

High-resolution single-shot DTI of the in-vivo human heart using asymmetric diffusion encoding

Christian T. Stoeck¹, Constantin von Deuster^{1,2}, Nicolas Toussaint², and Sebastian Kozerke^{1,2}

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

Introduction: Diffusion tensor imaging (DTI) of the heart has gained significant momentum over recent years [1-4]. The sensitivity of DTI encoding to cardiac motion has, however, limited the choice of sequences to the stimulated echo acquisition mode (STEAM) [5]. Free-breathing DTI-STEAM of the in-vivo heart is possible [3] but scan efficiency is very low as two consecutive heart beats are required to be at identical respiratory levels for successful STEAM encoding and decoding. While optical feedback systems may be used to guide healthy subjects in their respiratory action, such a system may prove difficult when examining patients. An additional limitation of STEAM is the inherent loss of half of the signal as only longitudinal magnetization is decoded. Spin echo (SE) sequences are an alternative capable of single shot diffusion encoding. However, the longer diffusion encoding periods make SE very vulnerable to cardiac motion and hence require careful adjustments of trigger delays besides the necessity of strong gradient amplitudes in excess of the standard 40 mT/m [5-6].

In this work we present a single-shot cardiac DTI-SE approach employing asymmetric (ASY) Stejskal-Tanner diffusion encoding. High-resolution multi-slice cardiac DTI data is acquired and 3D tensor reconstructions of the in-vivo heart are shown.

Materials and Methods: The b-value for conventional Stejskal-Tanner encoding is given by $b = \gamma^2 G^2 [\delta^2 (\Delta - \delta/3) + \zeta^3/30 - \delta\zeta^2]$ where b scales linearly with the spacing Δ of the diffusion gradient's waveform and with the power of three by their length δ and slope ζ (Fig. 1). Accordingly, the effective encoding duration can be

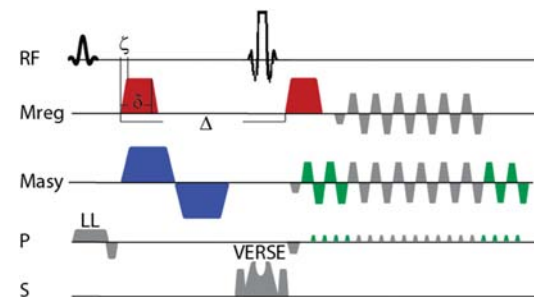


Figure 1: Sequence diagram of Stejskal-Tanner encoding (red) and asymmetric diffusion encoding (blue). Higher resolution is possible using (ASY-SE) as indicated by the additional readout lobes without prolonging the echo time.

minimized by applying a single bipolar gradient waveform instead of two single gradient lobes. Such an approach optimally utilizes any dead time between excitation and echo pulse. At the same time, a longer acquisition window is available allowing for higher resolution while keeping the echo time to a minimum. Since diffusion encoding is only applied during the period in-between excitation and echo pulse, the sequence is referred to as asymmetric diffusion encoded

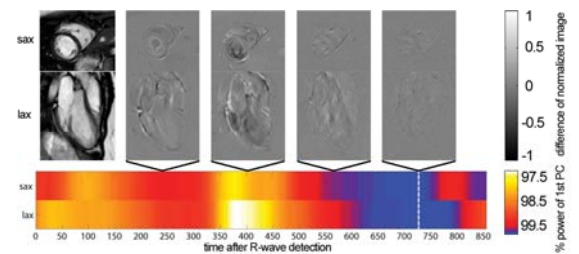


Figure 2: PCA based trigger delay estimation. The top row represents differences of the normalized image (in short axis: SAX and long axis: LAX) at the beginning and the end of the desired timing interval. The color-coding in the bottom row represents the amount of image information contained by the first principle component as function of the trigger delay.

spin-echo (ASY-SE). Figure 1 compares ASY-SE with the conventional Stejskal-Tanner SE experiment.

For in-vivo imaging the ASY-SE sequence was implemented on a 1.5T Philips Achieva system (Philips Healthcare, Best, The Netherlands) equipped with 80 mT/m gradients on each axis. A 5 channel cardiac array was used for signal reception. To define the trigger delay for ASY-SE cine 2D images were acquired in long- and short-axis views. The optimal trigger delay was determined automatically using sliding window principal component analysis (PCA) over time. The eigenvalue corresponding to the highest energy was used to identify quiescent phases. The maximum of the sum of the first eigenvalues from both cine scans was used as the optimal trigger time point for consecutive ASY-DTI. Short-axis ASY-DTI data were acquired in five slices covering the ventricle during free breathing of the subject. Navigator gating with a gating window of 5mm was employed. Scan parameters were as follows: FOV 230x102mm², spatial resolution 1.6x1.6mm², slice thickness 2mm, TR/TE 2R-R intervals/61ms, 90% partial Fourier, 18 averages, total scan duration 5:30min per slice. Diffusion was encoded along 8 directions [8] with a b-value of 500s/mm². A local look technique including VERSE echo pulses was applied [7]. For 3D tensor reconstruction, a whole heart balanced SSFP scan was acquired in addition. Conformal mapping using prolate spheroidal coordinates was performed as described previously [2].

Results: Figure 2 shows an example of the automated PCA based trigger-delay finder. The differences of the first and last image of two timing intervals at time points of maximal and minimal motion are shown. In Figure 3 in-vivo mean diffusion map (a) and the corresponding tensors (b) of a mid-ventricular slice out of the total set of 5 slices (Fig. 3c) are presented. The result of 3D tensor reconstruction of the entire LV is shown in Figure 3d). Using masking the helical structure is revealed (Fig. 3e).

Discussion: In this work a single-shot asymmetric diffusion encoding SE approach has been presented enabling acquisition of high-resolution tensor data of the in-vivo heart. A spatial resolution of 1.6x1.6 mm² was chosen here but even higher spatial resolution without prolonging TE if the partial Fourier factor is increased. Given the single-shot diffusion encoding and decoding process, respiratory motion will not affect signal quality as opposed to cardiac STEAM sequences. ASY-SE holds

great promise for diffusion tensor imaging of the in-vivo heart without the need for breathing instructions.

References: [1] Sosnovik et al. JCMR 2009, [2] Toussaint et al. MICCAI 2010; [3] Nielles-Vallespin et al. MRM 2012; [4] Mekkaoui et al. JCMR 2012; [5] Merboldt et al. MRM 1991, [6] Gamper et al. MRM 2007; [7] Stoeck et al. ISMRM 2011 ; [8] Jones et al. MRM 2004 ;

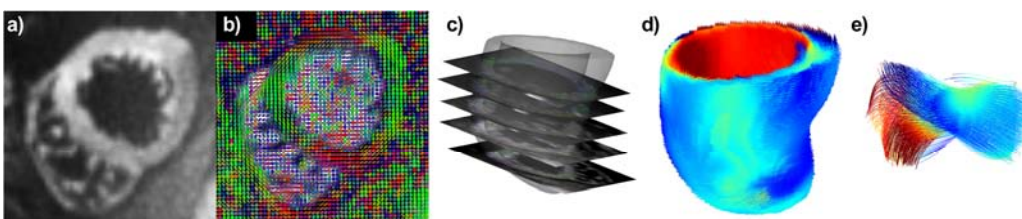


Figure 3: Mean diffusion map a) and tensors of a mid-ventricular slice b) out of a total of five acquired slices c); 3D LV tensor reconstruction based on conformal mapping using prolate spheroidal coordinates d) and extracted LV helical structure e).