Optimal Acquisition Protocol for White Matter Fiber Orientation Mapping using Generalized CSA-ODF Reconstruction

Amith J Kamath[1], Iman Aganj[2,3], Junqian Xu[4], Essa Yacoub[4], Kamil Ugurbil[4], Guillermo Sapiro[5], and Christophe Lenglet[4]

[1]*Electrical and Computer Engineering, University of Minnesota, Minneapolis, MN, United States,* [2]*Martinos Center for Biomedical Imaging, Massachusetts General Hospital, Harvard Medical School, Cambridge, MA, United States,* [3]*Electrical and Computer Engineering, MIT, Cambridge, MA, United States,* [4]*Center for Magnetic Resonance Research, University of Minnesota, Minneapolis, MN, United States,* [5]*Electrical and Computer Engineering, Duke University, Durham, NC, United States*

Introduction: Several reconstruction algorithms for high angular resolution diffusion imaging (HARDI) data have been proposed to estimate complex white matter fiber configurations. This work builds on an extension of the CSA-ODF model **[1]** to define an optimal diffusion MRI acquisition protocol. We exploit the incremental staggered gradient tables previously developed in **[2]**. The Camino toolkit **[3]** is used to perform realistic simulations and identify optimal regularization parameters, *b*-values and number of gradients directions as functions of the signal-to-noise ratio (SNR) and spherical harmonic (SH) approximation order. We conclude that, for this particular ODF reconstruction technique, the *b*-value combinations [1,2,3], [1,2,4], [1,2,5] and [1,2,6] × 1000 s/mm^2 are optimal candidates. Moreover, a total number of 200 gradient directions appears sufficient for accurate reconstruction and angular accuracy. Experimentations on human brain datasets acquired at 3T are also performed.

Method: The CSA-ODF algorithm uses a mono-exponential approximation for the diffusion signal when a single point (*b*-value) along any given radial direction in the *q*-space is available. The bi-exponential decay model is known to better fit the diffusion signal, but requires at least three radial data points to estimate its parameters. This necessitates the acquisition protocol to include points on three distinct shells, of which the choice of *b*-value is crucial for accuracy. For each *b*-value, the diffusion signal is approximated by a SH series. Due to the inverse-problem nature of this approximation, the optimal regularization parameter (based on the Laplace-Beltrami formalism) was exhaustively investigated using the generalized cross-validation (GCV) method **[4]** for nine scenarios (SH orders 4, 6, 8, and 1-, 2-, and 3-fiber configurations). For each scenario, eleven *b*-values ranging from 1000 s/mm^2 to 6000 s/mm^2 with 500 s/mm^2 increments and five SNRs (5, 15, 25, 35, and 45) were used, yielding a comprehensive list of regularization parameters. In all experiments, a maximum of 300 non-collinear directions was chosen, and distributed between the shells in a staggered fashion **[2]**. The synthetic data was generated using the Camino toolkit **[3]**. Based on a compartment model **[5]**, we used a fixed radius cylinder model with Gaussian phase distribution and a zeppelin model respectively for the intra- and extra-axonal components of each fiber compartment, and a dot model for the isotropic component. Two- and three-fiber orthogonal configurations were chosen as ground truth (generated using 11 *b*-values and SNR=40), and used to evaluate the reconstruction accuracy of various choices of *b*-values and number of gradients. In each case, the optimal regularization parameter identified using GCV was used. The error metrics are the L_2 distance between the SH coefficients, and the Kullback-Leibler divergence between ODFs. Human brain data from two healthy volunteers was acquired on a 3T Siemens scanner with the following parameters: **(**S1) Voxel size 1.5 × 1.5 × 1.5mm^3 with three shells: *b* = [1, 2, 3] × 1000 s/mm^2, 133 aligned gradient directions and 10 *b*0; (S2) Voxel size 1.25 × 1.25 × 1.25mm^3 with three shells: *b* = [1.5, 2.5, 3.5] × 1000 s/mm^2, 128 aligned gradient directions and 15 *b*0.

