The Brain Genomics Superstruct Project

R.L. Buckner1,2,3,4, M. Hollinshead1,2, A.J. Holmes1, D.G. Brohawn5, J.A. Fagerness5, T. O’Keefe1, V. Petrov1,3, G. Fariello1,3, L. Bakst1, S. Rubenstein1, T. Benner3, G. Sorensen3, B.R. Rosen3, J.L. Roffman4, J.W. Smoller1,5

Center for Brain Science, Harvard1, HHMF2, Radiology & Martinos Center, MGH/HMS3, Psychiatry, MGH/HMS4, Center for Human Genetic Research, MGH/HMS5

Introduction

We present our initial efforts to build a large, open repository of structural and functional neuroimaging data linked to genetic information and behavioral phenotypes. Our strategy was based on the observation that 3,000 to 5,000 individuals are enrolled each year in large-scale research studies involving matched MRI scanners across the Boston community. To take advantage of this existing research effort, we developed a rapid imaging protocol that could be tagged onto existing studies to obtain a common core acquisition protocol in 15 min or an extended imaging protocol with diffusion spectrum MRI (DSI) in 34 min. DNA was obtained from saliva. Extended behavioral prototypes including personality and cognitive assessments were obtained by asking participants to complete a series of web tests and surveys. We call the effort the superstruct project because superstruct means to build upon an existing infrastructure. Here the infrastructure is the existing neuroimaging research efforts already ongoing in the community. The initiative has captured data from over 3,000 participants to date. Example studies utilizing the collected data are illustrated.

Quantifying the Functional Connectome

Functional Connectivity Fingerprints

Functional Network Matrix

Brain Phenotypes Link to Behavioral Variation

Analysis of variation depends critically on the reliability of the estimates. Because subjects were enrolled from many studies, occasionally the same individual appeared in our sample more than once. This provides an opportunity to assess reliability under the same procedures used for acquisition of the full sample. Example analyses of structure (left, r = 0.98) and functional connectivity (middle, r = 0.46) reliability are illustrated. Targeted genotyping was also run on the independent saliva samples collected across sessions (right). Columns are individual SNPs. Rows are test-retest pairs where green = concordant, yellow = red, red = discordant.

References and Links


