Different diffusion schemes directly impacts the measured diffusion properties and tractography

[1,4]Ivanei Bramati; [1,2,4]Diego Szczupak, [1]Marina Monteiro, [1]Fernanda Meireles, [1,4]Rodrigo Basilio, [1]Rafael Chaves, [3,4]Ryan Dean, [1,4]Fernanda Tovar-Moll

[1]D'Or Institute for Research and Education, Image Processing Laboratory; [2]University of Pittsburgh, Neurobiology Department; [3]The University of Queensland, Queensland Brain Institute; [4]IRC5

Introduction

In a world where the imaging community is working to combine data pools, the comparability of different sequences is a challenge to be overcome.

Objective

Our objective is to understand how different diffusion schemes and resolutions can impact the dMRI (diffusion magnetic resonance imaging) metrics and the tractography of individual bundles in normal and CCD (corpus callosum dysgenesis) subjects, commonly used to answer biological questions related to white matter.

Methods

Diffusion-weighted images of 12 control subjects and 8 CCD patients were acquired in a SIEMENS PRISMA 3T Scanner with four different diffusion schemes (HARDI, MULTISHELL, DSI, and HCP). We measured the raw CNR, FA, MD and dispersion of each scheme in three different anatomical ROIs: corpus callosum, corona radiata, and center semi-ovale, to show the contribution of different diffusion schemes to dMRI metrics that are used to infer important biological features as white matter integrity.

Results

The diffusion properties of all ROIs are affected by the diffusion scheme. This effect does not seem to be linked with a particular brain region and is solely the effect of the diffusion scheme. Our data clearly shows that, although multiple sequences can resolve crossing fibers and reveal the principal fiber orientation per voxel, these sequences do not give the same dMRI properties values, making a comparison of different diffusion schemes a bigger challenge than previously thought. Furthermore, the tractography data from these sequences also reveal different fiber bundles, meaning that different sequences will affect the tractography output.

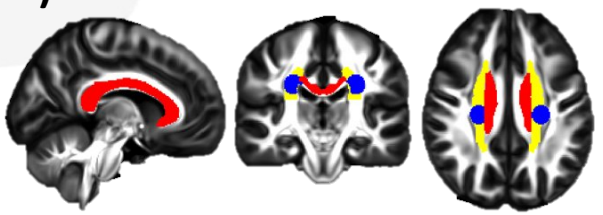
Conclusion

Our data show that the diffusion scheme directly impacts the diffusion properties and tractography in healthy controls and CCD patients. We are confident that the comparison of dMRI metrics with different diffusion schemes could lead to biased and false results. Therefore, combining data from different centers and protocols is a topic that deserves a great deal of attention.

References

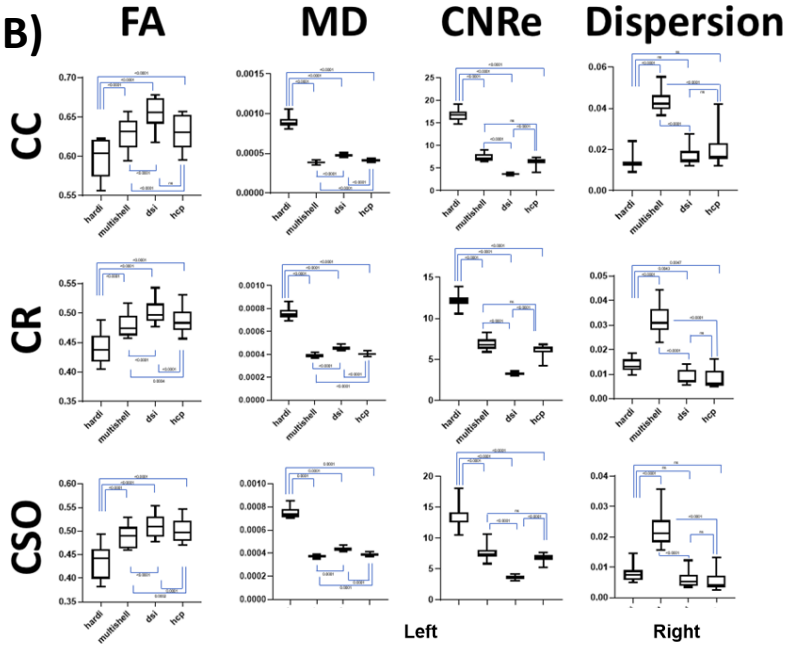
Andersson et al. -NeuroImage 125:1063-1078; Andersson et al.-NeuroImage 20:870-888; Andersson et al. -NeuroImage 141:556-572; Andersson et al. -NeuroImage 152:450-466; Andersson et al. -NeuroImage 171:277-295; Bastiani et al. -NeuroImage 184:801-812

A)

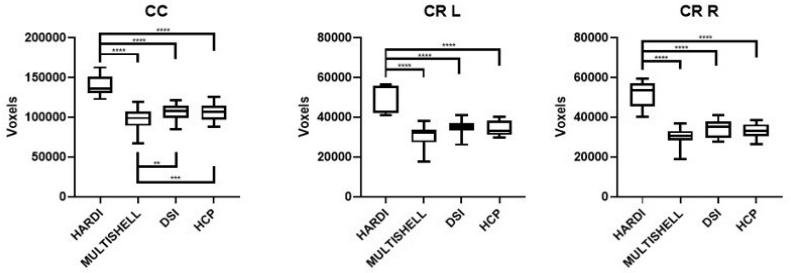


A) Selected ROIs: corpus callosum (red), corona radiata (yellow), and center semi-ovale (blue); **B)** The diffusion properties of all ROIs are affected by the diffusion scheme. This effect does not seem to be linked with a particular brain region and is solely the effect of the diffusion scheme. **C)** Our data shows, although multiple sequences can resolve crossing fibers and reveal the principal fiber orientation per voxel, these sequences do not give the same dMRI properties values; **D)** In CCD subjects, the tractography data from these sequences also reveal different volume (voxels) output from fiber bundles, meaning that different sequences will affect the tractography output.

B)



C)



D)