# A compressed sensing approach to super-resolution diffusion MRI from multiple low-resolution images

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**PURPOSE:** Diffusion weighted imaging (DWI) allows to study the neural architecture and connectivity of the brain. Typical spatial resolution of diffusion-weighted images on a clinical scanner is about 2x2x2 mm$^3$. Increasing the spatial resolution can have several advantages: 1) small white matter bundles can be traced and analyzed, 2) partial volume effects (PVE) can be substantially reduced, 3) cortical and sub-cortical areas can be clearly delineated, and 4) more accurate gray matter and white matter analysis becomes possible in neonates and infants. However, there are significant challenges to acquiring DWI images with very high spatial resolution (say, $1^3$ mm$^3$) due clinical scanner's limitations (limited gradient strength, signal loss due to $T_2$ decay and increased TE, etc). Further, the signal to noise ratio (SNR) decreases proportionately to the decrease in voxel size, thus requiring several acquisitions to obtain descent SNR. This makes the scan time prohibitively long. Using the classical concept of super-resolution[1], a few methods have been proposed that use multiple low-resolution (LR) volumes to obtain high resolution (HR) data[2,3,4]. In this abstract, we propose a novel method that combines the concepts of compressed sensing and classical super-resolution to obtain high-resolution (HR) diffusion images. The proposed super resolution reconstruction (SRR) framework uses *multiple anisotropic low-resolution DWI volumes together with a sparsifying basis called spherical ridgelets*[4] to estimate the HR diffusion images. Hence, it is capable of modeling complex fiber orientations with reduced number of measurements[5,6]. Moreover, in the spatial domain, the standard total-variation (TV) regularization is used to account for the correlation of diffusion signal in neighboring voxels. Further, each of the LR DWI volumes are acquired with a unique set of diffusion gradient direction which keeps the total acquisition time the same as in standard settings.

**METHOD:** Let $E_b(\boldsymbol{u}_n)$ denote the normalized diffusion signal at a b-shell along the diffusion gradient direction $\boldsymbol{u}_n \in \boldsymbol{S^2}, n = 1, \dots, N$. Let $\boldsymbol{s} \in \boldsymbol{R}^N$ denote a vector that stacks all the measurements. It was shown in[5] that $\boldsymbol{s}$ can be modeled as $\boldsymbol{s} = A_{\text{ridg}}\boldsymbol{x} + \boldsymbol{w}$, where the basis matrix $A_{\text{ridg}} \in \boldsymbol{R}^{N\times M}$ with $A_{\text{ridg}}(n,m) = a_m(\boldsymbol{u}_n)$ and $a_m(\cdot)$ being a spherical ridelget function that models the diffusion process of a certain degree of anisotropy and along a certain direction, $\boldsymbol{x} \in \boldsymbol{R}^M$ only has few number of non-zero entries, and $\boldsymbol{w}$ denotes the measurement noise. For better approximating isotropic signals in CSF areas, we expand the basis matrix as $A = [a_{iso}, A_{\text{ridg}}]$ where $a_{\text{iso}}$ denotes a vector having equal entries. Before introducing the SRR model, we let $S \in \boldsymbol{R}^{n_x n_y n_z \times N}$ denote the data matrix of a HR image which has $n_x \times n_y \times n_z$ voxels and is acquired at a single b-shell along $N$ directions. Similarly, we let $Y_l, l = 1 \dots L$, denote the corresponding LR images. Then, $S$ is modeled as $S = XA^T$ where each row of $X$ is sparse and denotes the representation vector of the signal in a particular voxel. The LR image $Y_l$ is modeled as $Y_l = D_l B S Q_l^T + W_l$ where $B$ denotes the blurring, $D_l$ is the down-sampling operator in spatial domain, $Q_l$ sub-samples the signal in q-space and $W_l$ denotes the measurement noise. Then the HR image is estimated by solving $\min_{S,V}\{\sum_{l=1}^{L}\|Y_l - D_l B S Q_l^T\|^2 + \lambda_1\|W \circ X\|_1 + \lambda_2\|S\|_{TV} \text{ s.t. } S = XA^T\}$ where $\|\cdot\|_1$ is used to promote the sparsity of $X$, $\|\cdot\|_{TV}$ is for the smoothness of the image, $\lambda_1, \lambda_2 \geq 0$ are used to weigh the relative importance of the sparsity and smoothness compared to the model fitting error, $W$ denotes a weighting matrix. Each row $W$ is of the form $[w, 1, \dots, 1]$ with $w > 0$. A probabilistic segmentation of a $T_1$-weighted image into gray, white and CSF areas is used as a prior to guide the reconstruction process. Thus, a smaller value for $w$ is used for CSF areas compared to other tissue types. Since the optimization problem involves very high dimensional variables, we have devised an optimization algorithm using the alternating direction of multipliers (ADMM) to decompose the problem into a sequence of simpler optimization problems. We first introduce an auxiliary variable $Z$ such that $S - Z = 0$ and replace $\|S\|_{TV}$ by $\|Z\|_{TV}$. Following the standard procedure of ADMM, we build an augmented Lagrangian and introduce two multipliers for the constraints. Then the solution is obtained by iterating the following three steps until convergence: (1) Update $X$ and $Z$ for a fixed $S$ by solving the $\ell_1$-regularization and TV-regularization problems. (2) Based on the $X$ and $Z$ obtained in (1), update $S$ by solving a least-squares fitting problem. (3) Update the multipliers. In particular, the $\ell_1$-regularization in (1) can be optimized in parallel, while the least-squares solution is easily obtained if the LR images are aligned.

