An Unbiased Bayesian Approach to Functional Connectomics Implicates Social-Communication Networks in Autism

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***Abstract*—We demonstrate that a hierarchical Bayesian analysis of whole-brain functional connectivity, as measured via resting-state fMRI (rsfMRI), supports the theory of impaired social cognition in Autism Spectrum Disorder (ASD). Our model captures multivariate dependencies between pairwise connections to infer both the region foci that are most affected by ASD and the corresponding network of functional abnormalities. We leverage the multi-site Autism Brain Imaging Data Exchange (ABIDE) and localize the disease foci to the temporal lobe and default mode network.**

I. Bayesian Analysis

Our model [1, 2] assumes that the connectivity differences induced by ASD can be explained by a set of K abnormal networks, where K is a user-specified parameter that controls the model complexity. Each network is characterized by impairments in a small subset of brain regions, or *foci*, which subsequently alter neural communication to the rest of the brain. The generative process consists of four probabilistic equations. The first equation defines a multinomial indicator vector that selects region hubs for Network 1 through Network K. The second equation specifies a latent tri-state functional template for the TDC population. Given the region labels and baseline template, the third equation defines a latent graph that combines the effects of each abnormal network. This induces differences in the observed rsfMRI data for the TDC and ASD groups, as specified by the final equation. We employ a variational Expectation-Maximization (EM) algorithm to estimate the latent posterior probability q_i of each region i and the model parameters from the observed data.

We analyze rsfMRI data of children and adolescents (7-19 years) from four ABIDE [3] institutions: the Yale Child Study Center, the Kennedy Krieger Institute, UCLA, and the University of Michigan. We used Freesurfer to segment the MPRAGE anatomical images into 86 cortical and subcortical regions. Standard functional connectivity preprocessing of the BOLD data was performed using FSL and MATLAB.

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II. Results

Fig. 1 illustrates the detected foci (posterior $q_i > 0.50$) and corresponding pathways for K=2. The first network localizes to the left middle temporal gyrus (q_i=0.97, p<0.001), the left posterior cingulate (q_i=1.00, p<0.01), the left supramarginal gyrus (q_i=1.00, p<0.01), and the right temporal pole (q_i=1.00, p<0.05). The abnormal pathways indicate a general reduction in long-range connectivity (blue lines) and an overall increase in short-range connectivity (magenta lines) in ASD. This global pattern has been well established in the autism literature. The second network consists of the left banks of the middle superior temporal sulcus (q_i=1.00, p<0.04), the right posterior superior temporal sulcus extending into inferior parietal lobule (q_i =0.86, p<0.08), and the right middle temporal gyrus (q_i=0.98, p<0.07). The corresponding functional pathways show reduced inter-hemispheric connectivity but largely increased intra-hemispheric connectivity. Automated decoding of these networks [4] implicates high-level concepts of *language*, *comprehension*, *social*, and *person* as the likely functional correlates.

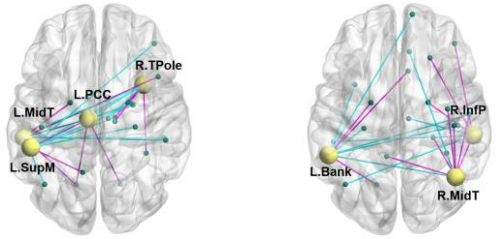

Figure 1. Estimated networks of abnormal connectivity for K=2 using the ABIDE dataset. The yellow nodes are disease foci (q_i>0.5). Blue lines indicate reduced functional connectivity and yellow lines denote increased functional connectivity in ASD patients.

References

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