Compressive Diffusion MRI - Part 2: Performance Evaluation via Low-Rank Model

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Purpose: Diffusion MRI, an emerging MRI technique that utilizes the diffusion process of water molecules in tissue as contrasts, has shown to be extremely powerful for exploring the integrity and connectivity of the brain white matter [1]. A major limitation of this technique is the long scan time and/or relatively low spatial resolution, which can be potentially improved by compressive MRI [2]. In another submitted abstract "*Compressive Diffusion MRI – Part 1: Why Low-Rank?*", we compared several sparsity models and found that the low-rank (LR) model is the most suitable for diffusion MRI. The purpose of this work is to retrospectively explore compressive MRI in the context of diffusion MRI via LR.

Methods: The diffusion MR data were simulated based on a randomly chosen healthy human subject. The imaging parameters of the data are: TR/TE=8500/95ms; $FOV=216\times256$, matrix size=108×128, 2mm isotropic resolution, GRAPPA=2, 60 diffusion directions (D=60), two averages with opposite phase-encoding directions for correcting susceptibility-related distortion [3]. After the removal of eddy current and susceptibility-related distortions, the principal (D1) and secondary (D2) diffusion orientations were estimated using FSL's partial volume model [4]. The estimated diffusion orientation in the middle slice of the subject's brain was subsequently used as the gold standard. After the orientation and the proportion of each diffusion compartment were estimated, simulated raw diffusion MR data based on the gold standard with various diffusion weighting (b=1000,2000,3000) as well as SNR (10, 20, 30) were generated for the evaluation purpose. For quantitative evaluation, we calculated the angular differences in D1 and D2 between the reconstructed images and the gold standard. Since the errors in gray matter (GM) could be larger than those in white matter (WM), we segmented the brain into GM, WM, and CSF and calculated the angular differences in GM and WM separately.

Results: The reconstructed images via LR with SNR=30 and 8-fold undersampling are presented in Figs. 1-3, which suggest that LR is able to accurately reconstruct the diffusion MR images from highly undersampled k-space (e.g., 8-fold undersampling). On the other hand, the angular differences are presented in Fig. 4 for various b values, SNRs, and undersampling ratios (2-fold, 4-fold, 6-fold, 8-fold, 10-fold). For example, with 8-fold undersampling, the angular difference of D1 for WM (resp. GM) is at most 18°, 15°, 13° (resp. 32°, 28°, 25°) for various SNRs, at b=1000, 2000, 3000 respectively.

Conclusion and Discussion: LR is able to accurately reconstruct the diffusion MR images from highly undersampled k-space, in terms of both the image quality and the angular differences in D1 and D2. And this should allow a significant reduction of the scan time (e.g., the conventional 20-minute scan is reduced to a compressive 3-minute scan through the 8-fold undersampling), which should greatly facilitate the time-sensitive patient scans, such as for autism, Parkinson and newborns.



Fig. 1. Image reconstruction at b=1000 via LR with 8fold undersampling. (a)The gold standard; (b) the reconstructed images; (c) the reconstruction difference.

Fig. 4. Angular differences in D1 and D2 between the reconstructed images and the gold standard. (a) b=1000, (b) b=2000, (c) b=3000. In each figure, the angular differences with various SNR values (10, 20, 30) are plotted in the region of white matter (WM) and gray matter (GM).

References: 1.Basser, *NMR in biomedicine*, 8, 333 (1995); 2. Lustig et al, *MRM*, 58, 1182 (2007); 3. Andersson et al, *NeuroImage*, 20, 870 (2003). 4. Behrens et al, *MRM*, 50, 1077 (2003). Fig. 2. Image reconstruction at b=2000 via LR with 8fold undersampling. (a)The gold standard; (b) the reconstructed images; (c) the reconstruction difference. Fig. 3. Image reconstruction at b=3000 via LR with 8fold undersampling. (a)The gold standard; (b) the reconstructed images; (c) the reconstruction difference.

