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Validating Validators: An Analysis of DWMRI Hardware and Software Phantoms

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Introduction

Diffusion Tensor Imaging (DTI) and its successor High Angular Resolution Diffusion Imaging (HARDI) are emerging MRI techniques for depicting *in-vivo* brain white matter, anatomy and connectivity. There is a wide range of utilizations of DTI and HARDI: from characterizing the local structure of the tissue, fiber tracking, segmentation, etc. However to apply any of the above-mentioned methods in a clinical setting, thorough validation is needed. The goal of the present work is to validate DTI and HARDI software phantoms, in regions of single and crossing fiber bundles, in relation to measured phantom data and in vivo data from human brain.

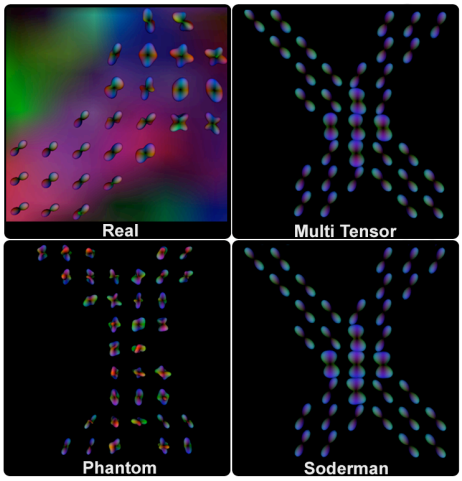

***Figure 1**: Q-ball glyphs with 4th order of Spherical Harmonics representation for the different datasets.*

Our Approach

1. The Multi-tensor (MT) model used in [3] and the Soderman (S) model [1] used in [4] for two fiber bundles crossing under 30˚, 50˚ and 65˚ were generated in a synthetic dataset creation tool developed in Mathematica, with parameters taken as similar as possible to the used MRI acquisition for the hardware phantom [2] and for the real brain: gradient sampling scheme and b values. Rician noise with realistic SNRs (corresponding to the used b values) was added to the signal.
2. For the in-vivo data we select a region of *corpus callosum* as linear part and known crossing between *corpus callosum* and *corona radiata.*

Results

We apply wide range of DTI and HARDI scalar measures on the four different types of` data. We also quantify the angular difference of the simulated linear direction and estimated main eigenvector in the DTI analysis, as well as the angular error and the standard deviation of the simulated and recovered angle in Q-ball.

In Fig. 2, the average normalized signal values for the analyzed voxels in the different datasets in the linear and crossing part are summarized. Signal decay (as to be expected) with increasing b value is observed in most of the cases, and the signals of the S model converge towards the MT model at high b values.

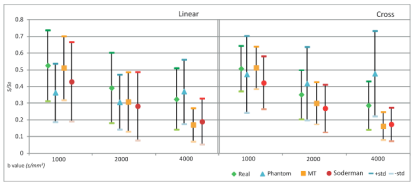

***Figure 2**: Average normalized signal values and standard deviation.*

The bolded results in Fig. 3 are the most similar to the real data. We observe similarity between the real and the MT model results. The results from the S model become similar to the *in-vivo* only at high b values, which can be useful in HARDI analysis, but for DTI analysis we recommend the MT model.

The qualitative results (see Fig. 1) suggest that the noise level for the selected b values is much lower in the S and MT model than for the scanned data.

b value (s/mm²)		Linear				Cross			
		real	*phantom*	*MT*	*S*	*real*	*phantom*	*MT*	*S*
1000	*FA*	**0.80**	0.40	**0.80**	0.88	**0.37**	**0.43**	0.55	0.67
	MD	**0.0008**	0.0012	**0.0008**	0.0011	**0.0008**	0.0010	**0.0007**	0.0009
	Cl	**0.59**	0.21	**0.60**	0.71	**0.10**	**0.20**	0.27	0.37
	Cp	**0.14**	**0.15**	0.05	0.05	0.31	0.23	0.27	0.28
	K1	**0.0023**	0.0037	**0.0023**	0.0032	0.0023	0.0030	0.0021	0.0028
	K2	**0.0011**	0.0007	**0.0011**	0.0019	0.0004	0.0006	0.0006	0.0011
	K3	**0.94**	0.53	**0.99**	**0.99**	-0.37	0.29	0.52	0.68
	Ang. Diff	-	17.58	**1.61**	1.77	-	-	-	-
4000	*GA*	**0.44**	0.07	**0.49**	0.63	**0.18**	**0.08**	0.32	0.41
	FMI	0.16	1.25	0.22	0.26	**0.88**	**0.96**	0.26	0.26
	Ang. err;std	-	-	-	-	-	13.58;7.28	**10.15;5.34**	10.6;7.76

***Figure 3**: Summary of DTI and HARDI measures.*

References

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