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Dense meta-analytical connectivity mapping of the cerebral cortex

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Dense mapping of cortical connectivity at the voxel/vertex level can provide a more precise view of connectomic organization compared to the conventional approach of studying connectivity at the level of brain areas. This approach has been previously applied to resting-state functional connectivity (RSFC), providing important insights into the organization of cortical networks (Yeo et al., 2011) and boundaries (Gordon et al., 2016; Schaefer et al., 2018), as well as principal gradients of connectivity variation (Margulies et al., 2016). However, RSFC characterizes task-free, spontaneous functional connectivity, and it remains unclear to what extent the connectomic organization observed in the resting state generalizes to task-related conditions. Meta-analytical co-activation modeling (MACM) characterizes consistent task-based co-activations across published neuroimaging studies, and thereby provides a marker of task-related functional connectivity (Langner & Camilleri, 2021). While MACM has often been applied to specific regions of interest, a dense whole-cortex characterization of MACM at the voxel/vertex level is lacking.

Here, we used a GPU-based implementation of specific co-activation likelihood estimation to calculate dense MACM across the cerebral cortex. We create a dense MACM matrix for 26,459 gray matter voxels in MNI space (4-mm resolution) using the BrainMap dataset. Cortical seeds were mapped to the CIVET surface (76,910 vertices) for the subsequent analyses.

We quantified MACM strength as the overall meta-analytical co-activation rate, which was highest in frontal medial cortex, middle temporal gyrus, supplementary motor area, posterior cingulate and precuneus (Figure 1A). Next, we computed similarity of MACM patterns across all cortical vertices, resulting in the MACM$_{corr}$ matrix. Clustering analysis on MACM$_{corr}$ using K-means showed relatively stable solutions with 4, 6, 11, and 19 clusters (Figure 1C). We focused on the six-cluster solution (instability = 0.13, variance explained = 66.8%; Figure 1B), on par with the seven canonical RSFC networks (Yeo et al., 2011). There was a broad correspondence between the MACM and RSFC networks (Figure 1D), with some of the MACM networks aligning with single RSFC networks (e.g., N1 and N2 corresponding to the visual RSFC network), and some spanning multiple RSFC networks (e.g., N6 spanning limbic and default mode RSFC networks). Next, we applied principal component analysis on MACM$_{corr}$ and identified three principal axes that explained 79.5% of variance (Figure 1E,F). We found the first and second principal axes of MACM to be largely co-aligned with the first and second gradients of RSFC (Figure 1G).

Together, we provide a dense high-resolution characterization of cortical MACM. Based on clustering and principal component analysis, we found that task-related co-activation shows a macroscale organization that is broadly aligned with RSFC, but has additional specific characteristics. As the next phase of this project, we plan to extend our analyses to higher spatial resolution, directly compare and integrate dense MACM with dense RSFC, and generate multimodal boundary maps of sharp transitions in co-activation and connectivity patterns.

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