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Globally Optimized Super-Resolution of Diffusion MRI Data via Fiber Continuity

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Abstract

In this paper, we introduce a technique for super-resolution reconstruction of diffusion MRI, harnessing fiber-continuity (FC) as a constraint in a global whole-brain optimization framework. FC is a biologically-motivated constraint that relates orientation information between neighboring voxels. We show that it can be used to effectively constrain the inverse problem of recovering high-resolution data from low-resolution data. Since voxels are inter-related by FC, we devise a global optimization framework that allows solutions pertaining to all voxels to be solved simultaneously. We demonstrate that the proposed super-resolution framework is effective for diffusion MRI data of a glioma patient, a healthy subject, and a macaque.

Keywords

Diffusion MRI; Super-resolution; Fiber continuity

1 Introduction

Diffusion magnetic resonance imaging (DMRI) with high angular and spatial resolution is plagued by low signal-to-noise ratio (SNR) and long acquisition time [1]. These are inevitable consequences of the smaller voxel size and the large number of diffusion-weighted (DW) volumes that need to be acquired for multiple diffusion directions and scales. Instead of relying on expensive scanner upgrades and sophisticated MRI sequences, super-resolution (SR) techniques can be used to infer high-resolution (HR) images from low-resolution (LR) images.

Regularization-based SR methods harness constraints such as smoothness, sparsity, and low-rank [2–7] to infer HR information. These methods leverage inter-voxel spatial redundancy that is typical in images for data recovery. For example, in [8], spatial regularization is used to improve estimation of orientation distribution functions. Ning et al. [6] coupled compressed sensing with SR for accelerated HR DMRI reconstruction and demonstrated that spatial regularization reduces sensitivity to noise.

Another form of regularization that is more specific to DMRI is fiber continuity (FC). FC is a biologically-motivated constraint that arises from the spatially-continuous nature of fiber tracts. The orientation information at each voxel location captures localized information about white matter pathways. Based on this observation, the FC constraint requires that orientations transit smoothly across voxels and is therefore a means of linking information within and across voxels. Recent studies have shown that FC [9–12] can be harnessed for enhancing image resolution and improving the estimation of fiber orientation distributions.

In this paper, we propose a technique for SR reconstruction of DMRI data by harnessing FC constraint based on intra-voxel orientation information. Note that our method does not rely explicitly on tractography. The term “fiber continuity” comes from the fact that at each voxel DMRI captures the local orientation of a fiber bundle. Since fibers are continuous spatially, the orientations are expected to vary smoothly across space. We show that FC in tandem with signal representation based on asymmetric fiber orientation distributions [12, 13] can be used to regularize the ill-posed inverse problem associated with the recovery of the HR DMRI data from its LR counterpart. We (i) formulate a novel SR technique that uses intra-voxel orientation information; (ii) use a global optimization framework for the spatio-angular recovery of multi-shell DMRI data, reducing sensitivity to noise; (iii) demonstrate the efficacy of the technique in tumorous and healthy human brains and a macaque brain; and (iv) demonstrate the utility of the technique in recovering HR data from highly incomplete or under-sampled LR DMRI data [14]. Experimental results indicate that our technique enables the recovery of rich structural details.

2 Methods

2.1 Forward Model

The LR DW volumes are considered as down-sampled versions of HR DW volumes that need to be estimated. For this purpose, we let $\mathbf{Y} \in \mathbb{R}^{N_v \times M_g}$ denote a set of LR DW volumes with N_v voxels per volume and M_g gradient directions across different shells. The LR volumes $\mathbf{Y}$ are related to the HR volumes $\mathbf{S} \in \mathbb{R}^{M_v \times M_g}$ by

$$\mathbf{Y} = \mathbf{D}\mathbf{S} + \boldsymbol{\mu}, \quad (1)$$

where $\mathbf{D}$ is a down-sampling matrix that averages neighboring voxels and $\boldsymbol{\mu}$ denotes noise. The sampling of $\mathbf{Y}$ can be encoded by a binary matrix $\mathbf{B}$ such that

$$\mathbf{B} \odot \mathbf{Y} = \mathbf{B} \odot (\mathbf{D}\mathbf{S} + \boldsymbol{\mu}), \quad (2)$$

where $\odot$ is the element-wise multiplication operator. The model is general and can account for different spatio-angular subsampling schemes determined by $\mathbf{B}$ and $\mathbf{D}$.