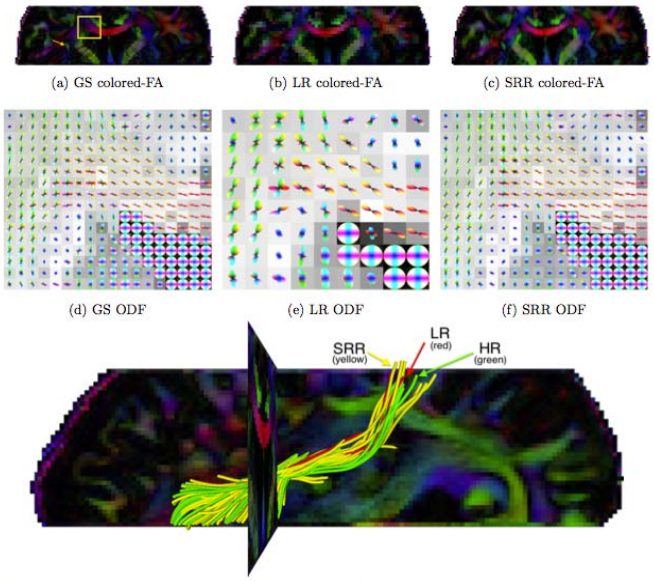


Figure 1: (a), (b), (c) are the colored FA images of the gold-standard (GS), low-resolution (LR) and SRR data sets, respectively. (d), (e), (f) are the corresponding ODF's for voxels in the rectangle area of (a). (g) shows the tractographies with ROI pointed out by the arrow in (a)

**RESULTS:** We validated the proposed method in a true SRR scenario using in-vivo human brain data. We acquired three LR data sets with high in-plane resolution (1.2 mm x 1.2 mm), which are shifted by 1.2 mm in physical space, but have a slice thickness of 3.6 mm. Each LR DWI volume had a unique set of 30 diffusion gradients at $b = 1000$. We recovered a HR image with isotropic voxels of size $1.2^3$ mm$^3$ and with 90 diffusion gradients. For comparison, we also acquired 9 HR scans ($1.2^3$ mm$^3$). Due to time limitations, the HR scans could be acquired only for a portion of the brain (partial brain coverage). The average of the 9 scans was considered as the gold-standard (GS) data set. We registered the whole-brain SRR image to the partial-brain GS image for comparison. To show the difference between HR and LR dMRI, we also down-sampled the GS image by averaging every $2 \times 2 \times 2$ neighboring voxels to create an isotropic LR image volume. Figure1 (a-c) are the coronal slices of the color FA images of the HR, LR and SRR data sets, respectively. Figure 1 (d-f) show the estimated ODF for voxels in the rectangle region of Figure 1(a) with $T_1$ images shown in background. Figure 1(g) shows tractography results for all three data sets with an ROI placed in the voxels pointed by the arrow in Figure 1(a). The LR data set shows fewer tracts than the HR and SRR data set, while the GS and SRR tracts overlap significantly, indicating accurate recovery of the data.

**Conclusion:** We presented a novel method for obtaining high-resolution diffusion data by combining the concepts of compressed sensing and classical super-resolution. Preliminary results show that the SRR method is capable of recovering complex fiber orientations at a very high spatial resolution, similar to a physically acquired "gold-standard" data. Hence it has potential to be applied in clinical settings to study mental diseases and to reduce PVE. Future work involves determining the minimum number of measurements required to obtain similar data quality as the gold standard.

**REFERENCES:** [1] M. Irani *et al.,* J Vis Commun Image Represent, 4 (4), 324-335, 1993. [2] S. Peled *et al.*, Magn. Reson. Med., 45 (1) 29-35, 2001. [3] D.H. Poot *et al.*, MICCAI, 615-622, 2010. [4] B. Scherrer *et al.,* Med. Image Anal., 16 (7), 1465-1476, 2012. [5] O. Michilovich *et al.*, IEEE Trans. Image Process., 19 (2) 461-477, 2010. [6] Y. Rathi *et al*. Med. Image Anal., 18 (7), 1143-1156, 2014.