Medical Image Analysis 18 (2014) 36–49

Contents lists available at ScienceDirect

Medical Image Analysis

journal homepage: www.elsevier.com/locate/media

Denoising and fast diffusion imaging with physically constrained sparse dictionary learning

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ARTICLE INFO

Article history:
Received 12 February 2013
Received in revised form 26 August 2013
Accepted 30 August 2013
Available online 10 September 2013

Keywords:
Diffusion-weighted imaging
Diffusion Spectrum Imaging (DSI)
Sparse coding
Denoising
Undersampling

ABSTRACT

Diffusion-weighted imaging (DWI) allows imaging the geometry of water diffusion in biological tissues. However, DW images are noisy at high *b*-values and acquisitions are slow when using a large number of measurements, such as in Diffusion Spectrum Imaging (DSI). This work aims to denoise DWI and reduce the number of required measurements, while maintaining data quality. To capture the structure of DWI data, we use sparse dictionary learning constrained by the physical properties of the signal: symmetry and positivity. The method learns a dictionary of diffusion profiles on all the DW images at the same time and then scales to full brain data. Its performance is investigated with simulations and two real DSI datasets. We obtain better signal estimates from noisy measurements than by applying mirror symmetry through the q-space origin, Gaussian denoising or state-of-the-art non-local means denoising. Using a high-resolution dictionary learnt on another subject, we show that we can reduce the number of images acquired while still generating high resolution DSI data. Using dictionary learning, one can denoise DW images effectively and perform faster acquisitions. Higher *b*-value acquisitions and DSI techniques are possible with approximately 40 measurements. This opens important perspectives for the connectomics community using DSI.

1. Introduction

Diffusion-weighted imaging (DWI) is able to non-invasively image the diffusion of water molecules in biological tissues. DWI was rapidly made popular by several clinical applications using apparent diffusion coefficient (ADC) imaging and diffusion tensor imaging (DTI) (Basser et al., 1994). However, the diffusion tensor is an over-simplified *Gaussian* view of the local diffusion phenomenon happening in each imaging voxel. The holy grail of DWI is to recover the full tridimensional (3D) probability distribution describing the local diffusion phenomenon. This is often called the ensemble average propagator (EAP) formalism (Tuch, 2002; Wedeen et al., 2005; Descoteaux et al., 2011), which provides a powerful framework to describe and predict the diffusion behavior in complex materials. The EAP contains the full 3D information about the water molecule diffusion within the imaging voxel, which goes beyond principal directions that can be used for tractography (Merlet et al., 2012b). The EAP can serve to estimate parameters that reflect the microstructural environment, such as axonal diameter in recent works (Assaf et al., 2008; Ozarslan et al., 2013).

EAP imaging can be long and demanding in terms of acquisition requirements (Descoteaux et al., 2011). Hence, the last 10 years have seen the emergence of numerous techniques to reconstruct the angular information of the EAP, the orientation distribution function (ODF) or other such angular distributions (Seunarine and Alexander, 2009; Descoteaux and Poupon, in press) from a reduced sampling scheme. These new techniques are most often restricted to a single shell in q-space with N uniform measurements for a single b-value (typically $b \in [1000, 3000]$ s/mm^2). This spanned the rich literature of high angular resolution diffusion imaging (HARDI), from compartment modeling to model-free and deconvolution techniques. These works are well covered in the following two book chapters (Seunarine and Alexander, 2009; Descoteaux and Poupon, in press).

In the last 2–4 years, Diffusion Spectrum Imaging (DSI) and 3D DWI have regained popularity, because of two applications. First, several works have shown that the radial information of the DWI signal is important and can be sensitive to white-matter anomalies caused by demyelination or brain damage (Assaf et al., 2008; Alexander, 2008). Consequently, new modeling and anisotropy

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http://dx.doi.org/10.1016/j.media.2013.08.006

measures from the EAP have appeared in the literature to better capture both the radial and angular information contained in the diffusion signal. Second, the recent fame of DSI (Wedeen et al., 2012) combined with connectomics studies (Hagmann et al., 2008; Honey et al., 2009), as well as the human brain connectome project[1] have made DSI a central acquisition protocol, despite the issue of long scanning time.

No matter what diffusion imaging protocol is used, be it scalar DWI, DTI, HARDI, or DSI, there is always a trade-off between quality of the data and acquisition time. Indeed, the higher the number of acquired images, the better the estimation of the diffusion signal will be. A common way of improving the signal-to-noise ratio (SNR), which is particularly poor for large b-values (see Fig. 6 for an example), is to repeat the acquisition of the same signal with the same sequence parameters and average them. However, for clinical requirements and applications, and considering the reduction of the risk of motion artifacts, an acquisition time between 3 and 15 min is the limit. A first challenge is therefore to be able to improve the SNR of a single acquisition of DWI with denoising algorithms. A second challenge is the ability to reduce the number of acquired images while offering the high resolution data required to estimate complex white matter structures, such as fiber crossing configurations, and microstructural features, such as axonal diameter (Assaf et al., 2008; Alexander, 2008). This paper addresses both of these challenges, providing validation and performance quantification using denoising metrics. The motivation for the use of a denoising benchmark is to compare the results obtained from undersampled data, with full resolution data after denoising using some well established methods. The experimental section focuses on DSI data, as it is a protocol with a dense sampling scheme using high b-value images. Two questions are of particular interest: Can we obtain DSI data with the same number of DWIs required for single b-value HARDI? How much can we subsample the q-space while keeping high spectral resolution in diffusion images?

