

Acceleration of High Angular Resolution Diffusion Weighted Images using Compressed Sensing

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Introduction: Diffusion tensor imaging (DTI) has become the state-of-the-art method for studying brain white matter architecture in-vivo. The technique achieves the goal by sampling tissues using a pulse sequence with diffusion gradients applied along various directions. One accepted fashion of representing the fiber architecture is to characterize their orientation using a tensor. Various acquisition schemes exist to realize this goal. On one extreme, there are low-resolution techniques that collect as few as 6 diffusion weighted (DW) images and fit a single tensor that captures the dominant fiber direction in each voxel [1]. Those methods fail to capture any crossing fibers present in the voxel. On the other extreme, there are techniques that collect large number of DW images at high b-values [2,3]. The information content in those techniques is unmatched and they can model diffusion of higher orders using non-parametric models. But they are plagued by their unreasonably long scan time and the lack of a parametric model. Intermediate group of techniques exists that sample fewer diffusion directions in reasonable scan time at low b-values [4,5]. Since the diffusion profile is broad at low b-values, techniques in this class only need fewer angular samples. Recently, compressed sensing has been applied to these methods to extract the high angular information from the data sampled with low angular resolution [6,7]. However, the broad profile of diffusion at low b-values limits the accuracy of such methods since they fail to resolve two adjacent orientations separately. In contrast, at high b-values, the diffusion profiles become narrower and hence to distinguish between adjacent orientations, sampling at high angular resolution is required.

In this work, we propose to use compressed sensing (CS) to achieve sampling of high angular resolutions within reasonable scan time. The reconstructed diffusion weighted images can then be used to obtain high-resolution parametric models of tissue microstructures. For compressed sensing to work, the data needs to be sparse in a transform domain, which can then be reconstructed accurately. In a typical brain voxel, the numbers of fiber orientations are sparse. By choosing basis functions that model diffusion in all possible discrete orientations, this sparse orientation information can be reconstructed. Our idea is to then randomly under-sample the k_x - k_y - $k_{diffusion}$ -space. Under sampling reduces the scan time, but introduces aliasing in individual diffusion weighted images. Using joint non-linear (sparse) reconstruction of the 3D diffusion data, aliasing-free 3D diffusion weighted images can be reconstructed which can be further used to fit multiple-tensors. Here we show that accelerated acquisition of high angular resolution is possible within reasonable scan time and within acceptable reconstruction errors.

Methods: A Gaussian mixture model is assumed for diffusion signal, with $S_k = S_0 [\sum_i f_i \exp(-bdg_k^T D_i g_k) + (1 - \sum_i f_i) \exp(-bd)]$, where S_k is the diffusion weighted data simulated for the k th diffusion direction (g_k), S_0 is non-diffusion weighted image, f_i is the unknown anisotropic volume fraction of the i th compartment with tensor oriented along D_i , b is the diffusion sensitizing constant and d is the mean diffusivity. A 128x128 dataset was simulated assuming two anisotropic compartments ($i=2$) and an isotropic compartment in each voxel. Using realistic values of f_i and S_0 obtained from a human brain data and the following parameters, the reference dataset S_k and its k -space samples X_k were generated: $b=12000$ s/mm², $d=1 \times 10^{-3}$ mm²/s, $D=R*[1 \ 0 \ 0; 0 \ 0 \ 0; 0 \ 0 \ 0]*R^T$ where R rotates the tensor to arbitrary directions. The k -space samples obtained were then randomly under-sampled for each diffusion direction.

The basis vectors for CS reconstruction were assumed as Gaussians oriented along all possible orientations of D_i . Here we chose 256 discrete directions uniformly distributed over the hemisphere. The model with the basis vectors was generated for all applied gradients g_k . With this setup, the model can be formulated as $Af=X$, where the left hand side combines the operation of multiplying the basis function by f , taking the Fourier transform and under-sampling. The aim is then to reconstruct the diffusion-weighted images that would give the correct the anisotropic volume fraction f_i present in each voxel from the under-sampled k -space data. A sparse reconstruction using iterative reweighted L1-norm of f_i subject to $Af=X$ was implemented using conjugate gradient algorithm.

