

Sequence timing optimization in multi-slice diffusion tensor imaging of the beating heart

C. T. Stoeck¹, N. Toussaint², P. Boesiger¹, P. G. Batchelor², and S. Kozerke^{1,2}

¹Institute for Biomedical Engineering, University and ETH Zurich, Zurich, Switzerland, ²Imaging Sciences, King's College London, London, United Kingdom

Introduction

Diffusion tensor imaging (DTI) of the beating heart has been a true challenge given the bulk motion encountered during diffusion encoding intervals. Several technical advances including the use of bipolar diffusion encoding gradients [1] in conjunction with strong system gradient performance and dedicated timing of diffusion encoding [2] have permitted acquisition of multi-slice data in the in-vivo heart [3]. Despite the progress the optimal timing can be difficult to determine in practice as it differs significantly in subjects.

In the present work, a dynamic diffusion scout sequence is proposed to facilitate determination of sequence timing for diffusion tensor imaging in the beating heart. It is demonstrated that the centre of mass of the diffusion encoding gradients is optimally set at the contraction upslope at points of minimal or maximal cardiac rotation. Whole-heart reconstructions of myocardial fiber orientations are presented based on optimized multi-slice data acquisitions.

Methods

For estimation of the optimal trigger delay a dynamic, navigator gated free-breathing 2D scout sequence was implemented (Figure 1). It consists of a spin echo sequence with TE/TR = 47/1500-2000ms and a single shot echo planar imaging (EPI) readout which is triggered to the R-wave using a vector ECG. Diffusion encoding is performed with a b-value of 350 s/mm² using velocity compensating double bipolar diffusion gradients [1]. In order to reduce the echo time partial Fourier sampling in combination with a local-look scheme was used [2]. The variable rate selective excitation algorithm (VERSE) [4] was utilized to design sufficiently short echo pulses. The trigger delays, measured from the R-wave to the centre of mass of the diffusion gradients, were dynamically increased starting from 65ms to 520ms in steps of 10ms for consecutive dynamic scans. A frequency selective fat saturation pulse was applied and two signal averages were acquired. A field of view of 230×100mm² was adjusted to image the heart in short-axis orientation at a spatial resolution of 2×2×4mm³. To assess cardiac mechanics, a cine 2D CSPAMM sequence [5] was acquired and circumferential strain and rotation were determined using HARMonic Phase (HARP) processing [6].

To determine the optimal trigger delay for the actual multi-slice DTI scan, signal-to-noise ratios were calculated in the entire myocardium in every dynamic scan of the diffusion scout and plotted against circumferential strain and rotation of the heart. Parameters for the multi-slice scan were identical with those of the diffusion scout sequence except for the number and directions of diffusion encodings. A total of fifteen diffusion directions was encoded with b-values of 350s/mm² in 5-8 slices depending on cardiac anatomy. For each set eight signal averages were acquired. For registration purposes, a standard whole-heart gradient echo sequence was used to cover the entire heart in a contiguous fashion.

In post-processing, the diffusion-encoded slices were registered to the whole-heart image volume and tensors were extrapolated using prolate spheroidal coordinates in order to reconstruct the entire left ventricular fiber architecture [3]. All measurements were performed on a 3T Philips MR system (Philips Healthcare, Best, The Netherlands) using a 6-element cardiac array coil for signal reception.

Results

Figure 2 shows the normalized signal-to-noise ratio (SNR) in the left ventricular myocardium as a function of the delay between the R-wave and the centre of mass of the diffusion gradients for diffusion encoding along the frequency (M), phase (P) and slice (S) encode directions along with normalized circumferential strain and rotation as determined from the tagged data. The region-of-interest for SNR estimation covered the entire myocardial tissue. The time axis was normalized to peak circumferential strain, which is considered 100% systole. In Figure 3 normalized myocardial SNR as a function of the trigger delay normalized to end-systole is plotted for different heart rates. Figure 4 illustrates the orientation and position of the multi-slice data relative to the anatomical scan along with reconstructed fibers of the left ventricle.

