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Multi-shell diffusion signal recovery from sparse measurements

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ABSTRACT

For accurate estimation of the ensemble average diffusion propagator (EAP), traditional multi-shell diffusion imaging (MSDI) approaches require acquisition of diffusion signals for a range of *b*-values. However, this makes the acquisition time too long for several types of patients, making it difficult to use in a clinical setting. In this work, we propose a new method for the reconstruction of diffusion signals in the entire *q*-space from highly undersampled sets of MSDI data, thus reducing the scan time significantly. In particular, to sparsely represent the diffusion signal over multiple *q*-shells, we propose a novel extension to the framework of spherical ridgelets by accurately modeling the monotonically decreasing radial component of the diffusion signal. Further, we enforce the reconstructed signal to have smooth spatial regularity in the brain, by minimizing the total variation (TV) norm. We combine these requirements into a novel cost function and derive an optimal solution using the Alternating Directions Method of Multipliers (ADMM) algorithm. We use a physical phantom data set with known fiber crossing angle of 45° to determine the optimal number of measurements (gradient directions and *b*-values) needed for accurate signal recovery. We compare our technique with a state-of-the-art sparse reconstruction method (i.e., the SHORE method of Cheng et al. (2010)) in terms of angular error in estimating the crossing angle, incorrect number of peaks detected, normalized mean squared error in signal recovery as well as error in estimating the return-to-origin probability (RTOP). Finally, we also demonstrate the behavior of the proposed technique on human *in vivo* data sets. Based on these experiments, we conclude that using the proposed algorithm, at least 60 measurements (spread over three *b*-value shells) are needed for proper recovery of MSDI data in the entire *q*-space.

1. Introduction

Diffusion MRI (dMRI) is an imaging modality that is sensitive to the neural architecture and connectivity of the brain. Consequently, it is increasingly being used in clinical settings for investigating several brain disorders such as, Alzheimer's disease, stroke, schizophrenia and mild traumatic brain injury (Thomason and Thompson, 2011; Shenton et al., 2012). Apart from more traditional Diffusion Tensor Imaging (DTI), it is nowadays standard to use High Angular Resolution Diffusion Imaging (HARDI), which involves acquiring diffusion signals at a single *b*-value (single *q*-shell) in several gradient directions spread over the unit sphere in a quasi-uniform manner (Tuch et al., 2003; Assemlal et al., 2011). While this protocol allows for resolving the complex angular structure of the neural fibers, it does not provide information about the radial signal decay, which is known to be sensitive to various anomalies of white matter (Cohen and Assaf, 2002).

To obtain accurate information about the neural architecture, diffusion spectrum imaging (DSI) was proposed by Wedeen et al. (2005). This dMRI technique involves acquiring multiple measurements over a Cartesian grid of points in the *q*-space, followed by application of discrete Fourier transform to obtain an estimate of the ensemble average propagator (EAP). Unfortunately, a large number of measurements required by DSI makes it impractical to use in clinical settings. Accordingly, to speed-up the acquisition of dMRI (and DSI) data, two complementary approaches have been proposed, namely: (i) the use of compressed sensing (CS) to reduce the number of measurements (Candès et al., 2006; Donoho, 2006), and (ii) the use of multi-slice acquisition sequences for faster data acquisition (Setsompop et al., 2011; Feinberg et al., 2010). This work focuses on methodology (i), i.e., CS-based reconstruction of diffusion signal from critically undersampled measurements.

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Several imaging and analysis schemes, which use fewer measurements than traditional DSI, have recently been proposed in the literature (Wu and Alexander, 2007; Jensen et al., 2005; Assemlal et al., 2011; Merlet et al., 2012; Barmpoutis et al., 2008; Descoteaux et al., 2010; Zhang et al., 2012; Ye et al., 2011; Ye et al., 2012; Hosseinbor et al., 2013). Each of these techniques captures a different aspect of the underlying tissue organization, which is missed by HARDI. Traditional methods of EAP estimation that account for the non-monoexponential (radial) decay of diffusion signals, require a relatively large number of measurements at high b-values (greater than 3000 s/mm^2) (Assaf et al., 2004; Mulkern et al., 2001). Consequently, their associated scan times are deemed to be too long for non-cooperative patients, which is the main motivation for reducing the number of measurements in dMRI scans.

Although not new in application to MRI, CS-based methods of signal reconstruction has gained significant attention in the diffusion imaging community over the last few years. Several works have proposed CS-based algorithms for recovering HARDI, MSDI as well as DSI data from undersampled (aka incomplete) measurements (Ye et al., 2011; Merlet et al., 2012; Landman et al., 2012; Gramfort et al., 2012; Duarte-Carvajalino et al., 2012; Freiman et al., 2013; Scherrer et al., 2013; Assemlal et al., 2011; Michailovich et al., 2011; Rathi et al., 2011). To this end, various types of signal representation bases have also been proposed, each having different sparsifying properties. For example, for HARDI data, spherical ridgelets were proposed in Michailovich et al. (2008), Michailovich and Rathi (2010), and for MSDI data, spherical polar Fourier (SPF) and its variants (SHORE) were proposed in (Assemlal et al., 2008; Ozarslan et al., 2008; Cheng et al., 2010; Merlet et al., 2012). In the case of the SHORE basis, to optimize the accuracy of signal reconstruction, one has to choose an appropriate scaling parameter, which could potentially be different for different types of tissue. To address this issue, (Merlet et al., 2012) used a dictionary learning technique to learn the scaling parameter and the appropriate polynomial to represent the radial decay term. On the other hand, in Özarslan et al. (2013), this scaling parameter was adaptively obtained in a data driven fashion by computing the eigenvalues of a tensor at each voxel. However, at a fundamental level, both these methods extend the original SHORE basis to sparsely represent the diffusion data. In this work, we will compare our technique with the SHORE-based reconstruction (Cheng et al., 2010; Merlet and Deriche, 2013), where sparsity is enforced through the standard l_1-norm minimization. In our earlier work (Rathi et al., 2011), we had also proposed a basis that combined the spherical ridglets with a radial term. However, the cost function used in that work was non-convex, making it quite susceptible to local minima. In this work, we propose significant modifications and address the limitations of our earlier work, as discussed in the next section.

