In vivo diffusion tensor imaging of the human heart with free-breathing in healthy volunteers

Hongjiang Wei[1], Magalie Viallon[1,2], Benedicte MA Delattre[1], Vinay M Pai[3], Han Wen[3], Hui Xue[4], Christoph Guetter[4], Marie-Pierre Jolly[4], Pierre Croisille[1,5], and Yuemin Zhu[1]

[1]CREATIS, CNRS (UMR 5220), INSERM (U1044),INSA Lyon,University of Lyon, Lyon, France, [2]Department of Radiology,University Hospitals of Geneva, Geneva, Switzerland, [3]Imaging Physics Lab, BBC/NHLBI/NIH, Bethesda, Maryland 20892, United States, [4]Siemens Corporation, Corporate Technology, Princeton, New Jersey 08540, United States, [5]5Jean-Monnet University, Saint-Etienne, France

Background

The cardiac fiber architecture, a complex arrangement of myocardium fibers, plays a deterministic role in studying the ventricular function. Diffusion tensor imaging (DTI) provides a non-invasive approach to the three-dimensional depiction of the myocardial fiber architecture. The biggest problem in *in vivo* cardiac DTI is the signal loss caused by motion. Recently, to cope with human physiological motion problem, a robust method called PCATMIP was proposed [1] that uses principal component analysis (PCA) filtering to improve the signal-to-noise ratio (SNR) and temporal maximum intensity projection (TMIP) approach to compensate the signal loss. While performing cardiac DTI during subject's breath-hold may not be realistic in clinical routine, free-breathing DTI acquisitions represent an ultimate objective. In this study, our objective was to obtain *in vivo* DTI indices of the human heart with free-breathing.

Method

All DTI acquisitions were performed on a MAGNETOM Avanto 1.5T (Siemens Healthcare, Erlangen, Germany) using a prototype diffusion EPI sequence. Six volunteers were involved in this study. To cope with intensity fluctuations arising from motion, our strategy was to acquire multiple diffusion weighted (DW) images at different time points during the diastole in each consecutive cardiac cycle. After each time frame was acquired, the trigger delay was increased by 10ms. At each trigger delay, we obtained the b0 image and 12 DW images corresponding to 12 gradient directions. We acquired 10 DTI slices across the whole heart. The total scan time is about 25 minutes at an average heart rate of 60bpm. The MRI parameters are: TE/TR=51/100ms, spatial resolution=2.6×2.6×6mm^3, acceleration rate=2 (GRAPPA), partial Fourier=6/8, matrix=90×160, and b=200s/mm². Free-breathing diffusion weighted (DW) images were then registered using a non-rigid registration algorithm that preserves high accuracy and consistency of the data [2]. Finally, PCATMIP algorithm was applied to the registered images to obtain motion corrected images.

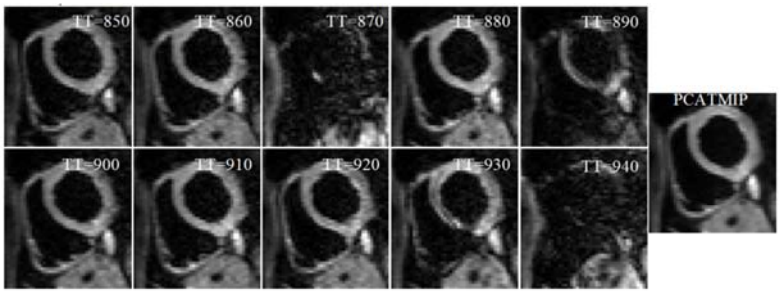

Fig. 1: Free-breathing cardiac DW images from 10 repetitions acquired at different time points and processed using PCATMIP. TT means trigger-delay time in ms.

