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A joint compressed-sensing and super-resolution approach for very high-resolution diffusion imaging

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ABSTRACT

Diffusion MRI (dMRI) can provide invaluable information about the structure of different tissue types in the brain. Standard dMRI acquisitions facilitate a proper analysis (e.g. tracing) of medium-to-large white matter bundles. However, smaller fiber bundles connecting very small cortical or sub-cortical regions cannot be traced accurately in images with large voxel sizes. Yet, the ability to trace such fiber bundles is critical for several applications such as deep brain stimulation and neurosurgery. In this work, we propose a novel acquisition and reconstruction scheme for obtaining high spatial resolution dMRI images using multiple low resolution (LR) images, which is effective in reducing acquisition time while improving the signal-to-noise ratio (SNR). The proposed method called compressed-sensing super resolution reconstruction (CS-SRR), uses multiple overlapping thick-slice dMRI volumes that are under-sampled in q-space to reconstruct diffusion signal with complex orientations. The proposed method combines the twin concepts of compressed sensing and super-resolution to model the diffusion signal (at a given b-value) in a basis of spherical ridgelets with total-variation (TV) regularization to account for signal correlation in neighboring voxels. A computationally efficient algorithm based on the alternating direction method of multipliers (ADMM) is introduced for solving the CS-SRR problem. The performance of the proposed method is quantitatively evaluated on several in-vivo human data sets including a true SRR scenario. Our experimental results demonstrate that the proposed method can be used for reconstructing sub-millimeter super resolution dMRI data with very good data fidelity in clinically feasible acquisition time.

Introduction

Diffusion-weighted Magnetic Resonance Imaging (dMRI) is a key technique for studying the neural architecture and connectivity of the brain. It utilizes multiple 3-dimensional diffusion-weighted images to probe the water diffusivity along various directions. Its importance has been proven in clinical settings for investigating several brain disorders such as Alzheimer's disease, schizophrenia and mild traumatic brain injury (Thomason and Thompson, 2011; Shenton et al., 2012). However, low signal-to-noise ratio (SNR) and acquisition time limit the typically spatial resolution of dMRI to the order of $2 \times 2 \times 2$ mm^3. Consequently, dMRI has been mainly used to study medium-to-large white matter structures. Further, partial volume effects (PVE) which occur at the interface of different tissue types (gray-white, gray-CSF (cerebrospinal fluid) and white-CSF) can have significant effect on the measured diffusion properties and can lead to erroneous inferences (Metzler-Baddeley et al., 2014; Alexander et al., 2001). While some of the effects of CSF contamination can be removed using free-water modeling (Metzler-Baddeley et al., 2012), yet large voxel sizes can lead to erroneous results in tractography. Consequently, increasing the spatial resolution of dMRI is imperative for investigation of small white-matter fascicles originating in small cortical and sub-cortical gray matter structures (such as, substantia nigra or sub-thalamic nucleus).

Reducing the voxel size of dMRI is challenging because the SNR is directly proportional to the voxel size if the readout time is fixed (see Nishimura, 1996, page 163). Although SNR could be enhanced by averaging multiple acquisitions, the increase in SNR is proportional to the square root of the number of averages. For example, reducing the voxel size from $2 \times 2 \times 2$ mm^3 to $1 \times 1 \times 1$ mm^3 requires 64 averages to obtain equivalent SNR, which makes it impractical to use such an "averaging" scheme in current clinical setting. Recently, several methods have been proposed to obtain high-resolution (HR) dMRI data. These methods can be classified into two categories based on their acquisition strategies. The first group of methods obtains high spatial resolution using a single low-resolution image via intelligent interpolation. These types of methods have been widely used for natural images (van Ouwerkerk, 2006) and more recently for MRI (Manjón et al., 2010;

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Rousseau, 2010) and dMRI (Coupé et al., 2013; Dyrby et al., 2014). Though, these methods preserve and enhance certain anatomical details, their performance still largely depends on the original image resolution, as pointed out in the work of Dyrby et al. (2014).

The second group of methods uses the concept of super-resolution to obtain high resolution data from multiple LR image volumes acquired according to specific sampling schemes. A HR image is estimated by intelligently fusing the LR images. This type of method was initially studied in Irani and Peleg (1993) for reconstruction of HR images using multiple LR stereo images. It has since been applied to obtain HR anatomical MRI images (Greenspan et al., 2002; Greenspan, 2009; Gholipour et al., 2010) by employing sub-pixel-shifted scans along the slice-select dimension. In the field of diffusion MRI, it was first proposed in Peled and Yeshurun (2001) to obtain high resolution diffusion tensor images. The authors in Scherrer et al. (2012) used acquisition from three orthogonal directions to perform super-resolution, while the authors in Poot et al. (2010) use a generalized version with arbitrary slice acquisition direction to obtain HR images. However, in most these methods, super-resolution was applied independently to each individual diffusion weighted volume and the correlation between diffusion signals in q-space was not taken into account during the reconstruction process. As a result, each of the LR images were either acquired or interpolated on the same set of diffusion gradients prior to obtaining the complete dMRI volume. Further, all of the LR volumes have to be corrected for EPI (echo-planar imaging) distortions, which are different for different slice-select directions. This requires accurate non-rigid registrations and blip-up blip-down acquisitions as in Sotiropoulos et al. (2013) for correcting the distortions, making the acquisition time significantly long. To address this problem, more recently, Van Steenkiste et al. (2013) introduced a method that used the diffusion tensor imaging (DTI) technique to model the diffusion signal in q-space. It was extended in Van Steenkiste et al. (2014) and Van Steenkiste et al. (2015) to allow the LR images to be acquired along different sets of gradients in q-space. Though this approach does reduce acquisition time and is robust to motion, a very simplistic diffusion tensor model is not appropriate for modeling more complex diffusion phenomena (crossing fibers). The proposed work is a generalization of this technique with no parametric model assumed about the diffusion signal and thus recovers the true underlying signal in its most general form (for a given b-value). A preliminary version of this paper has been accepted for publication in the conference on Information Processing in Medical Imaging (IPMI) 2015.

