Whole-brain quantitative diffusion MRI at 660 µm resolution in 25 minutes using gSlider-SMS and SNR-enhancing joint reconstruction

Justin P Haldar¹, Qiuyun Fan², and Kawin Setsompop²

¹Electrical Engineering, University of Southern California, Los Angeles, CA, United States, ²A. A. Martinos Center for Biomedical Imaging, Department of Radiology, Massachusetts General Hospital, Charlestown, MA, United States

Synopsis

We propose a novel approach to data acquisition and image reconstruction that achieves high-quality in vivo whole-brain human diffusion imaging at (660 µm)³ resolution in 25 minutes. The approach uses a powerful acquisition strategy (generalized SLice Dithered Enhanced Resolution Simultaneous MultiSlice, or gSlider-SMS) that enables high-resolution whole-brain imaging in 25 minutes (64 diffusion weightings + 7 b=0 images), but the resulting images suffer from low SNR without averaging. To address the SNR problem, we utilize a regularized reconstruction/denoising approach that leverages the shared spatial structure of different diffusion images. In vivo results demonstrate the effectiveness of this approach.

Purpose

It is extremely challenging to acquire whole-brain in vivo diffusion weighted images (DWIs) with sub-millimeter resolution using traditional approaches. This work proposes and evaluates a novel approach to diffusion MRI that can acquire 71 whole-brain DWIs (64 diffusion weightings + 7 b=0 images) at (660 µm)³ resolution in 25 minutes. Our approach is based on a novel generalization [1] of the previous Slider-SMS approach [2], combined with a regularized reconstruction method that has been demonstrated to substantially improve the SNR in both healthy [3] and injured [4] tissues with a minimal loss of spatial resolution.

Theory

The previous Slider-SMS acquisition strategy for diffusion MRI [2] combines multiple novel fast imaging technologies to achieve high-resolution whole-brain imaging:

- Blipped CAIPI [5] was used to enable SNR-efficient simultaneous imaging of multiple slices.
- Thick-slice super-resolution techniques [6] were used to increase resolution along the slice dimension. Thick-slice super-resolution techniques acquire overlapping thick slices, and then solve a linear system of equations to estimate the corresponding thin slices of interest. This is advantageous because thin slices can be recovered from an acquisition that exploits the higher SNR-efficiency of 3D volume encoding.

While Slider-SMS was effective at enabling high-resolution whole-brain diffusion MRI [2], it still suffers from blurring due to the inherent ill-conditioning of the thick-slice super-resolution inverse problem, which itself results from the large coherence between the encoding functions of the overlapping thick-slice acquisition. The novel gSlider-SMS acquisition approach [1] uses the same Blipped CAIPI and thick-slice super-resolution approaches as Slider-SMS, except that the excitation RF pulse is modified so that each thick slice has a specially-designed non-uniform phase profile along the slice dimension, which serves as an additional form of RF encoding. This RF phase encoding has the effect of substantially reducing the coherence between the shifted overlapping thick-slice encoding functions, which improves the conditioning of the inverse problem and enables higher-fidelity reconstruction.

While gSlider-SMS is very SNR-efficient, the extremely small isotropic voxel sizes mean that SNR is still a limiting factor for DWIs acquired with high b-values. To address this issue, we employ a variation of a previous regularized reconstruction method [3,4] that uses phase modeling to regain the resolution lost from partial Fourier acquisition, and simultaneously uses the structural similarity between different DWIs to reduce noise perturbation while preserving high-resolution image features.

Methods

Whole-brain gSlider-SMS DWI data was acquired at 660 µm isotropic resolution over a 220×118×151.8 mm FOV, with 7 b=0 images and 64 DWIs with b=1,500 s/mm². Each average was acquired in 25 minutes, and three averages were acquired to provide a gold standard reference. The acquisition used thick slices (5× larger than each thin slice) with 5 different RF encoding pulses, a multiband factor of 2, and 6/8ths partial Fourier encoding. The thick slices were first reconstructed using slice-GRAPPA reconstruction [7]. Subsequently, gSlider reconstruction, partial Fourier reconstruction, and denoising were performed simultaneously by solving

\[
\{p, \phi\} = \arg\min_{p,\phi} \|b - G(\phi \odot Ap)\|_2^2 + \lambda_1 R(\phi) + \lambda_2 J(p)
\]
where $\mathbf{b}$ is the vector of complex images obtained after slice-GRAPPA reconstruction, $\mathbf{p}$ is the unknown vector of DWI amplitudes (real-valued and nonnegative), $\mathbf{A}$ is the matrix modeling the thick-slice and RF encoded gSlider acquisition, $\phi$ is the unknown phase of each measured thick slice (phase is not consistent in diffusion MRI), and $\mathbf{G}$ is the matrix modeling the in-plane point-spread function of partial Fourier acquisition. The regularization penalty $R(\cdot)$ encourages $\phi$ to be smooth within each slice [8,9], while the $J(\cdot)$ penalty uses a Huber function to impose that $\mathbf{p}$ is smooth, but has edge structures that are shared between different DWIs [3,4,10]. Optimization is performed using a majorize-minimize approach that alternates between estimating $\mathbf{p}$ and $\phi$.

**Results**

Figure 1 shows an example of the substantial image-domain SNR-enhancement that is achievable using SNR-enhancing regularized reconstruction. Figure 2 shows that the SNR-enhancement also has a major impact on quantitative diffusion parameter estimation. Specifically, single-average data without SNR-enhancing regularization yields noisy biased parameter estimates, while single-average data with SNR-enhancing regularization yields similar results to the three-average reference data. As shown in Fig. 3, SNR-enhancing regularization also enables high-quality orientation estimation that is sensitive enough to detect the coherent orientation within gray matter.

**Discussion and Conclusions**

We proposed a novel acquisition and reconstruction strategy that uses gSlider-SMS together with regularized reconstruction to achieve a dramatic gain in SNR-efficiency relative to conventional 2D diffusion acquisition. We have leveraged these advances in SNR-efficiency to achieve a (660 µm)$^3$ resolution whole-brain quantitative diffusion MRI acquisition in 25 minutes, which we believe will prove useful across the full range of in vivo human diffusion MRI applications.

**Acknowledgements**

This work was supported in part by NSF CAREER award CCF-1350563 and NIH grants R01-NS089212, R24-MH106096, and R01-EB019437.

**References**


**Figures**

Single-average gSlider reconstruction of a (660 µm)$^3$ resolution $b=1,500$ s/mm$^2$ DWI (a) without joint regularization ($\lambda_2=0$) and (b) with joint regularization. The use of regularized joint reconstruction leads to substantial gains in image SNR without substantially reducing the image resolution.
Fractional anisotropy (FA) maps derived from (a) single-average gSlider without joint regularization, (b) single-average gSlider with SNR-enhancing joint regularization, and (c) three-average gSlider without joint regularization. Single-average gSlider yields biased noisy FA maps without regularization, which leads to a loss of contrast between white and gray matter in inferior portions of the brain. In contrast, the regularized results match quite well with the three-average results.

Whisker plots showing the primary orientations of diffusion tensors estimated from (a) single-average gSlider without joint regularization, (b) single-average gSlider with SNR-enhancing joint regularization, and (c) three-average gSlider without joint regularization. Orientations derived from single-average data without regularization are noisy, while the regularized results match closely with the three-average results, and are sensitive enough to detect coherent anisotropy in gray matter.