2.2 Fiber Continuity (FC)

Our method uses FC across voxels to regularize the inverse problem of recovering the HR volumes. FC [12] is a natural constraint supporting the fact that orientations should be consistent along fiber tracts. A model based on asymmetric fiber orientation distribution

functions (AFODFs) [12] is used to represent the sub-voxel configurations. In DMRI, the signal profile is typically assumed to be antipodal symmetric, implying that orientation in a positive hemisphere is always identical to its counterpart in the negative hemisphere. Symmetric FODFs are not sufficient in regions with, for example, fanning and bending fiber trajectories. To improve sub-voxel fiber continuity, we estimate AFODFs by incorporating information from neighboring voxels, allowing FODF asymmetry to better represent complex configurations [10, 13, 15]. The discontinuity of AFODFs, $\mathcal{F}_{\text{aniso}}$, over all voxels and directions ($\mathbf{u} \in \mathbb{S}^2$) is measured as

$$\Phi(\mathcal{F}_{\text{aniso}}) = \int_{\mathbf{u} \in \mathbb{S}^2} \|\mathcal{F}_{\text{aniso}}(\mathbf{u}) \otimes \mathbf{W}(\mathbf{u}) - \mathcal{F}_{\text{aniso}}(\mathbf{u})\|_{\text{F}}^2 d\mathbf{u}, \quad (3)$$

where $\mathbf{W}$ is a normalized directional probability distribution function as defined in [12] and $\otimes$ is a column-wise multiplication operator.

2.3 Spherical Convolution

We use a multi-tissue spherical convolution model to represent the diffusion signal at each voxel of $\mathbf{S}$. Specifically, $\mathbf{S}$ can be decomposed as $\mathbf{S} = \mathcal{R}\mathcal{X}$, with $\mathcal{R} = [\mathbf{R}_{\text{aniso}}, \mathbf{R}_{\text{aniso}}, \mathbf{R}_{\text{iso}, 1}, \dots, \mathbf{R}_{\text{iso}, n}]$ being the multi-tissue axially symmetric response function (RF) consisting of an anisotropic component $\mathbf{R}_{\text{aniso}}$ and n isotropic compartments $\{\mathbf{R}_{\text{iso}, i}\}_{i=1}^n$ as defined in [16]. Each column of

$$\mathcal{X} = [\mathbf{X}_{\text{aniso}}^+, \mathbf{X}_{\text{aniso}}^-, \mathbf{X}_{\text{iso}, 1}, \dots, \mathbf{X}_{\text{iso}, n}]^T$$

is the spherical harmonics (SH) coefficients of AFODF at each voxel location. The AFODF is represented by two sets of even-order spherical harmonics [12], capturing potentially asymmetric sub-voxel fiber configurations. That is,

$$\mathcal{F}_{\text{aniso}}(\mathbf{u}) = \begin{cases} \mathbf{A}(\mathbf{u}) \cdot \mathbf{X}_{\text{aniso}}^+, & \mathbf{u} \in \mathbb{S}_+^2, \\ \mathbf{A}(\mathbf{u}) \cdot \mathbf{X}_{\text{aniso}}^-, & \mathbf{u} \in \mathbb{S}_-^2, \end{cases} \quad (4)$$

where $\mathbf{A}(\mathbf{u})$ is the real even-order SH basis function sampled in direction $\mathbf{u}$, and the column vectors of $\mathbf{X}_{\text{aniso}}^+$ and $\mathbf{X}_{\text{aniso}}^-$ are the corresponding SH coefficients for the positive and negative hemispheres ($\mathbb{S}_+^2$ and $\mathbb{S}_-^2$).