Discussion

A dynamic diffusion scout has been used to determine the optimal trigger delay for cardiac diffusion tensor imaging. Maximum SNR and hence the optimal trigger delay was found to correspond to phases of contraction during which the heart moves approximately linear in accordance to previous reports [2]. Furthermore maximal SNR can be found at maxima and minima of cardiac rotational motion (60-70% peak circ. strain). The timing of the optimal trigger delay was confirmed to be weakly dependent on heart rates below 80 beats/min. Above 80 beats/min the absolute duration for the imaging window is narrowed due to early occurrence of peak contraction making it difficult to fit sequence preparations and the diffusion gradients into the interval between R-wave and optimal acquisition timing. To incorporate the sequence into a clinical protocol it is sufficient to shorten the trigger delay scout sequence and focus on the time window up to peak contraction, which reduces the scan duration to 80 heart cycles.

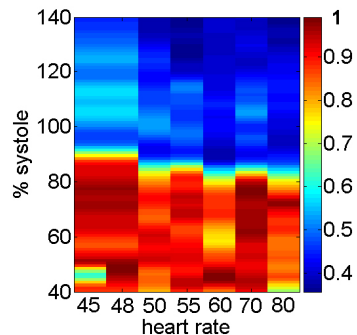


Figure 3: The normalized SNR is determined as function of trigger time and the subject's heart rate, using diffusion encoding in readout direction

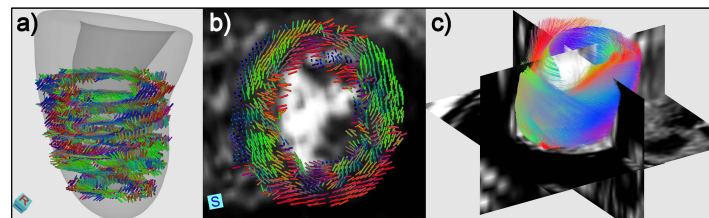


Figure 4: Slices for diffusion tensor imaging are acquired at different levels of the left ventricle (a). The reconstructed tensors are shown in one short axis slice (b) and the reconstructed fibers are mapped onto a 3D whole-heart volume (c).

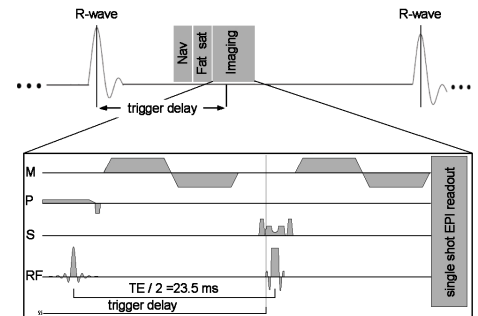


Figure 1: For the trigger delay scout the diffusion gradients are switched along the frequency encoding direction (M). The trigger delay spans from the subject's R-wave to the centre of mass of the diffusion gradients.

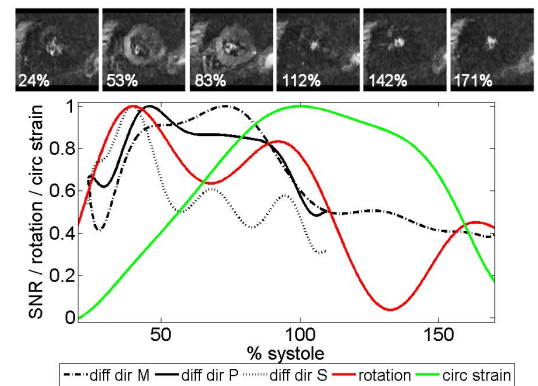


Figure 2: The myocardial SNR is shown as function of the timing of the diffusion gradient's center (three orthogonal directions). The myocardial rotation is plotted in red and the myocardial strain in green. The top row shows the corresponding images from the trigger delay scout at different time points during cardiac contraction.

References

- [1] Dou et al. MRM 2003 ;
- [2] Gamper et al. MRM 2007;
- [3] Toussaint et al. MICCAI 2010 ;
- [4] Hargreaves et al. MRM 2004 ;
- [5] Fischer et al. MRM 1993;
- [6] Osman et al. MRM 1999;