

# **In vivo cardiac diffusion tensor imaging: Selecting a b-value and acquiring the reference data**

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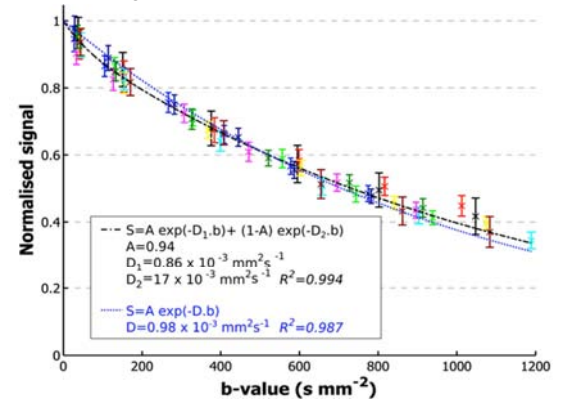
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**Target audience:** Physicists and clinicians with an interest in the cardiac microstructure.

**Purpose:** To investigate the influence of the diffusion weighting (the b-value) on *in vivo* cardiac diffusion tensor imaging (cDTI). This includes the diffusion weighting of the main diffusion weighted and reference images (referred to as *bref*) and the effect of the orientation of the diffusion weighting in the reference data.

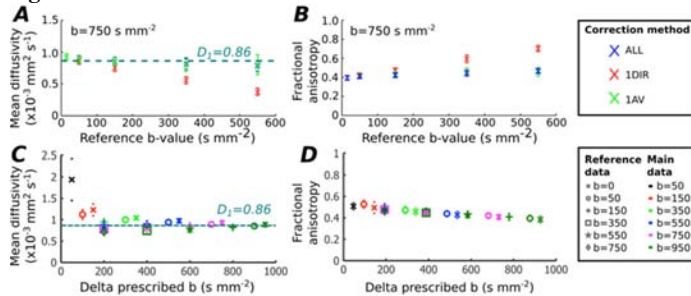
**Method:** cDTI was performed in 10 healthy subjects (7 male, age 23-57, Siemens Skyra) using the stimulated echo single shot EPI sequence with monopolar diffusion encoding, described previously<sup>1,2</sup>. GRAPPA parallel imaging and a reduced phase field of view (zonal excitation) were used to accelerate the acquisition. A single short axis slice in the mid-ventricle was imaged at a resolution of 2.8x2.8x8mm<sup>3</sup>. One average was acquired per breath hold and 8 averages were obtained. Each average consisted of 6 diffusion directions at  $b=50, 150, 350, 550, 750, 950$  smm<sup>-2</sup> and a reference image, where the effective diffusion weighting was  $b=15$  smm<sup>-2</sup>. In-house software<sup>2</sup> written in MATLAB (The Mathworks, Natick MA) was used for processing. Pixel wise diffusion tensors were calculated using each b-value with  $b=15$  smm<sup>-2</sup> and then also using all b-values less than the current b-value as *bref* (e.g.  $b=750$  vs. *bref*=15,50,150,350,550smm<sup>-2</sup>). Mean diffusivity (MD), fractional anisotropy (FA) and helical angle (HA) maps were derived in each case. To investigate the way the reference data is acquired, this was repeated using all averages and references (ALL), all averages of the first diffusion direction (1DIR) and 1 average of each direction as a reference (1AV). For each subject the average diffusion weighted signal (geometric mean over all directions) at each b-value was calculated in the left ventricle for comparison with the standard model of mono-exponential decay ( $S = A \exp[-b.D]$ , where  $S$  is signal, and  $D$  is the diffusivity).

**Figure 1:** Signal loss in the left ventricle with b-value.



Markers are coloured by subject.

**Figure 2:** The effect of reference and main b-value on MD and FA.



Parts A and B show parameters derived using a main b-value of 750 smm<sup>-2</sup> and increasing reference b-value for the three correction methods. Parts C and D, plot the parameters derived from all possible pairs of b-values (ALL correction method) vs. the difference between  $b$  and  $bref$  (delta prescribed  $b$ ). In C and D, marker style indicates *bref* and marker colour indicates  $b$ . FA and MD values are plotted as mean  $\pm$  standard deviation.

**Discussion:** When the *bref* is low, measured MD is augmented by another process with a high apparent diffusivity ( $D_2$ ), which is thought to be microvascular perfusion. Previous work in diffusion weighted imaging of the heart has also demonstrated a bi-exponential signal decay with b-value<sup>3</sup>, but this is the first *in vivo* work in cDTI to consider this effect. Here  $bref \geq 150$  smm<sup>-2</sup> resulted in sufficient suppression of the contribution of microvascular perfusion in the measured diffusion tensor.

Typically in cDTI the reference data is acquired with diffusion weighting along a single direction (i.e. the 1DIR case here), but using reference data acquired with diffusion weighting in 6 directions results in more stable values of MD and FA. Using 1 average of each direction (1AV) for the reference data produces similar results to using all 8 averages of all directions (ALL), without increasing the amount of data required. Most previous studies have used b-values around 350 smm<sup>-2</sup><sup>1,2,4,5</sup>, but increasing the b-value used in cDTI results in more uniform MD and FA, presumably due to an increase in the signal to noise ratio of the calculated diffusion tensor. In this work,  $b=750$  and  $bref=150$  smm<sup>-2</sup>, appeared to be optimal and MD was closest to the diffusion component ( $D_1$ ) in a bi-exponential model fitted to data from all 10 subjects.

**Conclusion:** Parameter maps obtained from *in vivo* cDTI data can be improved by using higher b-values than in previous studies. The contribution of microvascular perfusion to the measured diffusion tensor can be reduced by applying diffusion weighting to the reference data, the direction of which should change between averages.

**References:** 1. NIELLES-Vallespin 2013; MRM 70(2):454. 2. McGill 2012; JCMR 14:86. 3. Delattre 2012; Invest Radiol 47(11):662. 4. Wu 2009; Circ Imaging 2:32. 5. Reese 1995; MRM 34(6):786.

**Results:** Figure 1 shows the signal loss in the left ventricle with b-value. A bi-exponential fit (fitted to  $b < 1000$  smm<sup>-2</sup> to avoid the noise floor), with diffusion ( $D_1$ ) and microvascular perfusion ( $D_2$ ) components more closely matches the data than the standard mono-exponential model ( $R^2=0.994$  vs. 0.987). By  $b=150$ smm<sup>-2</sup>,  $D_2$  contributes approximately only 1% of the signal. Figure 2 plots mean MD and FA for: (A and B)  $b=750$ smm<sup>-2</sup> with increasing reference b-value for all three correction methods; and (C and D) for all possible pairs of b-values using the ALL reference method. Using the 1DIR method of correction, MD rapidly deviates from the  $D_1$  value obtained in figure 1 and FA steadily increases. However, using the 1AV method, MD remains close to  $D_1$ , FA shows only a small increase and both measures closely match those obtained with the ALL method, which should be more reliable. From parts C and D, with increasing *bref* the MD reduces and FA increases. With larger main b-values, maps are less noisy and there is less variation between subjects. MD is closest to  $D_1$  with  $b=750$  vs. *bref*=150smm<sup>-2</sup>. Figure 3 shows example cDTI parameter maps calculated using 4 pairs of b-values (using the ALL method of correction in the right hand data).

**Figure 3:** Example cDTI parameter maps obtained from data acquired using 4 pairs of diffusion weightings.