Our contributions

In this paper, we propose to combine the concepts of compressed sensing and super-resolution to reconstruct very high resolution diffusion data. In particular, we focus on a specific q-space sampling scheme known as high angular resolution diffusion imaging (HARDI) which uses several diffusion measurements at a single b-value shell (Tuch, 2004; Alexander, 2005). The proposed CS-SRR method reconstructs a HR image using multiple LR data sets which are also under-sampled in q-space. As illustrated in Fig. 1, given three thick-slice data sets that are sub-pixel-shifted along the slice-select dimension and have N_1, N_2 and N_3 gradient directions, respectively, we reconstruct a thin-slice high resolution dMRI data set that has $N_1 + N_2 + N_3$ gradients. Being a non-parametric method, the proposed approach is capable of resolving crossing of multiple fiber-bundles in the reconstructed high resolution image.

The proposed method uses spatial and q-space regularization techniques for reconstructing HR diffusion data. Additionally, we incorporate a-priori knowledge about the tissue type (gray, white or CSF) from a high-resolution T1-weighted image to adaptively reconstruct the HR diffusion data. Compressed sensing reconstruction from under-sampled data in q-space is achieved by means of a sparsifying basis of spherical ridgelets (Michailovich et al., 2011), whereas sparsity and smoothness in the spatial domain is incorporated by means of total-variation (TV) regularization. We design a convex cost functional and introduce an efficient optimization algorithm based on ADMM for solving the CS-SRR problem. We quantitatively evaluate the performance of our method by comparing short and long range fiber connectivity as well as the estimated diffusion measures such as fractional anisotropy (FA) and mean diffusivity or trace. The performance is evaluated for a synthetic scenario using the Human-Connectome-Project (HCP) data set and in a true SRR scenario, whereby quantitative comparison is made between high resolution data obtained using the proposed CS-SRR method and that obtained directly from the MR scanner (from repeated scans). We should note that, to the best of our knowledge, this is a first instance of combining compressed sensing and super-resolution to reconstruct the HR diffusion signal without any modeling assumptions of the diffusion process. The proposed acquisition and reconstruction scheme allows to reduce the scan time significantly (up-to 3 times) compared to the standard super-resolution reconstruction, which would require at-least 3 times more measurements than the proposed method. We thus expect the proposed method to be of great utility for future neuroimaging studies.

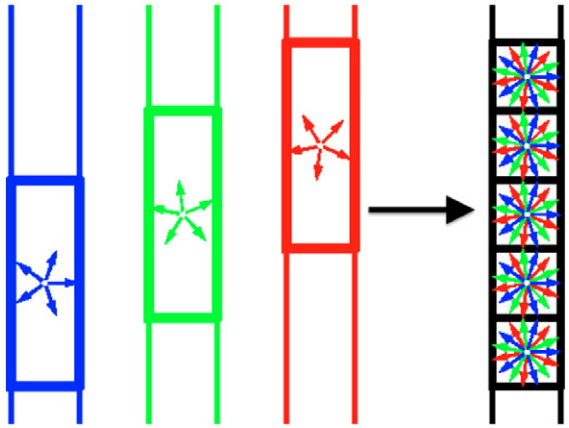

Fig. 1. An illustration of the proposed CS-SRR scheme: a high-resolution image is reconstructed using three overlapping thick-slice volumes with down-sampled diffusion directions.

Background

In this section, we provide a brief background on diffusion-weighted MRI, spherical ridgelets and the compressed sensing technique, which will be used subsequently in the proposed CS-SRR algorithm.

Diffusion-weighted imaging

Diffusion MRI is a favorite research tool for investigating the neural architecture and the connectivity of the brain. The ensemble average diffusion propagator (EAP) is usually estimated from the diffusion measurements to describe the average displacement of water molecules within a voxel during the sampling period, which provides important structural information about the underlying tissue. In the narrow pulse setting (for single pulse field gradient experiment), the diffusion signal $S(\boldsymbol{q})$ is related to the EAP $P(\boldsymbol{r})$ via the Fourier transform given by Stejskal and Tanner (1965)

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