

# Optimal diffusion weighting for *in-vivo* cardiac diffusion tensor imaging

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**Key words:** DTI; diffusion weighting; b-value; cardiac diffusion; microvascular perfusion

**Funding:** This work was performed at the National Institute for Health Research Cardiovascular Biomedical Research Unit at The Royal Brompton Hospital and Imperial College London.

**Running title:** Optimal b-values in cardiac DTI.

**Word Count:** 4998.

**Final published version available at:**

<http://onlinelibrary.wiley.com/doi/10.1002/mrm.25418/abstract>

## ABSTRACT

**Purpose:** To investigate the influence of the diffusion weighting on *in-vivo* cardiac diffusion tensor imaging (cDTI) and obtain optimal parameters.

**Methods:** 10 subjects were scanned using STEAM-EPI with 6 b-values, from 50 to 950 $\text{mm}^{-2}$ , plus  $b=15\text{mm}^{-2}$  reference. The relationship between b-value and both signal loss and signal to noise ratio measures was investigated. Mean diffusivity (MD), fractional anisotropy (FA) and helical angle (HA) maps were calculated using all possible b-value pairs to investigate the effects diffusion weighting of the main and reference data.

**Results:** Signal decay at low b-values was dominated by processes with high apparent diffusion coefficients, most likely microvascular perfusion. This effect could be avoided by diffusion weighting the reference images. Parameter maps were improved with increased b-value, until the diffusion-weighted signal approached the noise floor. For the protocol used in this study,  $b=750\text{mm}^{-2}$  combined with  $150\text{mm}^{-2}$  diffusion weighting of the reference images proved optimal.

**Conclusion:** MD, FA and HA from cDTI are influenced by the b-value of the main and reference data. Using optimal values improves parameter maps and avoids microvascular perfusion effects. This optimized protocol should provide greater sensitivity to pathological changes in parameter maps.

## Introduction

The ability to interrogate the microstructure of myocardial tissue has led to considerable interest in cardiac diffusion tensor imaging (cDTI) (1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14). Diffusion-weighted contrast (with magnitude described by the b-value) is the result of signal loss caused by incoherent motion within a mixing time between two diffusion-encoding gradients. Quantitative measures of diffusion are obtained by comparing images with a high b-value ( $b_{\text{main}}$ ) to equivalent images with a lower, typically minimal b-value ( $b_{\text{ref}}$ ). Tensor information is derived from images with the diffusion gradients orientated in  $\geq 6$  directions. The tensor is used to calculate mean diffusivity (MD), fractional anisotropy (FA) (15) and helical angle (HA) (9, 16) maps in the left ventricle (6, 7, 11, 17, 18). Published *in-vivo* cDTI studies have typically used  $b_{\text{main}}$  around 350  $\text{s mm}^{-2}$  ( $b_{\text{ref}}$  has been quoted in few previous studies (19, 20, 21)) with 6 diffusion directions. In reality, signal loss is caused by any intra-voxel incoherent motion and, therefore, contains contributions from both diffusion and microvascular perfusion (22, 23, 24). This has been studied in neurological applications (25, 26, 27), extensively in abdominal diffusion-weighted (i.e. without calculation of a full diffusion tensor) imaging (27, 28, 29) but there is limited work in the heart (24, 30, 31). Callot et al. (24) performed *in-vivo* diffusion-weighted imaging of dog hearts with and without infusion of a vasodilator. The results demonstrated that a two-component model (diffusion + microvascular perfusion) was a good fit to the data; that the component of the model related to perfusion increased after vasodilation; and that the signal loss from both components combined was reduced post-mortem. Using *in-vivo* diffusion-weighted imaging of the human heart Delattre et al. (31) similarly found that a two-component model was a good fit to the data in the heart and liver. However, the effect of microvascular perfusion on tensor parameters derived from *in-vivo* cDTI has, as yet, not been quantified.

In this study we consider how the diffusion weighting, both  $b_{\text{main}}$  and  $b_{\text{ref}}$ , influences the measured values of MD, FA and HA in the myocardium of healthy subjects and work towards determining an optimal pair of b-values. This

includes an investigation of the effects of the directionality of the diffusion weighting in  $b_{\text{ref}}$ .

## Methods

### Imaging sequence

All imaging was performed using a Skyra 3T MRI scanner (Siemens AG, Erlangen, Germany) with maximum gradient strength  $43\text{mTm}^{-1}$  and maximum slew rate  $180\text{Tm}^{-1}\text{s}^{-1}$  per axis. While other cDTI techniques exist (1, 4, 8, 10, 14, 31), the stimulated-echo acquisition mode (STEAM) echo-planar imaging (EPI) technique with monopolar diffusion encoding is a robust method (6, 7, 9, 18) and was performed in this work during a breath hold using the sequence shown schematically in figure 1 (7, 9). The EPI readout was shortened by using parallel imaging and zonal excitation in the phase encode direction (32). Each stimulated echo was formed over 2 cardiac cycles and each breath hold spanned 18 cardiac cycles. One stimulated echo was used for the EPI phase correction lines, the GRAPPA reference lines, the reference image and for each of the six diffusion encoded images. Diffusion encoding was achieved by using gradients of amplitude ( $G_d$ ) described in the scanner frame of reference ( $\hat{x}, \hat{y}, \hat{z}$ ) by  $G_d\hat{x} \pm G_d\hat{z}$ ,  $G_d\hat{y} \pm G_d\hat{z}$  and  $G_d\hat{y} \pm G_d\hat{x}$ . Spoiler gradients ( $G_{sp}$ ) are used in the reference acquisitions to spoil the gradient echo from the third RF pulse of the stimulated echo. Although smaller than  $G_d$ , the diffusion weighting ( $b_{\text{ref}}$ ) that  $G_{sp}$  imparts may be substantial (19). In this work  $G_{sp}$  were applied in the imaging frame of reference ( $(\hat{m}, \hat{p}, \hat{s})$  spoiler gradient  $=G_{sp}\hat{m} + G_{sp}\hat{p} + G_{sp}\hat{s}$ ) imparting a diffusion weighting of  $b_{\text{ref}}=15\text{ s mm}^{-2}$  to the reference acquisition (subsequently referred to as  $b_{\text{ref}15}$ ). The b-values were calculated (33) using software written in MATLAB (The Mathworks, Natick MA) and the output of the sequence simulator.

The echo-time (TE) was 24ms to enable the maximum prescribed  $b=950\text{ s mm}^{-2}$  used here (quoted, as all other “prescribed” b-values in this work, for an R-R interval of 1000ms). At this maximum b-value  $G_d=35\text{mT m}^{-1}$  per axis, ramp time  $660\mu\text{s}$  and flat-top time  $1680\mu\text{s}$ . Lower b-values were achieved by reducing  $G_d$ , while maintaining the timing parameters. Other parameters were similar to

those described previously (6, 7): repetition time 2 cardiac cycles; fat suppression; field of view 360 x 135mm<sup>2</sup>; slice thickness 8mm; acquired resolution 2.8 x 2.8mm<sup>2</sup>; reconstructed resolution 1.4 x 1.4mm<sup>2</sup>; GRAPPA factor 2; echo-train length 24 and echo-train duration 13ms.

