Three dimensional restoration of cardiac magnetic resonance diffusion weighted images based on sparse denoising

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Introduction

At present, diffusion weighted imaging is the only means for *in vivo* and nondestructive characterization of the three-dimensional (3D) diffusion and fibre architecture of human anatomical organs. However, The acquisition of diffusion weighted magnetic resonance image (DWI) is often contaminated by thermal noise, structure noise, chemical artifacts and electromagnetic interference artifacts. Moreover, the intensity of diffusion weighted signal is weaker than normal magnetic resonance signal. Therefore, DWIs present low signal to noise ratio [1]. If useful diffusion information cannot be obtained exactly from noisy data, it is impossible to calculate diffusion tensors accurately, which will greatly reduce the feasibility of myocardium fiber reconstruction [2]. In this abstract, a 3D restoration method based on sparse denoising (SAP-SPDN) is proposed for cardiac DWIs considering the image sparsity caused by self-similarity.

Methods

There are spatial correlations between adjacent layers in cardiac DWI sequence due to the organ consistency, and each DWI contains repetitive structures. Thus, sparsity could arise from self-similarity of cardiac DWIs. A structure adaptive sparse denoising algorithm based on image self-similarity is proposed herein for cardiac DWI. The principle of this algorithm is shown in Fig. 1. Given a reference patch, its similar patches are selected and grouped into 3D data. As shown in Fig. 1, the patch marked with "R" is the reference patch, and its similar patches grouped into 3D data $\mathbf{S}_{\mathbf{Y}(N_i)} = \{\mathbf{Y}(N_j) : j \in s_{N_i}\}$.

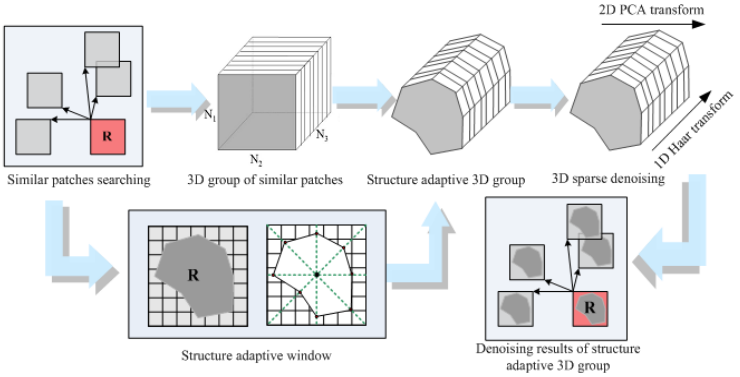

Fig. 1 Scheme of SAP-SPDN based on image self-similarity

Meanwhile, the structure adaptive neighborhood of the reference patch is searched, and then a collection of structure adaptive patches is extracted from the 3D data. Transform domain denoising for 3D data can be decomposed into 2D principal component analysis and 1D Haar transform. In 3D transform domain, after denoising the transform coefficients using Wiener filtering, the denoised 3D data is estimated by $\mathbf{S}_{\hat{\mathbf{X}}(N_i)} = \Gamma_{3D}^{-1}\left(\chi\left(\Gamma_{3D}\left(\mathbf{S}_{\mathbf{Y}(N_i)}\right)\right)\right)$, where Γ_{3D} and Γ_{3D}^{-1} denote 3D transform and inverse transform respectively, while χ is the Wiener filtering operator. The denoising results of each structure adaptive patch can then be obtained from the inverse 3D transform. Finally, a cardiac DWI is reconstructed by cumulative weighted average of the structure adaptive patches. To overcome the shortcoming of classical similarity measurement [3] for similar patches selection, a new similarity measurement with threshold constraint is defined as

$$w(i,j) = \begin{cases} \dfrac{1}{Z(i)} e^{\frac{\|\mathbf{Y}(N_i)-\mathbf{Y}(N_j)\|_2^2}{2\sigma_n^2 n^2}}, & \mu < \dfrac{\overline{\mathbf{Y}(N_i)}}{\overline{\mathbf{Y}(N_j)}} < \dfrac{1}{\mu} \text{ and } v < \dfrac{\mathrm{NSD}(i)}{\mathrm{NSD}(j)} < \dfrac{1}{v} \\ 0, & \text{otherwise} \end{cases}$$

where $\overline{Y(N_i)}$ and $\mathrm{NSD}(i)$ represent the mean and the non-stationary degree of the local neighborhood N_i at location x_i respectively. In this way, only the patches have similar mean and intensity variance with the reference patch are selected, without having to compute all the Euclidean distances between $\overline{Y(N_i)}$ and $\overline{Y(N_j)}$.

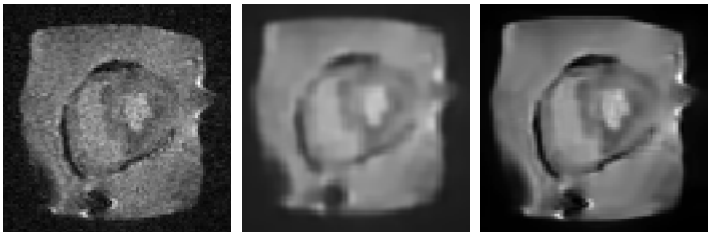

Fig. 2 Human cardiac DWIs. (a) Real image; (b) image denoised by BLS-GSM algorithm; and (c) image denoised by SAP-SPDN algorithm.

Results and Discussion

Fig. 2 shows denoising results of a real *ex vivo* human cardiac DWI using different algorithms. It is found that compared with BLS-GSM algorithm [4], SAP-SPDN can effectively filter out the noise in the cardiac DWI while preserving the image contrast and fine structures. Fig. 3 shows the myocardium fiber reconstruction before and after denoising cardiac DWIs. After denoising the DWIs, the fiber tracking of myocardium is more precise and robust with less break and warp. Myocardium fiber bundles exhibit small curvature, low bent, compact structure and helical structure through the wall [5]. These results demonstrate that SAP-SPDN algorithm has a good performance in denoising images with high structural redundancy. It can achieve a trade-off between image contrast and smoothness in denoising.

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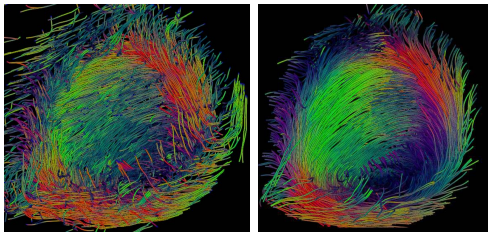

Fig. 3 Cardiac fiber reconstructions before (a) and after denoising (b).

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