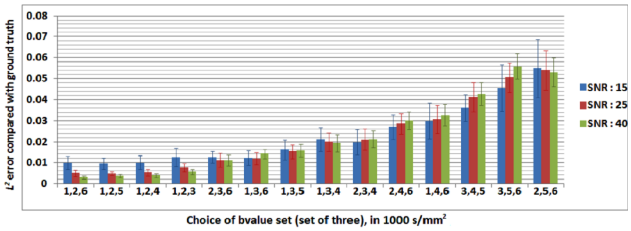

Figure 1. *Reconstruction error for order 6, single-fiber configuration.*

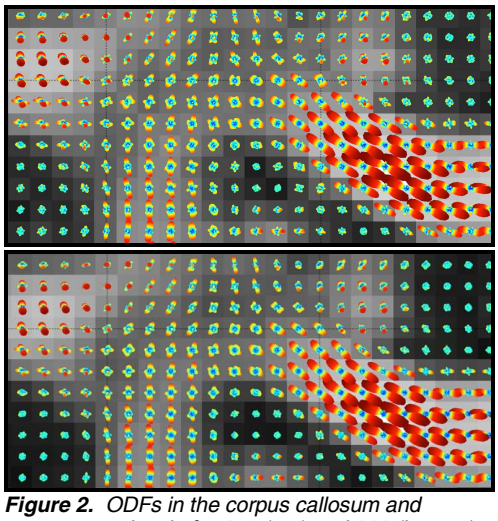

Figure 2. *ODFs in the corpus callosum and centrum semiovale for 150 (top) and 399 (bottom) total gradient directions.*

Results: Our comprehensive simulation studies revealed that the optimal regularization parameter varies sharply (10^{-4} to 10^{-1}) with the acquisition parameters (as compared to the previously used constant value of 0.006 **[6]**), and provides better reconstruction by incorporating prior information of the choice of *b*-value and SNR. With fourteen combinations of three *b*-values tested (**Figure 1**), optimal sets of *b*-values always comprise 1000 and 2000 s/mm^2, with a third shell in the range [3000, 6000] s/mm^2. Addition of a fourth shell, with the same overall number of gradients direction was found to only slightly improve ODF reconstruction. Moreover, reconstruction error was studied for a reduced number of total gradient directions, with all the other parameters remaining unchanged. We found that, for a wide range of three *b*-values combinations and the staggered sampling scheme, little additional information is achieved over 200 gradients. Simulating data with the identified optimal parameters (i.e. 200 directions and *b*=[1,2,6] × 1000 s/mm^2), reconstruction for two fibers with decreasing crossing angle shows that the generalized CSA-ODF algorithm distinguishes orientations up to a 35° limit, at SH order 8 and SNR 40. Finally, reconstructions on the human brain data S1 (**Figure 2**) with 90 to 399 directions demonstrate robust ODF estimation even with only 50 directions per shell (i.e. total number of 150 gradients). Tractography (**Figure 3**) experiments on S2 also demonstrate robust results from ODFs estimated with 192 vs. 384 directions.

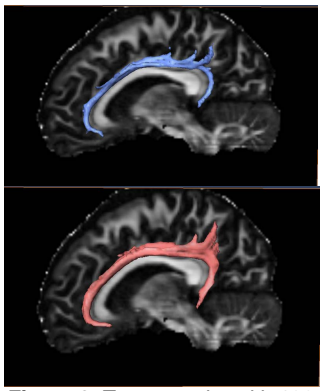

Figure 3. *Tractography with 192 (top) and 384 (bottom) total gradient directions.*

Conclusion: Using the CSA-ODF reconstruction technique for multi-shell HARDI data, we showed that specific sets of three *b*-values including 1000, 2000, and a third shell in the range [3000, 6000] s/mm^2, yield significantly better fiber orientation estimates, and that 200 total gradient directions appear sufficient to achieve good angular accuracy.

Acknowledgements: Work partly funded by NIH grants R01 EB008432, P41 EB015894, P30 NS057091, P30 NS076408, and the Human Connectome Project (U54 MH091657) from the 16 NIH Institutes and Centers that support the NIH Blueprint for Neuroscience Research.

References: **[1]** Aganj et al. *Magn. Reson. Med.*, 64(2):554-66, 2010; **[2]** Caruyer et al. *MICCAI Workshop on CDMRI 2011*; **[3]** Cook et al. *ISMRM* 2006; **[4]** Golub et al. *Technometrics*, 21(2):215-23, 1979; **[5]** Panagiotaki et al. *NeuroImage*, 59(3):22-54, 2012; **[6]** Descoteaux et al. *Magn. Reson. Med.*, 58(3):497-510, 2007; **[7]** Alexander et al. *Neuroimage*, 27(2):357-67, 2005.