**Comparison of two tractography approaches in healthy adults**

Yuri F. Ribeiro, Richard Frayne, and Adrian Tsang

Instituto de Sistemas Elétricos e Energia, Universidade Federal de Itajubá, Itajubá, MG, Brasil; Departments of Radiology and Clinical Neuroscience, Hotchkiss Brain Institute, University of Calgary, Calgary, Alberta, Canada; and Seaman Family MR Research Centre, Foothills Medical Centre, Calgary, Alberta, Canada

**Introduction:** Tractography is a 3D-modelling technique that uses diffusion tensor imaging (DTI) data to visually represent white matter (WM) fiber tracts in the brain. A common approach uses the tensor model to estimate fiber orientation on a voxel-by-voxel basis to delineate WM tracts.[1] This approach has been widely used in studies to investigate WM changes in disease and normal aging. However, it has been shown that the tensor model fails to correctly delineate WM tracts in voxels with multiple fiber orientations that accounts for 90% of WM voxels.[2] Constrained spherical deconvolution (CSD) is an approach proposed to mitigate the limitation of the tensor model using fiber orientation distribution in each voxel for WM tract delineation.[2,3] The objective of this study is to compare metrics that infer WM microstructure derived from both tensor and CSD methods in healthy subjects over the adult lifespan.

**Materials and Methods:** DTI data from 216 healthy participants (18 to 87 years) were collected as part of the Calgary Normative Study on a 3-T scanner (Discovery 750, General Electric). Raw diffusion images were corrected for subject motion and eddy-current-induced distortions. Four commonly used DTI data metrics: fractional anisotropy (FA), mean diffusivity (MD), axial diffusivity (AD) and radial diffusivity (RD) were obtained. Tractograms also were generated to visualize WM tracts from tensor model and CSD methods (MRTrix, [http://www.mrtrix.org](http://www.mrtrix.org)) [3]) using seed regions defined by seven template-defined resting state networks (RSNs).[4] Statistical analysis (SPSS Statistics, IBM) were conducted using paired *t*-test and Pearson correlation as appropriate.

|  |
| --- |
|  |
| *Fig.1: WM tracts depicted from DTI (left) and CSD (right) methods using a seed region in a representative subject.* |

|  |
| --- |
| *Table 1: Pearson correlation versus age in WM tracts associated with the default mode resting state network* |
| **DTI metric** | **tensor** | **CSD** |
| FA | -0.47 (*p*<0.001) | -0.39 (*p*=0.001) |
| RD, mm2 s-1 | 0.59 (*p*<0.001) | 0.73 (*p*<0.001) |
| AD, mm2 s-1 | 0.44 (*p*<0.001) | 0.69 (*p*<0.001) |
| MD, mm2 s-1 | 0.56 (*p*<0.001) | 0.73 (*p*<0.001) |

**Results:** The CSD method allowed visualization of more WM tracts compared to the tensor model and better delineated WM in voxels with crossing fibers, as expected (Fig. 1). Mean MD, AD and RD of WM tracts associated in each RSN were significantly (*i.e.*, *p<0.05*) higher, while mean FA was significantly lower, for CSD over the tensor model. Mean MD, AD and RD were positively correlated while mean FA was negatively correlated with age in all RSNs for both methods (Table 1).

**Discussion:** Our results agree with a recent study that compared metrics derived from tensor model and CSD methods in chronic stroke patients.[5] In addition, we demonstrated significant correlation between MD, AD, RD, and FA with age in most RSNs for both methods. At present, the tensor model is the most widely used tractography method, however, it has been shown to misrepresent the actual WM anatomy in certain brain regions compared to the CSD method.[2] Previous normal aging studies may have underestimated WM changes if they based their findings on the tensor model.

**Conclusion:** CSD method yields significantly different results than the tensor model and appears to provide more reliable result that better reflect anatomy and inferences about WM in normal aging.

**References:** [1] O’Donnell LJ, *et al*., *Neurosurg Clin N Am* **22**: 185-196, 2011; [2] Farquharson S, *et al*., *J Neurosurg* **118**: 1367-1377, 2013; [3] Tournier J-D, *et al*., *Int J Imaging Syst Technol*. **22**: 53-66, 2012; [4] Yeo BT, *et al*., *J Neurophysiol* **106**: 1125-1165, 2011; [5] Auriat AM, *et al*., *NeuroImage Clin* **7**: 771-781, 2015.