Moving away from single-shell?: a study on angular accuracy of constrained spherical deconvolution.

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Target audience: This work is intended for researchers who work with high angular resolution diffusion imaging (HARDI) datasets; single and multiple b-value data. In particular, for a given number of diffusion directions or a certain acquisition time slot, is it better to acquire a single or multiple b-value diffusion datasets?

Purpose: Diffusion MRI is commonly used to perform tractography, in which the local reconstruction algorithms prioritize the angular accuracy of the diffusion directions, describing the underlying white matter bundles. This is why single-shell HARDI is generally the acquisition scheme chosen for models such as Q-ball, CSA, CSD[1], or ball-&-stick. One downside of single-shell acquisitions is their inability to be applied in high-order models that need some information about the radial diffusion such as MAP[2], kurtosis[3] or multi-compartment models which can provide interesting microstructural diffusion features. But can we get at least equally satisfactory orientation reconstructions from multiple b-values diffusion data with the same amount of measurements as single b-value HARDI data? In this abstract, we present preliminary results showing that single-shell schemes can be outperformed by multi-shell schemes with an equivalent number of measurements.

Methods: We generated 362 single- and multi- shell sampling schemes by subsampling the MASSIVE dataset[4] gradient table. We enforced a good angular distribution of the samples on each shell and on the projection of all shells together. No direction is repeated across shells. These schemes were obtained by varying 1) the total number of diffusion samples N (N in [35, 60, 90, 120, 305]), 2) the number of shells S (S in [1, 2, 3, 4, 5] chosen from 5 possible shells: b-value = [500, 1000, 2000, 3000, 4000] s/mm^2) and 3) the "order" of the point distribution with respect to the shell number. For a sampling scheme of S shells, we compute [1,2,...,S]^order = [1,2^order,...,S^order], normalize it with respect to its sum and use the array as weight to set the number of points on each shell. For example, S = 2 with order = 0 gives a 1:1 ratio in the number of samples per shell, S = 3 with order = 2 gives a 1:4:9 ratio and S = 4 with order = 1 gives 1:2:3:4. Sampling schemes with less than 6 samples on a single shell were discarded. We generated a synthetic phantom consisting of single fibers, 2-fiber crossings and 3-fiber crossings at angles from 30 to 90 degrees. The data was simulated using the Tensor-Bingham-CSF model with parameters optimized to mimic human brain single fiber populations, which was the best out of 50 models in the recent paper[5]. Rician noise was added to simulate signal-to-noise ratio of 10, 20 and 30. We computed the fiber ODFs using the CSD implementation of Dipy[6] and extracted the diffusion directions. The reconstruction angular error was computed over 30 noise realizations for every sampling scheme. Note that the CSD implementation used does not attempt to use the multiple b-value aspect of the data; the whole signal is used as an input. It recovers the fiber ODFs from a single response function, implicitly used as a "mean response function across all shells". The response function was manually set to [0.015, 0.003, 0.003] x 10^-3 mm^2/s. The spherical harmonics order was set such that the number of unknowns in the model was lower than N, with a maximum order of 8.

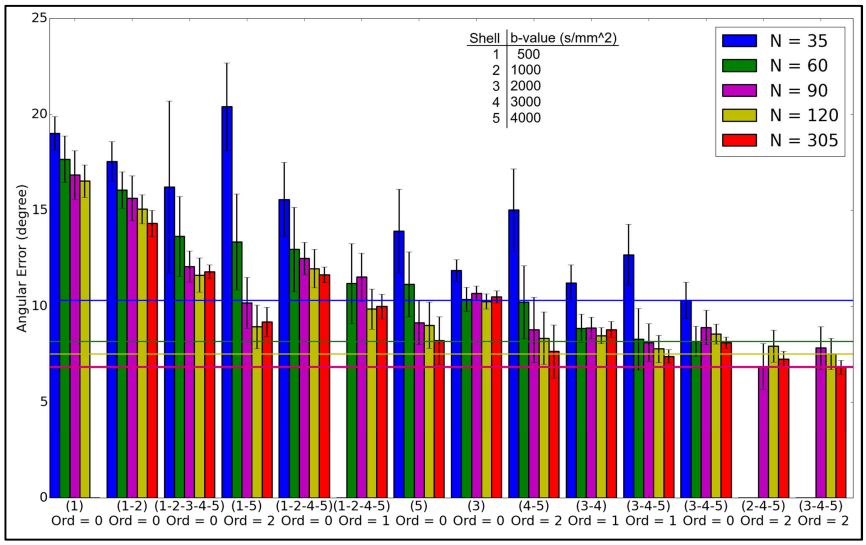

Figure 1: Angular Error with CSD reconstruction for SNR=20 for a few sampling schemes.

Results: Figure 1 shows the angular error of the reconstruction (with +/- 1 standard deviation) of CSD for SNR = 20 for each number of samples for a few hand-picked sampling schemes, ranging from the worst to the best (the numbers in parenthesis under the bars represent which shells are used). The horizontal bars represents the best observed angular error for each N for SNR = 20. For all N, the best results are obtained from 3-shells sampling scheme using the 2 highest b-value shells. These sampling schemes outperform any single-shell sampling scheme by at least 2 degrees for any given N. For example, N = 35 with scheme (3-4-5) order = 0 ((11, 12, 12) samples on shells 2000-3000-4000) performs as well as N = 60 on shell b = 2000, and N = 60 on the same 3-shell scheme performs as well as 305 samples on shell b = 4000. We also note that the best 3-shell sampling scheme uses order = 2 (64.3% of points on last shell, 28.6% on middle one and 7.1% on lowest b-value shell). This indicates that once N is big enough, the reconstruction seems to benefit more from the multiple b-values than from extra gradients directions on the same shell. This effect is even more pronounced looking at SNR = 10 (not shown).

Discussion and Conclusion: In summary, we have shown that even with a very naïve use of multi-shell data, the CSD still performs very well, arguably better than with single-shell, even in clinically feasible (low number of gradients) acquisition setting. It is clear that proper handling of multi-shell data in the CSD reconstruction would increase the fiber ODFs reconstruction accuracy, justifying the acquisition of multi-shell datasets rather than single-shell. This would also open new possibilities as one can now also use high-order models, giving access to new diffusion metrics at no increased acquisition cost nor accuracy loss in the regular diffusion orientation reconstruction (i.e. tracking).

References: [1] Tournier et al., NeuroImage, 2004. [2] Ozarslan et al., NeuroImage, 2013. [3] Jensen et al., MRM, 2003. [4] Froeling et al., ISMRM 2014. [5] Ferizi et al., MRM, 2013. [6] Garyfallidis et al., Frontiers Neuroinformatics, 2014.