

# Can we get around the crossing fiber problem by increasing resolution?

Kurt Schilling, Vaibhav Janve, Yurui Gao, Iwona Stepniewska, Bennett A Landman, Adam W Anderson  
Vanderbilt University Institute of Imaging Science, Vanderbilt University, Nashville, TN

**PURPOSE** It is now widely recognized that voxels with crossing fibers and complex configurations present a challenge for diffusion MRI (dMRI) reconstruction and fiber tracking algorithms. This “crossing fiber” problem has been estimated to affect anywhere from 30% [1] to 90% [2] of white matter (WM) voxels, and it is generally assumed that increasing the spatial resolution as much as possible will minimize the number of voxels containing multiple fiber populations. Here, using both dMRI and histology from the same brain, we investigate the prevalence of this crossing fiber problem across a range of spatial resolutions.

**METHODS** dMRI: an ex vivo macaque hemisphere was scanned on a 9.4T Agilent scanner (b-value 6,000 s/mm<sup>2</sup>; 101 gradient directions) at isotropic resolutions ranging from 800um to 300um, in increments of 100um. Crossing fibers were detected following [2], using constrained spherical deconvolution [3]. Histology: 16 histological sections were stained using Gallyas myelin stain and imaged on a Leica Brightfield microscope at 0.5um/pixel. Structure tensor (ST) analysis [4] was used to extract orientation estimates for every pixel in the image. The image was then downsampled to resolutions ranging from 32um to 1024um, and the FOD was derived for each downsampled block. FOD's were fit to single and mixture vonMises distributions to determine the presence of crossing fibers.

**RESULTS** Figure 1 shows the results of ST analysis in a region with in-plane fiber crossings. We find that, in both MRI and histology, the *percent of voxels with crossing fibers actually increases as we increase the resolution*. The middle and bottom rows highlight “single” fiber regions in red and “crossing” fibers as green, and qualitatively show that many regions with a “single” fiber population at a coarse resolution exhibit crossing patterns when processed at a finer resolution. This pattern was observed across the whole brain, in both MRI and histology, and in both gray and white matter. An analysis of the crossing angle in histology shows that the fibers tend to cross at more acute angles in the higher resolution datasets.

**DISCUSSION** The problem of crossing fibers appears to be a fundamental limitation associated with the anatomical geometry, rather than a technical problem that can be overcome with higher fields, stronger gradients, and technological advances that may increase spatial resolution. This increase in crossing fibers at higher resolution is likely a result of a decrease in partial volume effects between bundles that share similar, but not exactly the same, orientations. These complex configurations also take place in regions typically assumed to contain single fiber populations (i.e. corpus callosum), where heterogeneous fiber orientations are apparent in histological sections.

**CONCLUSION** Because voxels with complex fiber configurations will *always* exist in datasets, even at resolutions far beyond current dMRI capabilities, it is critical to focus on tissue models for describing the fiber geometry in voxels, rather than focus on pushing resolution (and sacrificing SNR) where gains in fiber reconstruction and fiber tracking will be minimal.

**REFERENCES** 1. Behrens, T. Neuroimage, 2007. 2. Jeurissen, B. Hum Brain Mapp, 2013. 3. Tournier, JD. Neuroimage, 2008. 4. Budde, MD, Frank, JA. Neuroimage, 2012.