### Data acquisition

Ten healthy subjects (7 male, age 23 – 57) were recruited in accordance with local ethical approval. A short-axis slice in the mid left ventricle was planned from a standard set of balanced steady-state free precession localisers. cDTI was performed in this plane using the sequence described above, triggered to the end-systolic pause ( $T_{\text{trigger}}$  in figure 1). To determine a suitable range of  $b_{\text{main}}$  to use in the study one subject was imaged over three sessions with 19 prescribed b-values from 50 to 3000 s mm<sup>-2</sup>. TE was increased where necessary but other parameters were constant. All subjects were then imaged with 8 averages for prescribed b-values of 50, 150, 350, 550, 750 and 950 s mm<sup>-2</sup> in a random order to avoid fatigue bias.

### Processing

The cDTI data were processed using in-house MATLAB software. All frames were examined visually to identify and reject frames corrupted by motion. A rapid multi-resolution rigid-registration algorithm (34) was used to register all images acquired in the same subject. The diffusion tensor was calculated at every pixel using the linear least squares “B-matrix approach” described in (35). As the mixing time is one cardiac cycle, the actual b-value varies with heart rate. In this work, the images used in the tensor calculation were not averaged so that the dependence of the b-value on heart rate could be accounted for in the B-matrix based on the image time stamps.

### Testing the mono-exponential model of diffusion

Typically in DTI, the diffusing water is assumed to be free, which results in a mono-exponential decay of the signal with diffusion weighting:

$$S = S_0 \exp(-b \cdot D) \quad (1)$$

where  $S$  is the measured signal,  $S_0$  is the signal without diffusion weighting,  $D$  is the diffusivity along the diffusion encoded direction and  $b$  is the magnitude of the diffusion weighting. Including a second, diffusion like, component, which is often performed to account for microvascular perfusion (23, 24, 31), produces a bi-exponential model:

$$S = S_0 \cdot [A \exp(-b \cdot D_1) + (1 - A) \exp(-b \cdot D_2)] \quad (2)$$

where  $D_1$  is the diffusion coefficient in the high b-value regime,  $D_2$  describes the diffusion like signal loss at low b-values and  $A$  describes the relative contribution of each term.

The relationship between b-value and signal loss was investigated. Trace diffusion-weighted images (8) were calculated for each subject and each b-value. A region of interest (ROI) was defined to cover the left ventricular myocardium in each subject, excluding the papillary muscles. The ratio of the mean trace diffusion-weighted signal and  $b_{\text{ref}15}$  signal in the ROI was plotted with the corresponding heart rate corrected b-value. The mono and bi-exponential models described in equations 1 and 2 were fitted to this data using the Levenberg-Marquardt algorithm in the MATLAB curve fitting toolbox with the bilinear option for robustness and starting points of  $A=1.0$ ,  $D_1=D_2=1.0 \times 10^{-3} \text{ mm}^2\text{s}^{-1}$ .

### Comparison of combinations of $b_{\text{main}}$ and $b_{\text{ref}}$ values

To assess the effect of  $b_{\text{main}}$ , the MD, FA and HA parameter maps were calculated for each subject using each of the 6 acquired b-values (prescribed as 50 – 950  $\text{s mm}^{-2}$ ) as  $b_{\text{main}}$  together with the  $b_{\text{ref}15}$  images.

To determine the effect of the diffusion weighting of the reference image on the parameter maps, diffusion-weighted images were used as a reference ( $b_{\text{ref}D}$  images). To determine the best way to acquire diffusion weighted reference data, 3 methods of defining the reference data were used:

**Method 1 – ALL:** All averages and directions were used for the reference data. This theoretically represents the best reference data, but in practice, means doubling the acquisition duration as 6 directions with 8 averages are used for both the  $b_{\text{main}}$  images and the  $b_{\text{refD}}$  images.

**Method 2 – 1DIR:** All averages of the first diffusion direction were used as reference images. This most closely approximates the diffusion weighting of the spoiler gradients used in the  $b_{\text{ref15}}$  images, although in general, the direction of the diffusion weighting of the  $b_{\text{ref15}}$  images is not parallel to any of the diffusion encoding directions. This scheme could be implemented without increasing the acquisition duration beyond the previously described protocol (7). The first direction was chosen here arbitrarily and this process also was repeated using the second (perpendicular to the first) and third (greatest sum of squares difference from the first direction) directions to test any dependence on direction.

**Method 3 – 1AVE:** The first average of all directions was used as reference data. Although with less signal to noise ratio (SNR) than in method 1 (ALL), this scheme could be implemented without increasing the acquisition duration beyond the previously described protocol (7).

For each subject and using each b-value as  $b_{\text{main}}$ , diffusion tensors and MD, FA and HA parameter maps were calculated using all possible  $b_{\text{refD}}$  with all three methods described above. Mean FA and MD in the left ventricle ROI was calculated for each case. HA varies approximately linearly from endo- to epicardium so the mean HA gradient and mean coefficient of determination ( $R^2$ ) from a linear regression of HA versus transmural depth (20, 21) was calculated to provide an indication of the changes in HA with  $b_{\text{main}}$  and  $b_{\text{ref}}$ . The number of negative eigenvalues in the calculated diffusion tensor within the ROI was also recorded. These values violate the assumption that the diffusion tensor is positive definite and they are, therefore, unphysical so are used as an indicator of

poor quality data where, for instance, the difference in signal between the voxels in the main and reference data was insufficient.

### Measures of SNR

The SNR was calculated from the trace diffusion-weighted images using the method described in Nielles-Vallespin et al. (7, 36), where SNR was defined as the ratio of the mean signal to the standard deviation between averages in each pixel. The mean SNR in the left ventricle and in each of 4 equal angle segments (septal, anterior, lateral and inferior) was calculated. In addition, minimum signal to noise floor ratio (MSNFR) was defined as the ratio of the minimum value (over the six directions) from the diffusion images after averaging all images with the same diffusion encoding, to the mean signal value in a ROI drawn in the blood pool in the left ventricle. The mean MSNFR was calculated in each of the 4 segments to indicate the proximity of the diffusion-weighted signal to the noise floor.

