# Concurrent dual-slice cardiac DTI of the in-vivo human heart

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# Introduction

The feasibility of diffusion tensor imaging (DTI) of the in-vivo human heart has been shown in previous works [1,2,3]. The Stimulated Echo Acquisition Mode (STEAM) provides robust diffusion weighted imaging of the heart [4,5] but requires diffusion encoding and decoding over two consecutive heartbeats. In addition, the SNR penalty of STEAM relative to spin-echo acquisitions makes additional signal averages necessary. Consequently, the image acquisition process is inherently slow. This becomes a particular challenge if multiple slices are acquired to reconstruct the 3D tensors of the whole heart [6]. In the present work, concurrent dual-slice single-shot EPI cardiac diffusion weighted imaging is proposed using multi-band STEAM and controlled aliasing in parallel imaging [7]. Magnitude images and 2D diffusion tensors for two short-axis slices are presented and compared to sequential single-slice acquisitions.

# Methods

The STEAM sequence spans over two consecutive heartbeats, with the first and third excitation pulse triggered on the R-waves of the ECG (Figure 1). In the current work, unipolar diffusion encoding gradients were played out in ten directions [9] with a b-value of 500s/mm<sup>2</sup>. The 90° RF pulses were replaced by dual band pulses for dual slice excitation. For RF-waveform generation the Shinnar-Le Roux algorithm [10] was used, producing two passbands corresponding to two slices with a slice thickness of 4mm and a stopband corresponding to a slice gap of 36mm. For a better conditioning of the separation of both slices during reconstruction a half Field Of View (FOV) shift was introduced for one of the two slices. To this end a phase difference of  $\pi$  between both slices was added for every second k-space line using gradient blips in slice selection direction [8] (Figure 1). To reduce the echo time and to shorten the readout duration, additional in-plane undersampling by a factor of 1.5 [11] was applied. Hence two sources of aliasing are present and up to four voxels originating from two slices can be folded onto each other forming aliased image  $I_x$  for coil x according to:

$\begin{pmatrix} I_1 \\ \vdots \\ I_{32} \end{pmatrix} =$	$\begin{pmatrix} C_{1.1} \\ \vdots \\ C_{32.1} \end{pmatrix}$	C <sub>1.2</sub> : C <sub>32.2</sub>	C <sub>1.3</sub> : C <sub>32.3</sub>	$\begin{pmatrix} C_{1.4} \\ \vdots \\ C_{32.3} \end{pmatrix}$ .	$\begin{pmatrix} M_1 \\ M_2 \\ M_3 \\ M_4 \end{pmatrix}$	(1)	$g_{ii} = \sqrt{[(C^{H}C)^{-1}]_{ii}[C^{H}C]}_{ii} $ (2)
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where *C* denotes coil sensitivity and *M* the desired unaliased image voxels. The g-factor is given as (2). In order to determine coil sensitivity matrix *C* a separate reference scan was acquired. All measurements were performed on a 1.5T Philips Achieva system (Philips Healthcare, Best, The Netherlands) equipped with a 32 channel cardiac receiver array. Fat suppression was achieved by frequency selective saturation prior to the first 90° excitation. For each diffusion encoding direction ten averages were acquired within one breath hold. To ensure consistency of breath hold levels respiratory navigator gating was used with a 1D navigator placed on the right hemi diaphragm (gating window: 5mm). The imaging parameters were as follows: resolution  $3 \times 3mm^2$ , slice thickness 4mm, FOV:  $360 \times 288mm^2$ , TE 24ms, TR: 2-R-R-intervalls, partial Fourier sampling (65 %).

## Results

Figure 3 shows the b=0s/mm<sup>2</sup> images of one mid-ventricular slice and one apical slice separated by 36mm according to Figure 2. Images presented in Figure 3 (a) and (c) were acquired with a standard single-slice DTI STEAM sequence within a total of 22 breathholds. Slices in Figure 3 (b) and (d) were acquired simultaneously using a total of 11 breathholds. Diffusion tensors upon image registration are shown in (e), (g) and (f), (h) for sequential single slice and concurrent dual slice acquisitions.

### Discussion

In this work a single-shot dual slice diffusion encoding sequence has been presented increasing scan efficiency of multi-slice cardiac STEAM DTI by a factor of two. Compared to sequential single-slice acquisitions,  $B_0$  homogeneity needs to be guaranteed over a larger volume potentially resulting in residual off-resonance artifacts as demonstrated in Figure 4. In order to address the issue, higher order shimming needs to be performed or off-resonance information to be incorporated into image reconstruction.

### References

[1] Tseng et al. MRM 1999; [2] Edelman MRM 1994; [3] Dou et al. MRM 2003; [4] Stoeck et al. ISMRM 2011; [5] Nielles-Vallespin et al. MRM 2012; [6] Toussaint et al. MICCAI 2010; [7] Breuer et al. MRM 2005; [8] Setsompop et al. MRM 2012; [9] Jones et al. MRM 1999; [10] Pauly et al. IEEE TMI 1991; [11] Pruessmann et al. MRM 1999; Acknowledgements

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Figure 4: Image distortion due to field inhomogeneity (a) and corresponding B0 map (b).



Figure 1: Cardiac STEAM DTI sequence with CAIPIRINHA blips (red) during singleshot readout.



Figure 2: Four chamber view with the slice locations used for multi-slice DTI.



Figure 3: Comparison of b=05/mm images to sequential single slice (a), (c) and concurrent dual-slice DTI (b), (d). Corresponding tensors are given in (e), (g) and (f), (h) for single and dual-slice acquisitions, respectively.