The intuition behind this paper is that the signal measured by multiple DWIs over the q-space is redundant and shares an underlying structure: the DSI acquisition on a 258 points half-space or on the full 515 points sampling contains redundant information that one can learn and then use to denoise or reduce the number of acquisitions. We show that a dictionary estimated from DSI data captures the geometry of white matter brain structures and can thus be used in 2 different setups: (i) intra-subject studies, for denoising purposes and (ii) inter-subject studies, to perform super-resolution of q-space data. The latter is done by acquiring subsampled DSI data (low resolution) and using a high resolution dictionary of DSI profiles learnt on another subject in order to recover the full DSI. This inter-subject validation setup was earlier proposed in our previous work (Gramfort et al., 2012), and by Bilgic et al. (2012a), although using an alternative non-physically constrained dictionary learning formulation (see next section). The key contribution of this work is to use sparse coding to estimate a dictionary of prototypical diffusion profiles constrained by physical properties of the signal. We indeed enforce symmetry and positivity for the atoms in the dictionary taking into account the structure of the signal present in multiple DWIs. See for example (Tournier et al., 2007), for a previous demonstration of the relevance of non-negativity constraints. As for symmetry, the physics of dMRI tells us that the measured local diffusion signal must also be symmetric (Tuch, 2002, Sections 3.3 and 8.3.2.3).

Results are presented on a publicly available simulation dataset and on two real DSI datasets, one from the Pittsburgh Brain Competition 2009 Challenge and one from our institute. The results of the proposed method are compared to the SNR improvements obtained by applying mirror symmetry through the q-space origin, Gaussian denoising and state-of-the-art non-local means denoising. A preliminary version of this work was presented at the MICCAI 2012 international conference (Gramfort et al., 2012). This manuscript complements it with more details on the method, an extensive simulation study and results on a new dataset (Pittsburgh Brain Competition 2009).

2. Theory

2.1. Diffusion-weighted imaging and diffusion spectrum imaging

Under the narrow pulse assumption (Stejskal and Tanner, 1965), there is a Fourier relationship between the measured DWI signal and diffusion propagator, $P(\mathbf{R})$,

$$P(\mathbf{R}) = \int_{\mathbf{q}\in\Re^3} E(\mathbf{q}) e^{-2\pi i \mathbf{q}\cdot\mathbf{R}} d\mathbf{q}, \tag{1}$$

with $E(\mathbf{q}) = S(\mathbf{q})/E_0$, where $S(\mathbf{q})$ is the diffusion signal measured at position $\mathbf{q}$ in q-space, and E_0 is the baseline image acquired without any diffusion sensitisation ($q = 0$). We denote $q = |\mathbf{q}|$ and $\mathbf{q} = q\mathbf{u}$, $\mathbf{R} = r\mathbf{r}$, where $\mathbf{u}$ and $\mathbf{r}$ are 3D unit vectors. The wave vector $\mathbf{q}$ is $\mathbf{q} = \gamma\delta\mathbf{G}/2\pi$, with γ the nuclear gyromagnetic ratio of water molecules and $\mathbf{G} = g\mathbf{u}$ the applied diffusion gradient vector. The norm of the wave vector, $\mathbf{q}$, is related to the diffusion weighting factor (the b-value), $b = 4\pi^2 q^2 \tau$, where $\tau = \Delta - \delta/3$ is the effective diffusion time with δ the duration of the applied diffusion sensitizing gradients and Δ the time between the two pulses. Note that the Fourier relationship between the EAP and the diffusion signal of Eq. 1 is strictly valid only if the narrow pulse assumption is met, which is rarely the case in *in vivo* 3D q-space MRI. Nonetheless, we can measure the approximation of the average diffusion propagator by taking the ensemble average over the imaging voxel, hence the name Ensemble Average Propagator, EAP (Tuch, 2002).

The current state-of-the-art acquisition technique to reconstruct the 3D diffusion propagator is DSI. The original DSI protocol (Wedeen et al., 2005) measured $S(\mathbf{q})$ on a Cartesian grid restricted to a sphere of radius 5, resulting in 515 q-space discrete measurements $S(\mathbf{q})$. Then, a simple 3D inverse Fast Fourier Transform (FFT) is applied to recover the EAP at every imaging voxel. Finally, the diffusion ODF, Ψ, can be extracted by numerically computing the radial integral over the discrete DSI grid, $r \in [0,5]$, as

$$\Psi(\mathbf{u}) = \int_0^5 P(r\mathbf{u}) r^2 dr. \tag{2}$$

DSI acquisition is a long process. A typical full brain coverage acquisition with 60 axial slices, 2 mm isotropic voxels, parallel imaging, a repetition time of approximately TR = 11 s, a full DSI grid with 515 directions and b-values from 0 to 6,000 s/mm^2 or so, takes 1h45 min of acquisition (Descoteaux et al., 2011). Because diffusion is symmetric (Tuch, 2002), one can reduce acquisition time by half if only the half-space is acquired, resulting in 257 directions (Hagmann et al., 2008). The missing half is then obtained by applying mirror symmetry through the q-space origin.

2.2. Dictionary learning

Sparse coding, equivalently referred to as dictionary learning, applied to diffusion weighted images such as DSI data reveals the latent structure of the diffusion in white matter voxels. However, sparse coding is not compressed sensing (CS). Compressed sensing consists of three ingredients: a linear sensing process, a linear transformation to the data that generates sparsity and is incoherent to the sensing basis, and a solver used for signal recovery that promotes sparse estimates, *e.g.* using ℓ_1 norm or ℓ_0 non-linear

[1] http://www.humanconnectomeproject.org/.