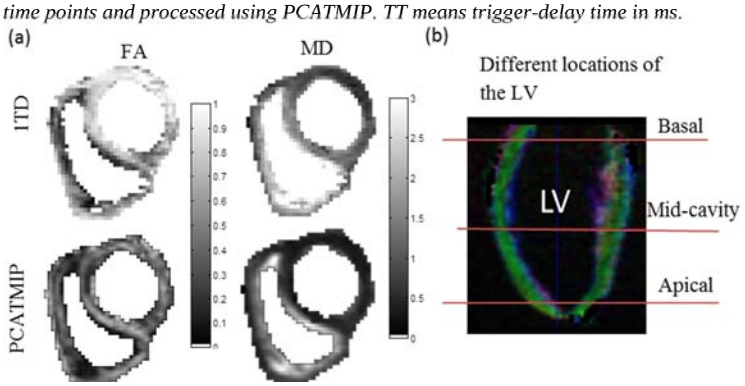

Fig. 2: (a) FA and MD maps calculated from tensor fields for a mid-cavity slice in a healthy volunteer. Images show FA and MD maps developed by 1TD and PCATMIP approaches. Top: 1TD; Bottom: PCATMIP; (b) Different locations of the LV.

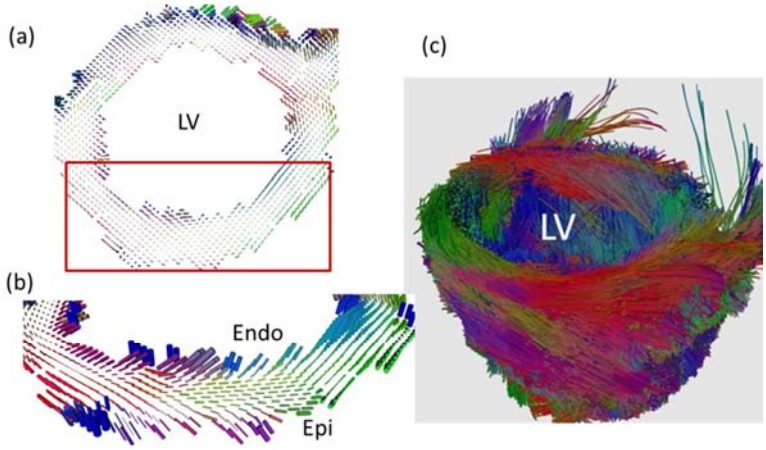

Fig. 3: (a) Tensor field of the LV, (b) zoomed tensor field corresponding to the red block in (a), (c) 3D fiber architecture of the LV.

Results

Free-breathing DW images are affected in a more important manner by signal loss due to physiological motion. Lost signal was recovered and the intensity of DW images was substantially enhanced by repeated acquisitions and PCATMIP post-processing (Fig. 1). Fig. 2 gives the FA and MD maps for the same volunteer as in Fig. 1, and shows significant differences between one trigger delay (1TD) and PCATMIP methods ($p<0.001$). With 1TD, the signal loss increased and resulted in an overestimation of MD values. The FA and MD values at different locations of the LV myocardium are given in Table 1. Overall, for each slice, FA and MD values are higher in 1TD than in PCATMIP. No statistically significant difference between different heart locations were observed ($p>0.05$). After processing by PCATMIP, both FA (0.40±0.01) and MD (0.8±0.06×10^{-3} mm^2/s) are smaller than those obtained from 1TD acquisition (0.59±0.04 and 1.37±0.10×10^{-3} mm^2/s, respectively). The tensor field and 3D fiber architecture calculated over the LV (Fig. 3) reveal a circular symmetry of its myocardial fiber orientations, which reflects the rotation characteristic of cardiac fibers.

Table 1: Mean ± SD FA and MD values at different locations of the LV mean for the 6 volunteers. MD values are in units of 10^{-3}mm^2/s.

		Basal	Mid-cavity	Apical
FA	1TD	0.56±0.16	0.63±0.17	0.59±0.15
	PCATMIP	0.39±0.09	0.40±0.1	0.39±0.08
MD	1TD	1.40±0.37	1.43±0.28	1.34±0.24
	PCATMIP	0.75±0.16	0.79±0.20	0.87±0.21

Discussion and Conclusion

This study demonstrates the feasibility of *in vivo* cardiac DTI in healthy volunteers. The PCATMIP can be used to minimize motion-induced signal loss that is the main problem in cardiac DTI. The proposed acquisition and processing scheme allow us to obtain *in vivo* diffusion tensor parameters in free-breathing subjects, and open interesting perspectives for clinical applications. The main drawback of the PCATMIP method is that it is time-consuming. On the other hand, the present study is under the free-breathing condition, which leads to a reduction in scan time.

REFERENCES:

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