2. Our contributions

The framework of spherical ridgelets (SR) proposed in Michailovich et al. (2011) was used to recover HARDI data on a single b-value shell from highly undersampled set of diffusion measurements. In this work, we propose a novel extension of this basis for recovering multi-shell diffusion data. Towards this end, we incorporate a novel radial decay term which is a monotonically decreasing function with its range bounded between 0 and 1. This property is quite desirable, since it is known that the values of normalized diffusion signals lie within this range (Clark and Le Bihan, 2000; Schwarcz et al., 2004; Mulkern et al., 2009). In this work, we use spherical ridgelets to perform CS-based reconstruction of MSDI signals over each of their associated b-value shells (q-shells), while using the radial decay term for representing the signal attenuation with increasing b-values. To obtain an optimal consensus solution that ensures spatially smooth signal recovery, we propose a novel computational framework based on the ADMM algorithm. We perform extensive testing of the proposed algorithm on a physical phantom data set and compare it with the SHORE-based method. We provide quantitative results in terms of the error in estimation of the orientation, incorrect number of peaks detected, normalized mean squared error (NMSE) in the estimation of the signal as well as NMSE in the estimation of the return-to-origin probability (RTOP). We also provide similar quantitative results on human *in vivo* data set.

The primary aim of the algorithm presented in this work is the recovery of diffusion signal from sub-critically sampled measurements. Following this, any model or methodology (such as, multi-compartment models, kurtosis, diffusion propagator and free-water) can be used to compute diffusion measures or features (Özarslan et al., 2013). Thus, in this work, we do not focus on recovering model specific diffusion properties as they can be computed once an estimate of the diffusion signal in the entire q-space is available using the proposed method.

3. Background

3.1. Diffusion MRI

Under the narrow pulse assumption, the diffusion signal $S(\mathbf{q})$ in the q-space is related to the EAP $P(\mathbf{r})$ via the Fourier transform as given by Stejskal and Tanner (1965)

$$P(\mathbf{r}) = \int_{\mathbf{r}\in\mathcal{R}^3} E(\mathbf{q}) \exp(-i2\pi\mathbf{q}\cdot\mathbf{r}) d\mathbf{q},$$

where $E(\mathbf{q}) \triangleq S(\mathbf{q})/S(0) : \mathbb{R}^3 \rightarrow [0,1]$ is the *normalized* diffusion signal, with $S(\mathbf{q})$ and $S(0)$ being the measured diffusion signal and its corresponding $b = 0$ value, respectively. Alternatively, E can be written as a function of b-value and a unit vector $\mathbf{u} \in \mathbb{S}^2$, such that $E(b,\mathbf{u}) : \mathbb{R}^+ \times \mathbb{S}^2 \rightarrow [0,1]$, where $b = \gamma^2\delta^2(\Delta - \delta/3)\|\mathbf{g}\|^2$ s/mm^2, with δ being the duration of the gradient pulse, Δ is the mixing time (i.e., the time between the two diffusion-encoding gradients), γ is the gyromagnetic constant, and $\|\mathbf{g}\|$ denotes the Euclidean norm of the diffusion-encoding gradient $\mathbf{g}$. In the context of MSDI, the signal E is measured along N discrete orientations $\{\mathbf{u}_k\}_{k=1}^N$ for several different values of b. Thus, for each b value shell, the sampling points are spread over the unit sphere, thereby giving the measurements a multi-shell structure.

3.2. Compressed sensing

The theory of CS provides the mathematical foundation for accurate recovery of signals from their discrete measurements acquired at sub-critical (aka sub-Nyquist) rate (Candès et al., 2006; Donoho, 2006; Candes et al., 2011). The theory relies on two key concepts: *sparsity* and *incoherence*, although the latter requirement could be relaxed in certain cases (Candes et al., 2011). Sparsity implies that the signal of interest should have a sparse representation in some basis/frame $\Psi \in \mathcal{R}^{N\times M}$, which we term as the representation dictionary. The signal $E \in \mathcal{R}^N$ is said to admit a sparse representation in Ψ if its expansion coefficients contain only a small number of significant coefficients, i.e. if $E = \Psi\mathbf{c}$, then most of the elements of $\mathbf{c} \in \mathcal{R}^M$ are zero. If only K elements of $\mathbf{c}$ are nonzero, then the signal E is said to be K-sparse in Ψ, where $K \ll M$.

The framework of CS also relies on a sensing or sampling basis Φ. In the context of diffusion MRI, since we have a single value $E(\mathbf{q})$ associated to each point $\mathbf{q}$ in the q-space, we assume that the