2.4 Super-Resolution Reconstructions

Based on Eq. (2), we estimate $\mathbf{S}$ and $\mathcal{X}$ by solving

$$\min_{\mathbf{S}, \mathcal{X}} \frac{1}{2} \|\mathbf{B} \odot (\mathbf{Y} - \mathbf{D}\mathbf{S})\|^2 + \lambda \|\mathcal{L}\mathcal{X}\|^2, \text{ s.t. } \begin{cases} \mathbf{S} = \mathcal{R}\mathcal{X}, \\ \mathcal{A}\mathcal{X} \geq 0, \\ \Phi(\mathcal{F}_{\text{aniso}}) \leq \epsilon, \\ \mathbf{S} \geq 0, \end{cases} \quad (5)$$

where the Laplace-Beltrami regularization [17] is realized via $\mathcal{L} = \text{diag}[\mathbf{L}, \mathbf{L}, 0, \dots, 0]$ where $\mathbf{L}_{jj} = \ell(\ell+1)$ with ℓ being the order associated with the j -th coefficient. λ is the regularization parameter and the matrix $\mathcal{A} = \text{diag}[\mathbf{A}, \mathbf{A}, a_0, \dots, a_0]$ maps the SH coefficients $\mathcal{X}$ to the AFODF amplitudes for imposing AFODF non-negativity. $a_0 = \sqrt{\frac{1}{4\pi}}$ is the 0-th order SH basis function.

Problem (5) is solved using alternating direction method of multipliers (ADMM) [18]. Specifically, the problem can be cast as a strictly convex quadratic programming (QP) problem, which can be solved by an operator splitting solver for quadratic programs (OSQP) [19]. Following common SR frameworks [5–7], we used linearly interpolated data to initialize ADMM.

2.5 Implementation Details

A white matter (WM) RF is estimated for each b-shell from the average of the reoriented diffusion signal profiles of voxels with high anisotropy in WM. Also isotropic RFs are set with diffusivity values ranging from $0.1 \times 10^{-3} \text{ mm}^2/\text{s}$ to $3 \times 10^{-3} \text{ mm}^2/\text{s}$ and step size $0.2 \times 10^{-3} \text{ mm}^2/\text{s}$. This will allow better characterization of tissue microstructure in healthy and tumorous brains.

We used k-fold cross-validation to determine the optimal regularization parameter λ in (5). Two thousand random WM voxels from an HCP DMRI dataset and 61 candidate values for λ , logarithmically spanning the interval between 0.01 and 10, were considered [12, 13]. We found that the optimal value was 0.01. This value was applied to all experiments.

3 Experimental Results

We compared our method, fiber-continuity super-resolution (FCSR), with four existing methods, including bicubic interpolation, Lanczos-3 resampling, TV-L1 reconstruction [20], and TV-L2 reconstruction [21]. We assumed that LR DW volumes $\mathbf{Y}$ are spatially downsampled from HR DW volumes $\mathbf{S}$ by a factor of 2 for each dimension. Objective evaluation was performed using Blind/Referenceless Image Spatial Quality Evaluator (BRISQUE) [22] and Naturalness Image Quality Evaluator (NIQE) [23]. Both BRISQUE and NIQE are no-reference image quality scores, with lower values indicating better image quality. Three datasets, summarized in Table 1, were used for validation, involving (i) a pre-surgical glioma patient [24]; (ii) a healthy subject with data acquired using slice-interleaved diffusion encoding (SIDE) [14]; and (iii) a macaque with histological data [25].

3.1 Glioma Dataset

Representative results for fractional anisotropy (FA), isotropic volume fraction (IVF), apparent diffusion coefficient (ADC), intra-cellular volume fraction (ICVF)¹, and tissue maps are shown in Fig. 1. Among the methods, FCSR recovers more structural details, especially in the zoomed-in regions. Moreover, FCSR retains the shape of the tumor, similar to the T1-weighted image that is shown in the insets. FCSR results in lower BRISQUE and NIQE scores, indicating better image quality. Figure 2 shows that FCSR improves the tractography of fiber bundles connecting cortical or sub-cortical regions.