### Results

cDTI was successfully performed in all subjects and no breath holds were repeated due to poor image quality. The mean number of rejected frames per acquisition was  $3.1 \pm 7.5\%$  and the number of rejected frames did not correlate significantly with prescribed b-values ( $R^2=0.0025$ ,  $p=0.81$ ). The median acquisition duration for the cDTI data acquisition was 32 minutes (range 28 – 40 minutes). The median for all 10 subjects of the average RR interval was 1.055 s with a range of 0.83 – 1.22 s corresponding to b-values from 623 – 915  $\text{s mm}^{-2}$  for a prescribed b-value of 750  $\text{s mm}^{-2}$  (which, in combination with  $b_{\text{ref}}=150 \text{ s mm}^{-2}$ , we later find to be optimal). The median within-subject standard deviation of the RR interval was 0.05 (range 0.03 – 0.06 s), suggesting that at a prescribed b-value of 750  $\text{s mm}^{-2}$  and a mean RR interval of 1s the b-value typically varied within a subject from 675 to 825  $\text{s mm}^{-2}$  (-2 standard deviations to +2 standard deviations). Figure 2 shows example images at each of the prescribed b-values before and after averaging in one typical subject. Artifacts caused by insufficient spoiling of the gradient echo pathways were observed in



some  $b_{\text{ref}15}$  images (Figure 2a arrow). These artifacts were not present in any of the other diffusion-weighted images, due to the higher b-values and more effective spoiling in these images.

Plots of MD, FA, SNR and MSNFR versus prescribed  $b_{\text{main}}$  up to  $3000 \text{ s mm}^{-2}$  (with  $b_{\text{ref}15}$ ) for the pilot subject are provided in the supplementary material (S1). MD initially fell rapidly until  $b_{\text{main}} \approx 250 \text{ s mm}^{-2}$  and then more slowly. FA reduces with increasing  $b_{\text{main}}$ , with a more rapid reduction beginning between prescribed  $b_{\text{main}} = 750 \text{ s mm}^{-2}$  and  $b_{\text{main}} = 950 \text{ s mm}^{-2}$ . Visual analysis suggests that signal in some areas of the myocardium reaches the noise level at around prescribed  $b_{\text{main}} = 950 \text{ s mm}^{-2}$  and the MSNFR is less than 2 at this point. Based on these results, prescribed b-values from 50 to  $950 \text{ s mm}^{-2}$  were chosen to image the 10 volunteers.

Figure 3 shows maps of MD, FA and HA from one typical subject with all  $b_{\text{main}}$  values and  $b_{\text{ref}15}$  reference images. The parameter maps appear more consistent between  $b_{\text{main}}$  values as  $b_{\text{main}}$  increases.

Figure 4 shows a plot of the mean myocardial signal intensity in the trace diffusion-weighted images plotted against the heart rate corrected b-value. The fit of equations 1 and 2 to the data after excluding data at b-values  $> 1000 \text{ s mm}^{-2}$  to avoid the noise floor is also shown. The bi-exponential model (equation 2) demonstrates better agreement with the data than the mono-exponential model,  $R^2 = 0.994$  vs.  $R^2 = 0.987$  respectively. The fitted parameters for the bi-exponential model were  $D_1 = 0.86 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$  (95% confidence interval (C.I.) =  $0.83 - 0.90 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$ ),  $D_2 = 17 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$  (C.I. =  $5.6 - 29 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$ ) and  $A = 0.94$  (C.I. =  $0.92 - 0.96$ ). The mono-exponential model over-estimates the diffusivity when compared to the bi-exponential model as  $D = 0.99 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$  (C.I.  $0.95 - 1.00 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$ ).

Diffusion tensors and the parameter maps were calculated for every subject with all  $b_{\text{main}}/b_{\text{ref}D}$  combinations using all three methods. Figure 5 shows the mean MD, FA, HA gradient,  $R^2$  from the transmural linear regression of HA and

percentage of negative eigenvalues plotted against  $\Delta b$  (where  $\Delta b$  is the difference between the prescribed  $b_{\text{main}}$  and  $b_{\text{ref}}$ ). For clarity, the results obtained using  $b_{\text{ref}15}$  are shown for each  $b_{\text{main}}$  value and the full set of results using all possible  $b_{\text{ref}D}$  values is only provided for  $b_{\text{main}}=750 \text{ s mm}^{-2}$  and the 1AVE method (the complete set of results is provided in supplementary material, figure S2).

When the  $b_{\text{ref}15}$  images are used as a reference, the MD initially falls rapidly with  $\Delta b$  and then more gradually when  $\Delta b > 150 \text{ s mm}^{-2}$  (figure 5.a). With increasing  $b_{\text{ref}D}$  MD falls slowly. There is little difference in MD values between the ALL, 1DIR and 1AVE methods (see supplementary material, figure S2. a-c).

There is a significant linear trend for decreasing FA with increasing  $\Delta b$  using ALL ( $R^2=0.95$ ,  $p<0.001$ ,  $\text{FA}=0.49 - 0.00013 \Delta b$ ), 1DIR ( $R^2=0.93$ ,  $p<0.001$ ,  $\text{FA}=0.50 - 0.00014 \Delta b$ ) and 1AVE ( $R^2=0.94$ ,  $p<0.001$ ,  $\text{FA}=0.49 - 0.00013 \Delta b$ ) (see figure 5.b and supplementary material, figure S2, d-f).

The percentage of negative eigenvalues is high (up to 23%) for small values of  $\Delta b$  ( $\leq 200 \text{ s mm}^{-2}$ , see figure 5.c), suggesting that the data is unreliable in this regime. At low  $\Delta b$  the percentage of negative eigenvalues increases with increasing  $b_{\text{ref}D}$ ; more so when 1DIR or 1AVE is used (see supplementary material figure S2, g-i). However, when  $\Delta b > 200 \text{ s mm}^{-2}$ , the maximum mean number of negative eigenvalues was 0.8%.

When  $\Delta b \leq 200 \text{ s mm}^{-2}$ , there is a small increase in HA gradient for some combinations of  $b_{\text{main}}$ ,  $b_{\text{ref}}$  and reference method (see supplementary material figure S2, m-o). The  $R^2$  value from the linear regression of transmural HA change primarily depends on  $b_{\text{main}}$  and is low at low  $b_{\text{main}}$ , then plateaus around  $b_{\text{main}}=550 \text{ s mm}^{-2}$ . When the 1AVE or 1DIR methods are used there is a small drop in  $R^2$  value with increasing  $b_{\text{ref}}$  value (see supplementary material, figure S2, j-l).

While there is a greater proportion of negative eigenvalues at small  $\Delta b$  when using 1AVE or 1DIR compared to using ALL, differences in HA gradient, FA and

MD between the methods are small. As the ALL method is time consuming and appears to offer little benefit, either of 1DIR or 1AVE should be considered optimal.

Tables 1 and 2 provide mean MD and FA values calculated from all pairs of prescribed  $b_{\text{main}}$  and  $b_{\text{refD}}$  using the 1AVE method of calculating  $b_{\text{refD}}$ . MD is closest to  $D_1$  when prescribed  $b_{\text{main}}=950 \text{ s mm}^{-2}$  and  $b_{\text{refD}}=50 \text{ s mm}^{-2}$  ( $\text{MD}=0.859\pm 0.053 \text{ s mm}^{-2}$ ) and next closest when  $b_{\text{main}}=750 \text{ s mm}^{-2}$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$  ( $\text{MD}=0.870\pm 0.063 \text{ s mm}^{-2}$ ).

