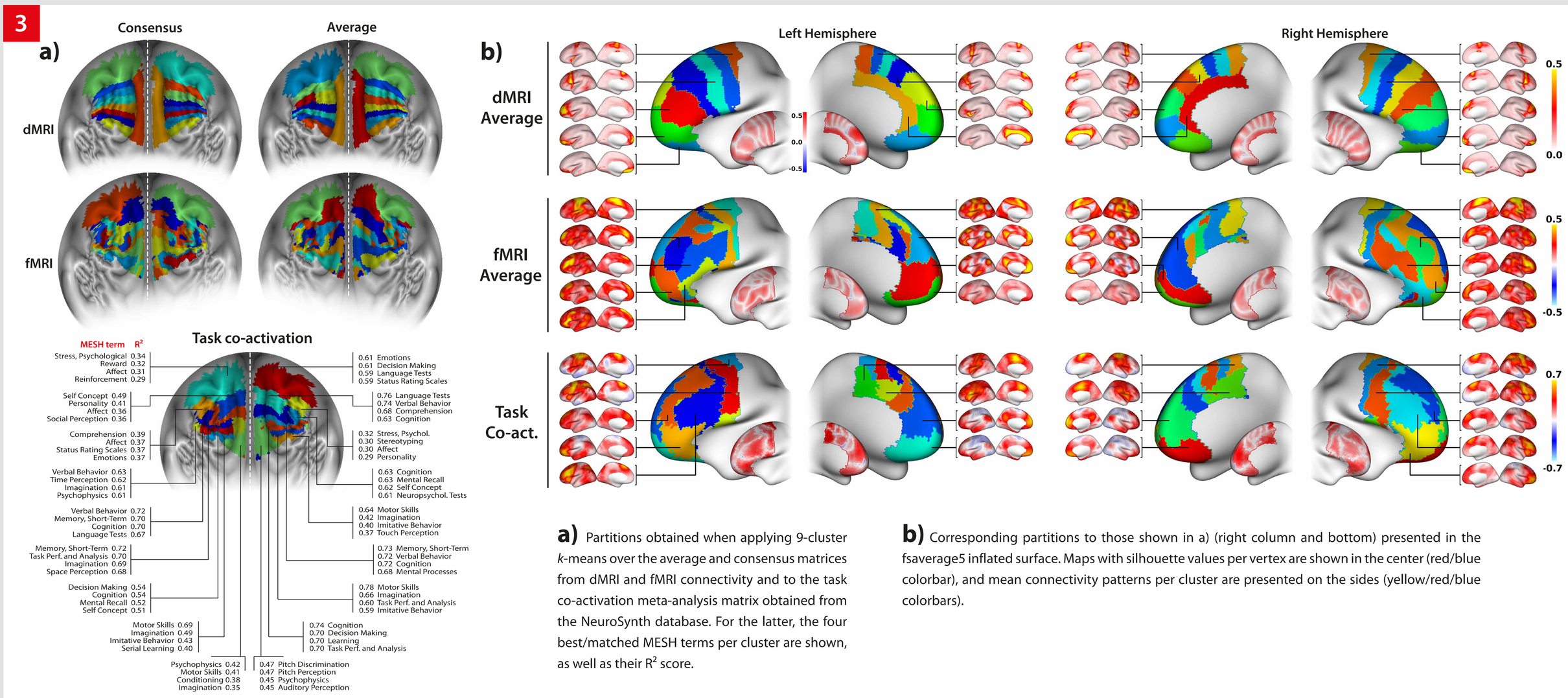
1



Schematic of the processing pipeline

Results

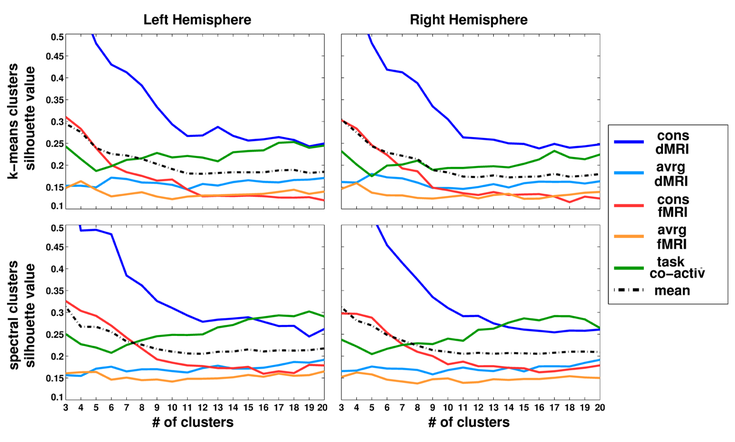
3



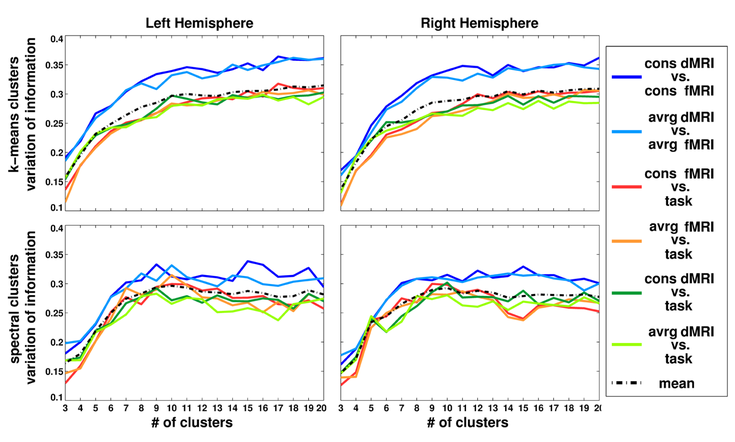
a) Partitions obtained when applying 9-cluster *k*-means over the average and consensus matrices from dMRI and fMRI connectivity and to the task co-activation meta-analysis matrix obtained from the NeuroSynth database. For the latter, the four best/matched MESH terms per cluster are shown, as well as their R^2 score.

b) Corresponding partitions to those shown in a) (right column and bottom) presented in the fsaverage5 inflated surface. Maps with silhouette values per vertex are shown in the center (red/blue colorbar), and mean connectivity patterns per cluster are presented on the sides (yellow/red/blue colorbars).

2



Silhouette values for *k*-means and spectral clustering solutions in the range of 3 to 20 clusters obtained from dMRI and rs-fMRI (from averaged and consensus matrices) and task co-activation data. Mean values across all graphs are also shown in dashed line.



Variation of information across modalities for *k*-means and spectral clustering solutions in the range of 3 to 20 clusters obtained from dMRI and rs-fMRI (from averaged and consensus matrices) and task co-activation data. Mean values across all graphs are also shown in dashed line.

Discussion

Clustered cortical parcellations offer a medium for comparing the different methods for characterizing the connectome. By integrating neuroimaging software via Nipype, we have written a modular pipeline used to cluster subregions of the frontal lobe. The pipeline allows us to explore various combinations of analytic and preprocessing strategies, and offers the possibility of flexible investigation of cortical parcellation across modalities and datasets.

References

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OHBM, 2014