3.2 SIDE Dataset

We also evaluated FCSR with SIDE [14] data acquired with acceleration factors $R = 2, 4$, and 10. Collecting the full data ($R = 1$) took a total acquisition time of 8.32 min. Therefore, the acquisition time is $8.32/R$ minutes for acceleration factor R . The results are summarized in Fig. 3, demonstrating that FCSR recovers more structural details especially in the cortical regions. The effectiveness of FCSR is further confirmed by the lower NIQE and BRISQUE scores. Note that $R = 10$ corresponds to less than one minute of acquisition time. Coupling SIDE with FCSR allows rich information on tissue microstructure to be collected in a very short amount of time.

We also evaluated FCSR by ICVF values along tractography streamlines. Figure 4(d, e) show that FCSR improves the tractography of u-fibers connecting small cortical or subcortical regions, with high consistency between full acquisition (i.e., FCSR (HR)) and acquisitions with different acceleration factors.

Figure 5 compares the FODFs generated by (a) spatially upsampled SH coefficients [17] of the full LR data ($R = 1$) and (b) FCSR. It can be seen that details near the cortex cannot be sufficiently recovered by upsampling via interpolation. On the other hand, FCSR yields superior orientation details in the cortical region, critical for mitigating gyral bias and improving the estimation of cortico-cortical connections [12].

3.3 Macaque Dataset

Figure 6 summarizes the results for the macaque dataset, including color FA, axon diameter index, and tissue maps. Note that HR and SR DMRI data are reconstructed from original LR and HR DMRI data, respectively. The results again indicate that FCSR is superior in preserving details and consistent across HR and SR reconstruction. The efficacy of FCSR is confirmed by the mean squared error (MSE) and structural similarity index (SSIM), which are computed between the reconstructed HR data and the original HR data, averaged across volumes.

4 Conclusion

We demonstrated that spatial resolution can be improved using the fiber-continuity constraint in a global whole-brain optimization framework. Our evaluation with datasets

¹Computed using AMICO [26].

acquired with different resolutions, imaging sequences, and scanners for humans and non-human primates indicate that our method is effective in resolution enhancement.

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Fig. 1. Color FA, IVF, ADC, ICVF, and WM tissue maps of a patient with glioma. NIQE and BRISQUE scores are shown on the right. The T1-weighted reference image is shown in the insets of the IVF results.

Fig. 2.

Fiber bundles given by (a) the original LR data, (b) bicubic interpolation, (c) Lanczos-3 resampling, (d) TV-L1 reconstruction, (e) TV-L2 reconstruction, and (f) FCSR.

Fig. 3. Color FA map, WM tissue map, GM tissue map, ICVF map, and FODF glyphs of the SIDE data acquired from a healthy subject. NIQE and BRISQUE scores are shown on the right.

Fig. 4.

The tract streamlines and along-tract ICVF values for five major white matter bundles. On the right, the ICVF values averaged across streamlines in a bundle are plotted along-tract locations. The Pearson correlation coefficients (r) and the p -values of mean ICVF values between the full and accelerated acquisitions are shown.

Fig. 5.

Comparison of HR FODFs computed by (a) upsampling the SH coefficients and (b) FCSR of the full LR data ($R = 1$). Close-up views are shown for the cortical region marked by the red rectangle.

Fig. 6.

Color FA, axon diameter, and GM tissue maps of the macaque brain. MSE and SSIM values are shown on the right. FCSR (HR) and FCSR (SR) are reconstructed from original LR and HR DMRI, respectively.

Table 1.**Datasets**

	Glioma [24]	SIDE [14]	Macaque [25]	
			LR	HR
Dimensions	$96 \times 96 \times 60$	$128 \times 128 \times 100$	$48 \times 96 \times 64$	$96 \times 192 \times 128$
Resolution	2.5 mm^3	1.5 mm^3	0.8 mm^3	0.4 mm^3
Acceleration	N/A	Multiband = 5	N/A	
b-value (s/mm ²)	700,1200,2800	500,1000,2000,3000	3000,6000,9000,120000	
# Gradient directions	100	160	404	
# Non-DW volumes	2	1	16	