SNR and MSNFR were highest in the septal segment and lowest in the lateral segment. Plots of mean SNR and MSNFR in the septal and lateral segments with b-value are provided in the supplementary material (figure S3). As expected SNR and MSNFR decrease with increasing b-value. In the lateral wall the MSNFR at prescribed  $b=950 \text{ s mm}^{-2}$  is  $1.47\pm 0.28$ , which is 1.7 standard deviations away from the noise floor and it might be expected that the signal in some subjects may lie within the noise floor. At prescribed  $b=750 \text{ s mm}^{-2}$ , MSNFR is  $1.74\pm 0.37$ , which is 2.0 standard deviations from the noise floor and in the large majority of healthy subjects the signal avoids noise floor effects.

Figure 6 shows example parameter maps (MD, FA and HA) in one subject when prescribed  $b_{\text{main}}=750 \text{ s mm}^{-2}$  and the prescribed  $b_{\text{ref}}$  is increased from 15 to 550  $\text{s mm}^{-2}$  using the 1AVE (part i) and 1DIR (part ii) methods of calculating  $b_{\text{refD}}$ . There is little difference between the parameter maps produced using 1AVE and 1DIR, except a slightly greater visible increase in noise in the FA and MD maps as  $b_{\text{refD}}$  is increased using 1AVE.

When the processing was repeated using the 1DIR method of calculating the  $b_{\text{refD}}$  images using the second diffusion encoding direction as a reference, there was an average difference in MD of  $+2.3 \pm 2.7\%$  and FA of  $-2.1\pm 2.6\%$  (direction 1 – direction 2) at  $b_{\text{main}}=750 \text{ s mm}^{-2}$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$ . The equivalent results using the third diffusion encoding direction as a reference were a difference in MD of  $+1.5\pm 3.5\%$  and in FA of  $-1.3\pm 3.1\%$  (direction 1 – direction 3). When

$b_{\text{main}}=350 \text{ s mm}^{-2}$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$ , there was an MD difference of  $+2.9 \pm 7.2\%$  and an FA difference of  $-2.5 \pm 5.6\%$  when comparing direction 1 to direction 2. The equivalent results comparing direction 1 to direction 3 were an MD difference of  $+3.4 \pm 9.2\%$  and an FA difference of  $-2.8 \pm 7.0\%$ .

Figure 7 shows FA maps, MD maps and superquadric glyphs representing the full measured diffusion tensor in each pixel for one subject with prescribed  $b_{\text{main}}=350 \text{ s mm}^{-2}$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$ , using the 1DIR method (figure 7a, c, e and f) and with prescribed  $b_{\text{main}}=750 \text{ s mm}^{-2}$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$  using the 1AVE method (figure 7b, d, g and h). Table 3 compares values for MD, FA, HA gradient and  $R^2$  for prescribed  $b_{\text{main}}=350$  and  $750 \text{ s mm}^{-2}$  when  $b_{\text{ref15}}$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$  (all three methods) are used as a reference. These b-values were chosen to most closely match those in previous work from both our group (6, 7, 19, 21) and others (9, 11, 12, 20), compared with the values chosen as optimal in this work.

## Discussion

In this work we have described developments, which go some way towards addressing two of the difficulties faced in *in-vivo* cDTI: the intrinsically low SNR of the technique and the contribution of other intra-voxel incoherent motions to the measured diffusion. We have demonstrated the dependence of the measured myocardial diffusivity on  $b_{\text{main}}$ . This is partly caused by a deviation of the signal intensity versus b-value relationship from the mono-exponential model shown in equation 1. A bi-exponential model fits the data well. At low b-values the signal loss is a combination of the diffusion of water molecules (described by  $D_1$ ) and a second process with a much higher apparent diffusion coefficient ( $D_2$ ), which, it has been suggested (31), is associated with microvascular perfusion. In this study, using  $b_{\text{ref}}=150 \text{ s mm}^{-2}$  was sufficient to reduce the contribution of the  $D_2$  component to 0.5% of the remaining signal, making MD less dependent on the  $b_{\text{main}}$ . One limitation of this analysis was that it did not consider any directionality of the two components. Previous work (24, 30) has suggested that the fast (or  $D_2$ ) component is predominantly aligned with the myocyte orientation, but others (31) have assumed  $D_2$  to be isotropic.

Our results demonstrate that when a similar number of  $b_{\text{ref}}$  images are used, mean values of FA, MD and HA gradient are similar whether the reference images have diffusion encoding in a single direction (1DIR) or the direction is rotated (1AVE). However, we did demonstrate within-subjects differences in FA and MD depending on which diffusion encoding direction was used as a reference with the 1DIR technique. And while it was not investigated as part of this work, it would seem reasonable to acquire reference data with diffusion encoded in several directions to avoid any directional bias in  $D_2$  (24). Parameter maps are improved using the ALL method, but it is not clear from this work whether time would be better used to acquire more data at  $b_{\text{ref}}$  or  $b_{\text{main}}$ . In future studies  $b_{\text{refD}}$  images may be acquired instead of or in addition to the existing  $b_{\text{ref15}}$  images; acquiring both may allow an estimation of  $D_2$  which could be physiologically interesting.

Prescribed  $b_{\text{main}}$ , particularly for low SNR techniques such as STEAM, should be as high as possible to maximise the signal intensity differences between the main and reference data, and hence, increase the SNR of the derived tensors. With increasing  $b_{\text{ref}}$  derived parameters become more variable and at low  $\Delta b$  values, there are more negative eigenvalues. The minimum value of  $b_{\text{ref}}$  required to suppress the signal from microvascular perfusion should therefore, be used. The longer diffusion gradients required for higher b-values increase TE slightly, but the disadvantages of this should be outweighed by the improvements in the parameter maps. At sufficiently high b-values the signal approaches the noise floor and the derived parameters will be artifactually affected (37). The signal is closer to the noise floor in the lateral wall than in the septal wall, but MSNFR (and SNR) is more variable in the septal wall (see the standard deviations in supplementary figure S2). This is due to the combination of the proximity of the septal wall to the anterior surface coil, the rapid change in coil sensitivity in this region and the subject specific cardiac geometry. We calculated parameter maps using prescribed  $b_{\text{main}}$  values up to  $950 \text{ s mm}^{-2}$ , without noticing detrimental effects. However, limiting prescribed  $b_{\text{main}}$  to  $750 \text{ s mm}^{-2}$  maintained MSNFR at 2 standard deviations above the noise floor in healthy subjects. In patients the

prescribed  $b_{\text{main}}$  may need to be reduced below  $750 \text{ s mm}^{-2}$  as patients often have a higher body mass index and poorer breath-hold performance, both of which reduce SNR.

For the protocol used in this study, we selected a combination of  $b_{\text{main}} = 750 \text{ s mm}^{-2}$  with  $b_{\text{refD}} = 150 \text{ s mm}^{-2}$  as optimal. This was based on reducing the contribution of  $D_2$  to less than 1% of the remaining signal, avoiding severe noise floor effects at high b-values, matching the mean MD value to the  $D_1$  value obtained and maximising the linearity of the transmural HA progression ( $R^2$ ). It is possible that a different combination would be optimal for FA, which reduced linearly with  $\Delta b$ . Improvements in the appearance of FA maps were observed with increasing  $\Delta b$  but without a gold standard for myocardial FA, this remains a limitation.

