# State of the Art in Hardware, Acquisition & Analysis for In-Vivo Connectivity

Lawrence L. Wald[1]

[1]*A.A. Martinos Center for Biomedical Imaging, Massachusetts General Hospital Dept. of Radiology*
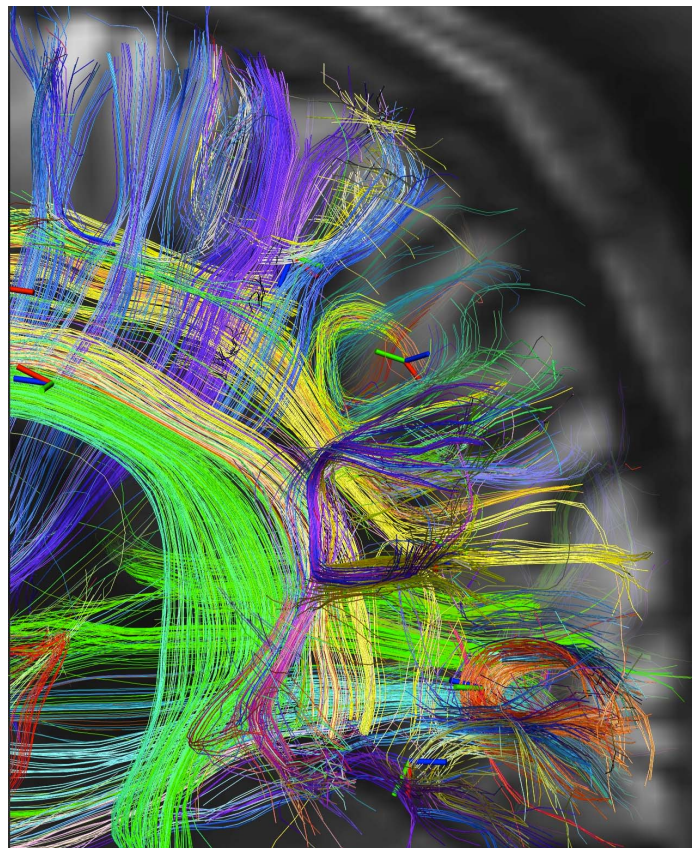*Harvard Medical School, Boston MA, USA.*

Perhaps more than any other "-omics" endeavor, the accuracy and level of detail obtained from mapping the major connection pathways in the living human brain will depend on the capabilities of the imaging technology used. The current tools are remarkable; for example allowing the formation of an "image" of the water diffusion probability distribution in regions of complex crossing fibers at each of half a million voxels in the brain. Nonetheless our ability to map the complex organization of connection pathways *in vivo* is acquisition limited. The problem is one of sensitivity, image resolution, and also resolution in encoding the diffusion probability distribution for diffusion tractography.

The goal of our work in the MGH-UCLA Human Connectome Project is two-fold; optimize the acquisition sequence over the wide and non-orthogonal parameter space of the acquisition methods, and also to fundamentally increase the breadth of this space by optimizing the hardware of the MRI scanner specifically for the connectome problem. We have therefore examined the MR scanner architecture and developed a scanner from the ground up, optimized for diffusion structural connectivity measurements. By increasing the gradient strength 7 fold with a gradient coil and novel quadrature drive geometry to achieve a whole body sized gradient capable of sustained, high duty-cycle imaging at 300mT/m (30G/cm), we allow high diffusion contrast imaging with substantially lower loss to T2 decay as well are reduced "blurring" of the resultant map of the water Probability Distribution function (PDF) by shortening diffusion times. In addition to beneficial effects on diffusion contrast through TE and diffusion time, the gradients also presented many imaging challenges such as strong concomitant gradient terms and eddy currents.

The project also focused on improving the detection coils (via a 64 channel brain array) and the efficiency of the diffusion acquisition sequence thorough the introduction of Simultaneous Multi-Slice (SMS) acquisitions using a blipped CAIPIRIHINA approach to reduce the g-factor to acceptable levels. The latter is important since previous attempts at simultaneous slice acquisition had either g-factors that were too high for diffusion applications or image blurring or readout lengthening issues. The net result is nearly a factor of 10 improvement in Contrast-to-Noise ratio in high b-value diffusion imaging which is beginning to provide new levels of detail to the connectome measurement as well as allow the exploration of white-matter microstructure through methods such as AxCaliber, previously accessible only in samples and animal models.

In summary, these tools have provided rich engineering challenges and are found to be enabling technology for improved structural connectomics with MRI.



Detail from a 515 direction DSI scan, b=15,000s/mm$^{2,}$ 1.5mm spatial resolution scan, acquired on the connectome scanner.