Results: Simulations were performed in MATLAB for under-sampling of the k -space data by factor of up to 8 and at various levels of noise. Only random under-sampling was studied at this time. Two error metrics were defined to check the error in various phases of reconstruction: data consistency error reporting the % sum of squares error (SSE) in k -space ($Af-X$), reconstruction error reporting the % SSE in reconstruction of DW images. From Table 1, it can be seen that even at 8-fold under-sampling and in the presence of 50dB noise, the reconstruction error are less than 3%.

Table 1: Error metrics for various under-sampling levels and noise

Error metric	No noise	With noise	
		SNR=100dB	SNR=50dB
US=2	Data consistency	6.8e-3%	7.6e-3%
	Reconstruction	.014%	.017%
US=4	Data consistency	.01%	.027%
	Reconstruction	.11%	.2%
US=8	Data consistency	.06%	.1%
	Reconstruction	1.8%	2.3%

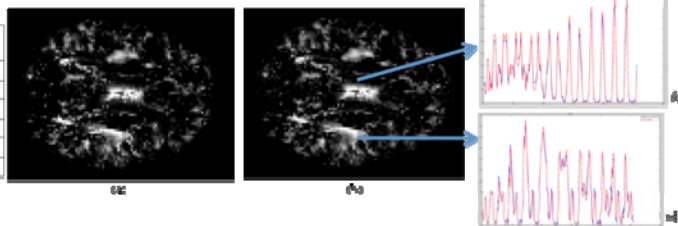


Figure 1: (a) shows the original DW image for one diffusion direction, (b) CS reconstructed DW image, (c) and (d) shows the plot of original DW image (red) and CS reconstructed DW image (blue) for all 256 directions from two voxels marked by arrows.

Discussion: Current CS methods in DTI uses few angular samples acquired at low b-values to reconstruct high angular information.

But, the accuracy of resolution achievable is limited due to the broad profile of diffusion at low b-values. High angular sampling schemes fit non-parametric models to the rich data and fail to generate parametric maps that are of clinical interest. Also, in comparison to a typical clinical DTI scan that acquires 30-60 diffusion directions, they requires about 8 times the scan time to sample 256-512 directions which limits their practical application. We have shown that it is possible to reconstruct the diffusion-weighted images from its randomly under-sampled k -space samples using the idea of CS. Under-sampling by factor of up to 8 was tested with different noise levels and was found to give reasonable reconstruction results. In practice, this could translate to 8-fold gain in acquisition time for the high angular resolution sampling. Methods such as parallel imaging can be combined with the CS technique to further lower the scan time. Our choice of basis function for reconstruction also enables to fit a parametric model to the high angular resolution DW data. In contrast to the existing methods that fit the model to the data voxel-wise, we note that we do a joint reconstruction of the 3D data. In the current implementation, positivity of anisotropic volume fractions is not enforced during reconstruction. Once this is implemented, it may be possible to reconstruct the multiple diffusion tensor orientations directly, bypassing an otherwise two-step procedure.

References: [1] P. J. Basser, et al, *NMR Biomed.*, 2002. [2] D. S. Tuch, "Q-ball imaging," *Magnetic Resonance in Medicine*, 2004. [3] D. S. Tuch, et al, *Magnetic Resonance in Medicine*, 2002. [4] J. Parker and D. Alexander, *Proc. IPMI*, 2003. [5] Behrens, T.E.J., et al., *Magn. Reson. Med.*, 2003. [6] A. Ramirez-Manzanares, et al, *IEEE Trans. Med. Imag.*, 2007. [7] B. A. Landman et al, *Proceedings of SPIE, ser. Medical Imaging*, San Diego, CA, February 2010.