Until now there has been little consideration of the optimal b-values for *in-vivo* cDTI. Previous work in neuro-imaging has suggested that  $\Delta b$  should be approximately  $1.11/\text{diffusivity}$  (38) (ignoring T2), suggesting that  $\Delta b$  should be larger than the value of  $600 \text{ s mm}^{-2}$  ( $b_{\text{main}}=750$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$ ) selected here as optimal. While future improvements (39) may permit larger  $\Delta b$  values, a detailed assessment, including simulations of the effects of noise should be performed first.

The FA and MD obtained here using prescribed  $b_{\text{main}}=350 \text{ s mm}^{-2}$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$  calculated using the 1DIR method are within 1 standard deviation of those obtained by Nielles-Vallespin et al. (prescribed  $b_{\text{main}}=350 \text{ s mm}^{-2}$ ) after the correction for  $b_{\text{ref}}$  (prescribed at  $135 \text{ s mm}^{-2}$ ) was applied (7, 19) (FA= $0.471 \pm 0.041$  vs.  $0.46 \pm 0.04$  and MD= $0.987 \pm 0.082 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$  vs.  $1.14 \pm 0.15 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$ ). Wu et al. (12) found MD= $0.64 \pm 0.03 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$  in healthy subjects, imaged at the sweet spot to avoid strain effects, using monopolar STEAM EPI ( $b_{\text{main}}=300 \text{ s mm}^{-2}$ ). We found higher MD values (MD= $1.049 \pm 0.047 \times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$  using prescribed  $b_{\text{main}}=350 \text{ s mm}^{-2}$  and  $b_{\text{ref}15}$ ), but acquired at peak systole, where strain affects measurements, but motion is less problematic. Using similar sequences ( $b_{\text{main}}=350 \text{ s mm}^{-2}$  and  $b_{\text{ref}}=15\text{-}20 \text{ s}$

mm<sup>-2</sup>) also acquired in peak systole, Lau et al. (20) and Tunncliffe et al. (21) obtained closer values of MD=1.19±0.10 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup> and MD=1.06±0.06/1.13±0.13 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup> (two-centre comparison (21)) respectively. Using diffusion-weighted imaging, Rapacchi et al. (8) found MD=7.1 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup> using a spin-echo EPI sequence with b=0, 50 and 100 s mm<sup>-2</sup>, which is greater than we found (MD=1.90±0.46 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup> using prescribed b<sub>main</sub>=50 s mm<sup>-2</sup> and b<sub>ref15</sub>). At low b<sub>main</sub> the measured MD is elevated due to the inclusion of microvascular perfusion and the high ratio of noise to signal difference between the main and reference images. The same group also fitted a bi-exponential model to diffusion-weighted data acquired with b-values from b=0 to b=550 s mm<sup>-2</sup> (31). They found values equivalent to our D<sub>1</sub>, D<sub>2</sub> and A of D<sub>1</sub>=2.44±0.99 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup>, D<sub>2</sub>=76.5 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup> and A=0.792±0.057. Using a larger range but fewer b-values, we found a smaller proportion of microvascular perfusion (A=0.94) and lower values for both D<sub>1</sub>=0.86 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup> and D<sub>2</sub>=17 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup>. One key difference with our work is the mixing time, which is ~10ms for the spin-echo sequence and ~1s for the monopolar STEAM sequence. *Ex-vivo* work has demonstrated time dependent diffusivity in myocardial tissue (5), however it is unclear how this would translate to *in-vivo* imaging. Work in *in-vivo* canine myocardium using a monopolar STEAM EPI sequence (14 b-values, 0-600 s mm<sup>-2</sup>, mixing time 1 cardiac cycle) has found values equivalent to D<sub>1</sub>=1.26±0.10 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup> and D<sub>2</sub>=14.13±2.56 x 10<sup>-3</sup> mm<sup>2</sup> s<sup>-1</sup> (24).

We have demonstrated a dependence of FA on the b-values. We obtained mean FA values from 0.372 (prescribed b<sub>main</sub>=950 s mm<sup>-2</sup> and b<sub>ref15</sub>) to 0.495 (prescribed b<sub>main</sub>=150 and b<sub>ref15</sub>). In healthy volunteers Wu et al. (12), measured FA=0.34±0.02 at b<sub>main</sub>=300 s mm<sup>-2</sup>, whereas Tseng et al. (11) quote higher values of FA=0.72 and 0.78 in the free wall and septum respectively (b<sub>main</sub>=400 s mm<sup>-2</sup>). However, FA might be elevated at the higher spatial resolution used by Tseng et al. (3x3x3mm<sup>3</sup>) (11). Using a protocol similar to that used here, similar values to our result of FA=0.445±0.042 (using b<sub>ref15</sub> and b<sub>main</sub>=350 s mm<sup>-2</sup>) were found by Lau et al. (20) (FA=0.44±0.05) and Tunncliffe et al. (21) (FA=0.41±0.05 and 0.40±0.07 at two sites).

The values of HA gradient obtained by Tunncliffe et al. (21) were similar to those obtained here ( $8.7 \pm 1.4$  and  $9.0 \pm 1.4$  ° mm<sup>-1</sup> at two different sites vs.  $9.3 \pm 1.1$  ° mm<sup>-1</sup> here using  $b_{\text{main}}=350$  s mm<sup>-2</sup> and  $b_{\text{ref15}}$ ), but Lau et al. (20), found a lower value of  $4.5 \pm 1.5$  ° mm<sup>-1</sup>. HA gradient appears to change little with b-values but using the coefficient of determination of the linear fit ( $R^2$ ) appears to be an indicator of data quality and demonstrated that HA is most linear when  $b_{\text{main}} \geq 550$  s mm<sup>-2</sup>.

The results we have presented here apply to the monopolar STEAM technique and the optimal parameters will vary with subject and protocol. The dependence of the b-value on the heart rate means that it is important that the dependence of measured diffusion parameters on the b-values is minimized to enable between-subjects comparisons. It is also possible parameters could vary with heart rate due to a mixing time dependence of the measured diffusion which is typical in biological tissues (40). However, from *ex-vivo* work, we expect the changes to be small for typical variations in heart rate (5). While we did not eliminate the dependence of FA and MD on b-values, work in the brain (41, 42, 43) has demonstrated that a mono-exponential model is insufficient at higher  $b_{\text{main}}$  values, due to the complex structure of biological tissues. In fact previous work in *ex-vivo* myocardium, has shown reductions in FA and MD (13) and deviation from mono-exponential behavior in isolated beating hearts (30) at high  $b_{\text{main}}$  values. As described by Jones et al. (37), there is a signal bias effect before we reach the noise floor which would account for some of the changes we observed in MD and FA (37). Also, we did not account for strain (9, 44, 45), but it should have similar effects on any intravoxel incoherent motion and we believe our findings still apply.

