**The Human Connectome Project**

Bruce Rosen², Van J. Wedeen², John D. Van Horn¹, Bruce Fischl², Randy L. Buckner², Lawrence Wald³, Matti Hamalainen², Steven Stufflebeam², Joshua Roffman¹, David W. Shattuck¹, Paul M. Thompson¹, Roger P. Woods¹, Nelson Freimer³, Robert Bilder³, and Arthur W. Toga¹

¹Laboratory of Neuro Imaging (LONI), Department of Neurology, UCLA, Los Angeles, CA 90025; ²Athinoula A. Martinos Center for Biomedical Imaging, MGH, Harvard Medical School, Boston, MA; ³Cognitive Neuroscience Laboratory, Department of Psychology, Harvard University, Cambridge, MA; 4Jane & Jerry Seidman Institute for Neuroscience and Human Behavior, UCLA, Los Angeles, CA 90025; 5Center for Neurobehavioral Genetics, UCLA, Los Angeles, CA 90025

---

**Introduction**

Mapping of the human connectome offers a unique opportunity to understand the complexity of neural connectivity (Sporns et al., 2005, Wedeen et al., 2008, Hagmann et al., 2007). The Human Connectome Project (HCP) is a project to construct a map of the complete structural and functional neural connections in vivo within and across individuals. The HCP represents the first large-scale attempt to collect and share data of a scope and detail sufficient to begin to address fundamental questions about human connectional anatomy, inter-regional communication, and their variations. Via a close collaboration between MGH and UCLA, this portion of the overall HCP is being developed to employ advanced neuroimaging methods, and to construct an extensive informatics algorithms infrastructure to analyze these data, derive detailed connectivity models capable of also accommodating phenotypic and genotypic data, building upon existing multidisciplinary and collaborative efforts currently underway.

**Methods**

The HCP is leveraging key scientific domains that together yield a steady release of increasingly detailed connectomics data and tools. First, we have begun collecting data for the release of a very large, existing connectomic, behavioral and genomic dataset, including connectivity data from MZ/DZ twin pairs, to encourage broad participation in the HCP by the larger research community. These rich data will also allow us to quantify genetic (Chiang et al., 2009) and behavioral variation of white matter fiber pathways and functional correlations for analysis by the entire community, and help define an optimized methodology for collection of a definitive connectome dataset using diffusion spectrum imaging (DSI, V. J. Wedeen, 2005). Concurrently, we are refining and optimizing the spatial and functional resolution of our connectome neuroimaging techniques, to enhance acquisition of still further optimized HCP data, to be shared with the community as the data are acquired. This necessitates deployment of the next generation of MRI scan technology, specifically built to extend the limits of DSI. Additionally, our connectome efforts include the acquisition of high resolution neuroimaging data in a small subset of ex vivo whole brain specimens, as well as detailed chemo- and cytoarchitectonic analysis and planar polarimetry of these specimens. These datasets will allow us and others to examine correlations between cytoarchitecture and the connectome (Burgel et al., 2006), as well as help validate in vivo results. All the while, we will continuously build and refine vital infrastructure to support the analysis, archiving, and broad-scale dissemination of HCP data and informatics tools.

---

**Conclusions**

This project is presently working to achieve the following goals: 1) optimize advanced imaging technologies and computational methods to map the in vivo human connectome using DSI; 2) validate these data against those collected at other HCP sites (Washington University in St. Louis and the University of Minnesota); 3) through joint effort between UCLA and MGH, construct sophisticated software tools for high-throughput connectomics analysis; 5) develop and disseminate data acquisition and analysis, educational, and training outreach materials.

---

**Results**

Through this comprehensive white matter and functional connectivity mapping project – using next generation neuroimaging technologies – we will provide the neuroscience research community with novel data and capabilities for measuring connectivity that will significantly enhance our understanding of the neuroanatomical and functional connectedness of the human brain.

---

**References**


