Q-space signal reconstruction from sparse samples

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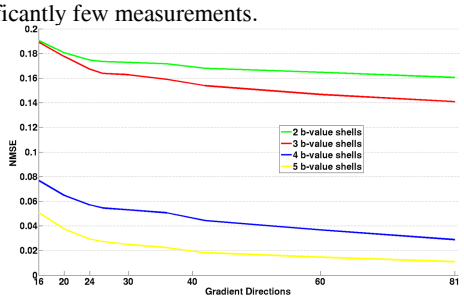
Purpose: Diffusion Spectrum Imaging (DSI) as well as several other imaging schemes (diffusion propagator imaging, multi-shell imaging) require a lot of measurements making the scan time clinically impractical, specifically for children and patients with several types of psychiatric disorders. While the information obtained by sampling the entire q-space is quite sensitive to neural tissue changes (Assaf2002), its current feasibility is quite limited. Thus faster acquisition/analysis schemes are required to reduce the scan time and bring these advanced diffusion MR imaging (dMRI) protocols to the clinic. In this work, we use the concept of compressive sampling (CS) to dramatically reduce the number of measurements required to obtain the same information as that of a standard fully sampled multi-shell scan, thus reducing the scan time significantly (by a factor of 4).

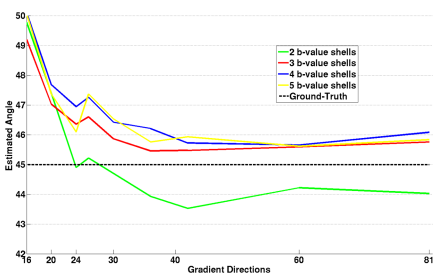
Methods: We propose to extend the spherical ridgelets (SR) basis (Michailovich2010) from single to multi-shell data by introducing a novel radial decay term, which is guaranteed to be monotonically decreasing with increasing b-value. This model of decay was chosen based on the prior knowledge that the signal decay is either single or bi-exponential in the radial q-domain. This is in contrast to existing methods that do not enforce this behavior leading to erroneous estimation of the diffusion propagator. In particular, we propose a novel framework, which enforces sparsity in the spherical domain via the SR basis (which is known to have sparse representation), sparsity in the radial q-domain via the novel radial decay term and sparsity in the spatial domain (of the 3D image volumes) via the total-variation based norm to reconstruct the diffusion signal from a sparse set of samples. The radial decay function in terms of the b-value (b) is given by: $f(b)=(1+b)^{-}$, ≥ 0, ≥ 0. This function can model mono-exponential as well multi-exponential signal decay using two parameters (,). Combining the sparse representations in all three domains, the cost function we minimize is given by: $\mathbf{min}\ \{\ \|\mathbf{Ac}-\mathbf{s}\|^2 + \lambda_1\|\mathbf{c}\|_1 + \lambda_2\|\mathbf{F}(\ ,\ )-\mathbf{s}\|^2 + \lambda_3\|\mathbf{Ac}\|_{TV}\ \}$, where A is a block-diagonal matrix of SR basis functions arranged for multi b-value data, c is the sparse set of SR coefficients to be estimated, F is a vector representation of the radial decay function (f(b)) and TV denotes the total-variation norm of the reconstructed signal. This composite cost functional can be estimated using the Alternating Directions Method of Multipliers (ADMM) algorithm (Boyd2011), which gives the optimal solution by harmonizing the competing solution to each of the above terms.

Results: We did extensive validation of the proposed technique on physical phantom data set with a crossing angle of 45°. Data was acquired for b-values of b={1000,2000,3000,4000,5000} mm^2/s, at each of the following set of gradient directions u = {16,20, 24, 26, 30, 36, 42, 60, 81}. The data had 5 repetitions of each set, which were used to see the effect of noise on the estimation process. In addition, a total of 10 repetitions were acquired for the set with 81 gradient directions and an averaged data was constructed to obtain the "gold standard" data. All quantitative comparisons were done against this data set**. Our goal was to test the minimal number of measurements required (gradient directions and number of b-value shells) to obtain an accurate reconstruction of the dMRI signal at each voxel.** We compare our work with the 3D-SHORE basis (Cheng2010) and show superior reconstruction quality with significantly few measurements.

NMSE – SR basis



NMSE – SHORE basis



AAE – SR basis

The figures above show the Normalized mean squared error (NMSE) in reconstruction of the dMRI signal in the entire q-space where the gold standard data was sampled. Also shown is the average angular error (AAE) in estimation of the principal diffusion direction. Note that, the SR basis has NMSE error that is lower than 2% in all cases, while the 3D-SHORE basis reaches a 2% error only if ALL the samples (405) are used. In terms of the angular error, the SR basis shows an error of only 1-2°, whereas for the SHORE basis the error was at-least 7°. We also computed the percentage of voxels where the 2-peaks in the phantom data were not detected and found that for 20 gradient directions and 3 –bvalue shells (total of 60 measurements), the error was 5%. This is in sharp contrast to the 3D-SHORE basis, which failed to find the two peaks in the ODF if less than 162 measurements were used.

Conclusion: With at-least 60 measurements, we were able to reconstruct the diffusion data in the entire q-space with very minimal error (NMSE =1.5%, AAE =1.5°, and incorrect peak in 5% of the cases). This data used 20 gradient directions over 3 b-value shells. More measurements would lead to better results, but the payoff may not be as high given the amount of time required to scan the additional data. Additionally, if we used 2 b-value shells with 30 directions each (total 60), this reduced the AAE to 1°, but had higher number of incorrect peaks (7%). Thus, spreading the measurements over more b-value shells is slightly better. Overall, the proposed method significantly reduces the scan time by requiring 60 measurements to recover dMRI signal in the entire q-space. This could make computation of diffusion propagator practical in clinical settings.

References: Assaf2002: NMR in Biomedicine, Michailovich2010: MICCAI, Cheng2010: Cheng,MICCAI. Boyd2011:Foundations &Trends in machine learning.