In conclusion, we have demonstrated how *in-vivo* cDTI may be improved by using optimal b-values. We have demonstrated the dependence of MD, FA and transmural HA linearity on diffusion weighting and shown that at low b-values the signal loss in *in-vivo* cDTI is dominated by a second process with a high diffusion coefficient. We believe this additional process to be microvascular perfusion and its contribution to the measured diffusivity can be avoided by



using diffusion-weighted reference images. Also, using increased diffusion weighting in the main diffusion-weighted images improves the MD, FA and HA maps, as long as the diffusion-weighted signal remains sufficiently far from the noise floor. While the noise floor depends on many parameters, a combination of prescribed  $b_{\text{main}}=750 \text{ s mm}^{-2}$  and  $b_{\text{ref}}=150 \text{ s mm}^{-2}$  was optimal for the protocol used here and is recommended as a starting point for future developments. The improvements in parameter maps provided by using these optimal b-values might enable detection of the seemingly small changes caused by disease and contribute to advances in the understanding of cardiac microstructure.

### Acknowledgements

This work was performed at the National Institute of Health Research funded Cardiovascular Biomedical Research Unit at the Royal Brompton Hospital, London, UK.

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## Tables

**Table 1: Mean ( $\pm$ SD) of global left ventricular MD using the 1AVE method of calculating the reference images.**

$b_{ref}$	$b_{main}$	$b_{main}$	$b_{main}$	$b_{main}$	$b_{main}$	$b_{main}$
	50	150	350	550	750	950
$b_{ref15}$	1.90 $\pm 0.46$	1.21 $\pm 0.17$	1.049 $\pm 0.047$	0.983 $\pm 0.041$	0.930 $\pm 0.037$	0.879 $\pm 0.041$
50		1.19 $\pm 0.16$	1.012 $\pm 0.053$	0.954 $\pm 0.055$	0.906 $\pm 0.053$	0.859 $\pm 0.053$
150			0.97 $\pm 0.16$	0.914 $\pm 0.092$	0.870 $\pm 0.063$	0.827 $\pm 0.053$
350				0.89 $\pm 0.12$	0.826 $\pm 0.075$	0.784 $\pm 0.072$
550					0.823 $\pm 0.087$	0.763 $\pm 0.082$
750						0.72 $\pm 0.14$

The cells highlighted grey indicate where the calculated MD deviates by 10% or less from the value of  $D_1$  calculated in figure 4. MD values are given in units of  $\times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$  and b-values are prescribed and in units of  $\text{s mm}^{-2}$ .

**Table 2: Mean ( $\pm$ SD) of global left ventricular FA using the 1AVE method of calculating the reference images.**

$b_{ref}$	$b_{main}$	$b_{main}$	$b_{main}$	$b_{main}$	$b_{main}$	$b_{main}$
	50	150	350	550	750	950
$b_{ref15}$	0.481	0.492	0.445	0.411	0.393	0.372
	$\pm 0.023$	$\pm 0.062$	$\pm 0.042$	$\pm 0.026$	$\pm 0.021$	$\pm 0.029$
50		0.491	0.461	0.424	0.404	0.382
		$\pm 0.045$	$\pm 0.042$	$\pm 0.029$	$\pm 0.023$	$\pm 0.030$
150			0.483	0.444	0.419	0.396
			$\pm 0.068$	$\pm 0.045$	$\pm 0.036$	$\pm 0.038$
350				0.461	0.448	0.420
				$\pm 0.043$	$\pm 0.029$	$\pm 0.027$
550					0.453	0.435
					$\pm 0.042$	$\pm 0.031$
750						0.451
						$\pm 0.059$

b-values are prescribed and are given in units of  $s\ mm^{-2}$ .

**Table 3: Comparison of the 3 methods of acquiring reference data**

$b_{\text{main}}$	$b_{\text{ref}}$	Ref. method	MD (mean $\pm$ SD)	FA (mean $\pm$ SD)	HA gradient (mean $\pm$ SD)	$R^2$ (mean $\pm$ SD)
350	15	$b_{\text{ref}15}$	1.049 $\pm$ 0.047	0.445 $\pm$ 0.042	9.3 $\pm$ 1.1	0.861 $\pm$ 0.067
350	150	ALL	0.960 $\pm$ 0.076	0.482 $\pm$ 0.032	9.2 $\pm$ 1.2	0.870 $\pm$ 0.059
350	150	1DIR	0.987 $\pm$ 0.082	0.471 $\pm$ 0.041	9.4 $\pm$ 1.1	0.856 $\pm$ 0.063
350	150	1AVE	0.974 $\pm$ 0.157	0.483 $\pm$ 0.068	9.2 $\pm$ 1.1	0.850 $\pm$ 0.062
750	15	$b_{\text{ref}15}$	0.930 $\pm$ 0.037	0.393 $\pm$ 0.021	9.1 $\pm$ 1.0	0.908 $\pm$ 0.035
750	150	ALL	0.875 $\pm$ 0.070	0.418 $\pm$ 0.023	9.17 $\pm$ 0.97	0.912 $\pm$ 0.038
750	150	1DIR	0.883 $\pm$ 0.055	0.412 $\pm$ 0.023	9.1 $\pm$ 1.0	0.909 $\pm$ 0.036
750	150	1AVE	0.870 $\pm$ 0.064	0.419 $\pm$ 0.036	9.0 $\pm$ 1.0	0.910 $\pm$ 0.032

MD values are quoted in units of  $\times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$ .

HA gradient is quoted in units of  $^\circ \text{ mm}^{-1}$ .

$R^2$  is the coefficient of determination for the linear regression of transmural HA progression.

b-values are prescribed and are given in units of  $\text{s mm}^{-2}$ .

The grey rows highlight the protocol which approximately replicates the method used in McGill et al. (6) and Nielles-Vallespin et al. (7, 19) (prescribed  $b_{\text{main}}=350 \text{ s mm}^{-2}$ , 1DIR method  $b_{\text{refD}}=135 \text{ s mm}^{-2}$ ) compared to the parameters proposed for future studies (prescribed  $b_{\text{main}}=750 \text{ s mm}^{-2}$ , 1AVE method  $b_{\text{refD}}=150 \text{ s mm}^{-2}$ ).



## Figures

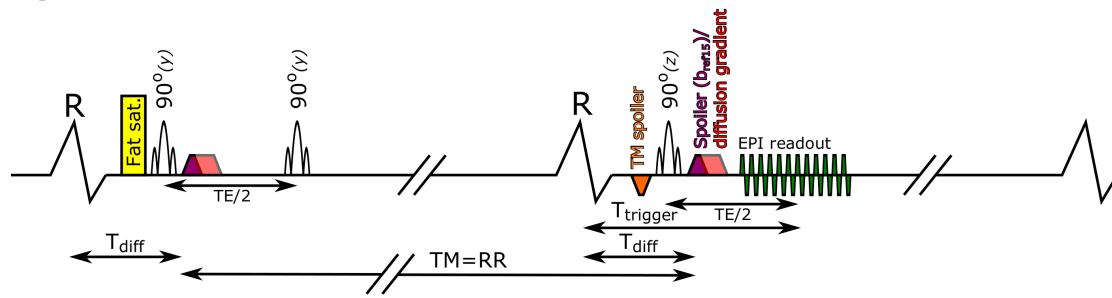


Figure 1: The monopolar STEAM EPI sequence used in this study. TM = mixing time, TE = echo time,  $T_{Trigger}$  = trigger time for imaging,  $T_{diff}$  = time the diffusion gradients are applied.

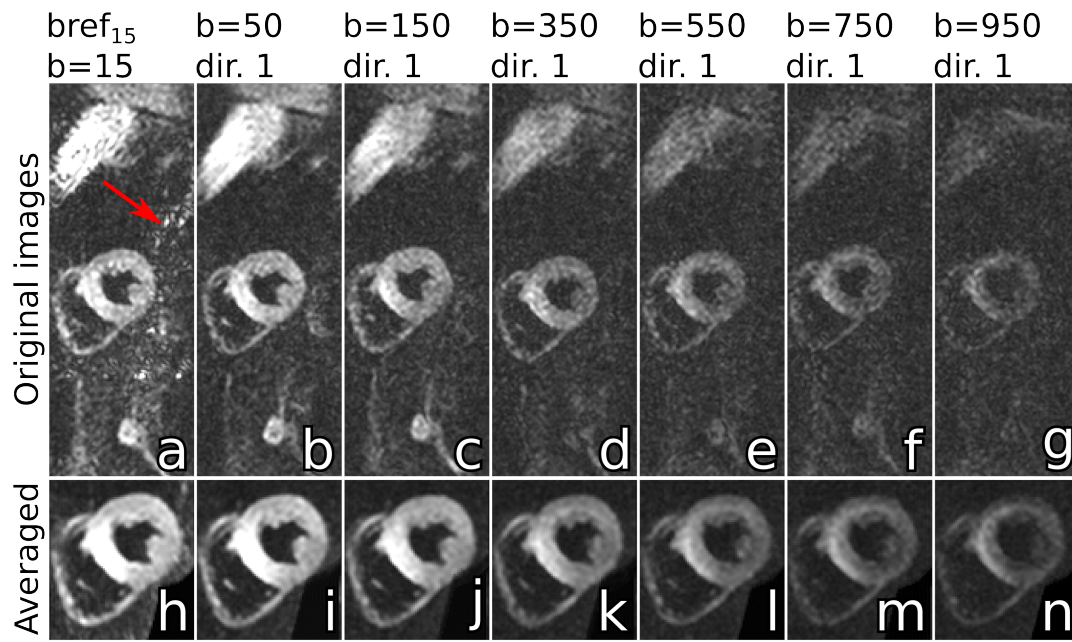


Figure 2: Example diffusion encoded images with increasing diffusion weighting, both with one average (a – g) and after motion correction and averaging (h – n). Artifact is observed in the  $b_{ref15}$  images before averaging (arrow), thought to be due to incomplete spoiling of gradient and spin echoes at low b-values. b-values are prescribed (not heart rate corrected) in units of  $s\ mm^{-2}$ .

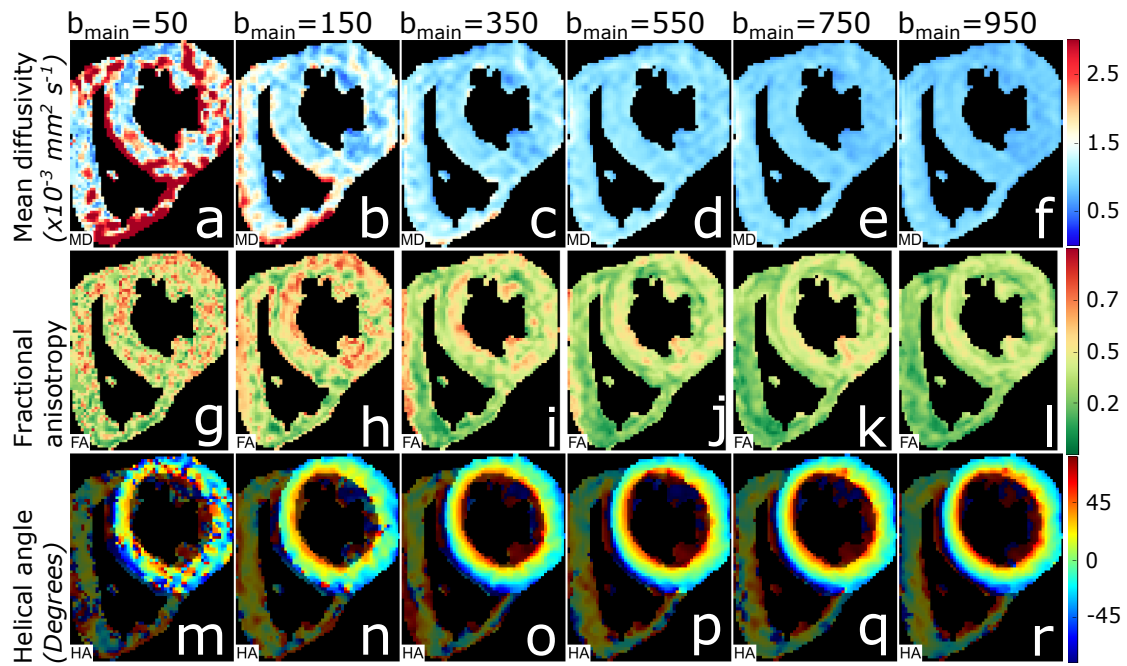


Figure 3: Example cDTI parameter maps (MD, FA and HA) from one example subject with  $b_{\text{main}}$  from 50 to 950  $\text{s mm}^{-2}$ . In each case  $b_{\text{ref}15}$  was used as a reference. The  $b$ -values given are those prescribed (before heart rate correction) in units of  $\text{s mm}^{-2}$ . The shaded region in the HA maps indicates the areas excluded from the left ventricular region of interest.

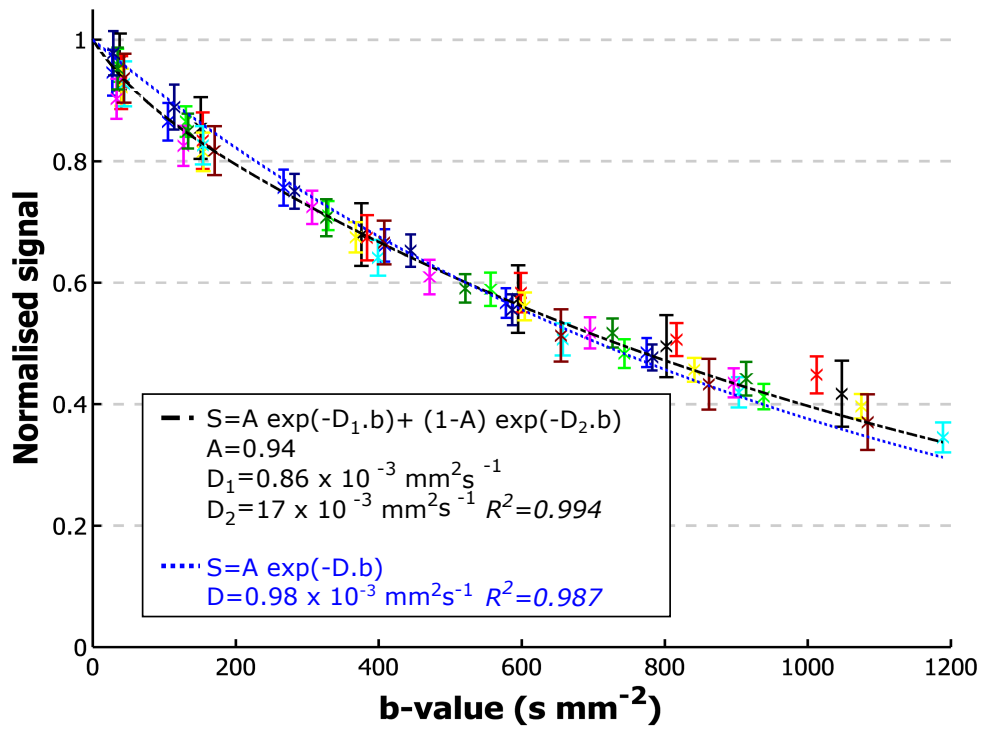


Figure 4: Normalised signal in the trace diffusion-weighted images plotted with the b-value (corrected for heart rate) with the mono and bi-exponential models fitted to the data.

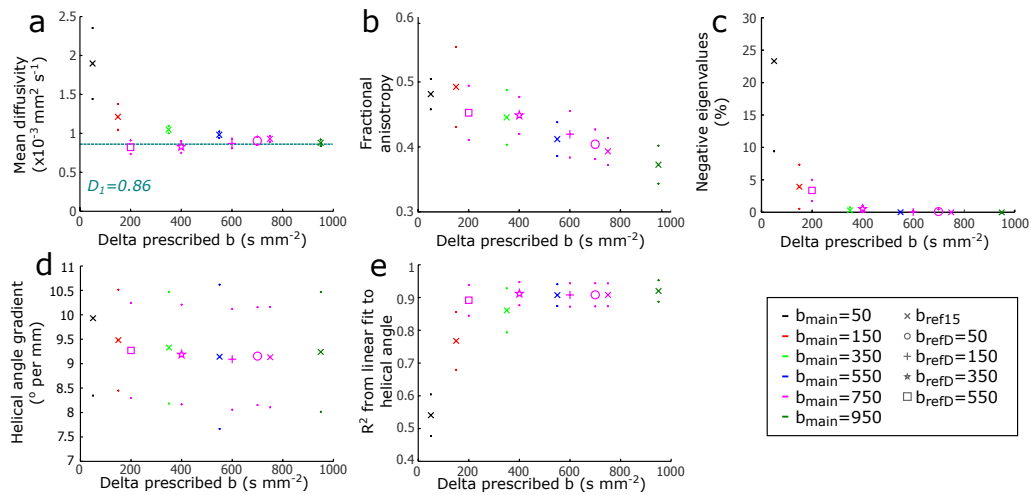


Figure 5: MD (a), FA (b), percentage of negative eigenvalues (c), transmural HA gradient (d) and the coefficient of determination ( $R^2$ ) for the linear regression of transmural HA (e) derived using the 1AVE method and plotted with the difference in prescribed  $b_{\text{main}}$  and  $b_{\text{ref}}$  (defined as  $\Delta b$  in the text). For each parameter, the mean is plotted  $\pm$  the standard deviation shown as small point markers. The main markers are colour coded by the  $b_{\text{main}}$  and the marker style indicates  $b_{\text{ref}}$ . The value of  $D_1$  from the bi-exponential model described by equation 3 and calculated in figure 4 is shown on the plots of MD. The upper error markers for  $b_{\text{main}}=50 \text{ s mm}^{-2}$  are not shown in parts c and d as the errors are large and lie far outside the displayed scale. Also see figure S2.

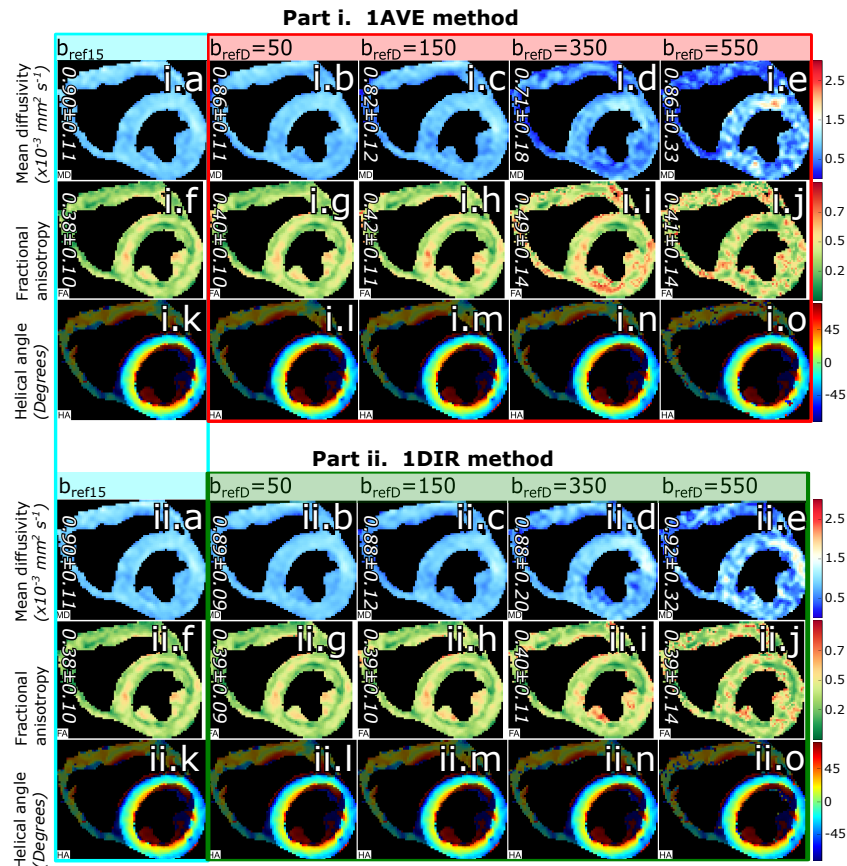


Figure 6: Example cDTI parameter maps calculated using a  $b_{\text{main}}=750 \text{ s mm}^{-2}$  with increasing  $b_{\text{ref}}$ . Reference images were calculated using the 1AVE method (part i) and 1DIR method (part ii). The  $b_{\text{ref}15}$  images are the same in both cases. The mean  $\pm$  standard deviation of the left ventricular MD and FA is shown on the corresponding images. The b-values given are those prescribed (before heart rate correction) in units of  $\text{s mm}^{-2}$ .

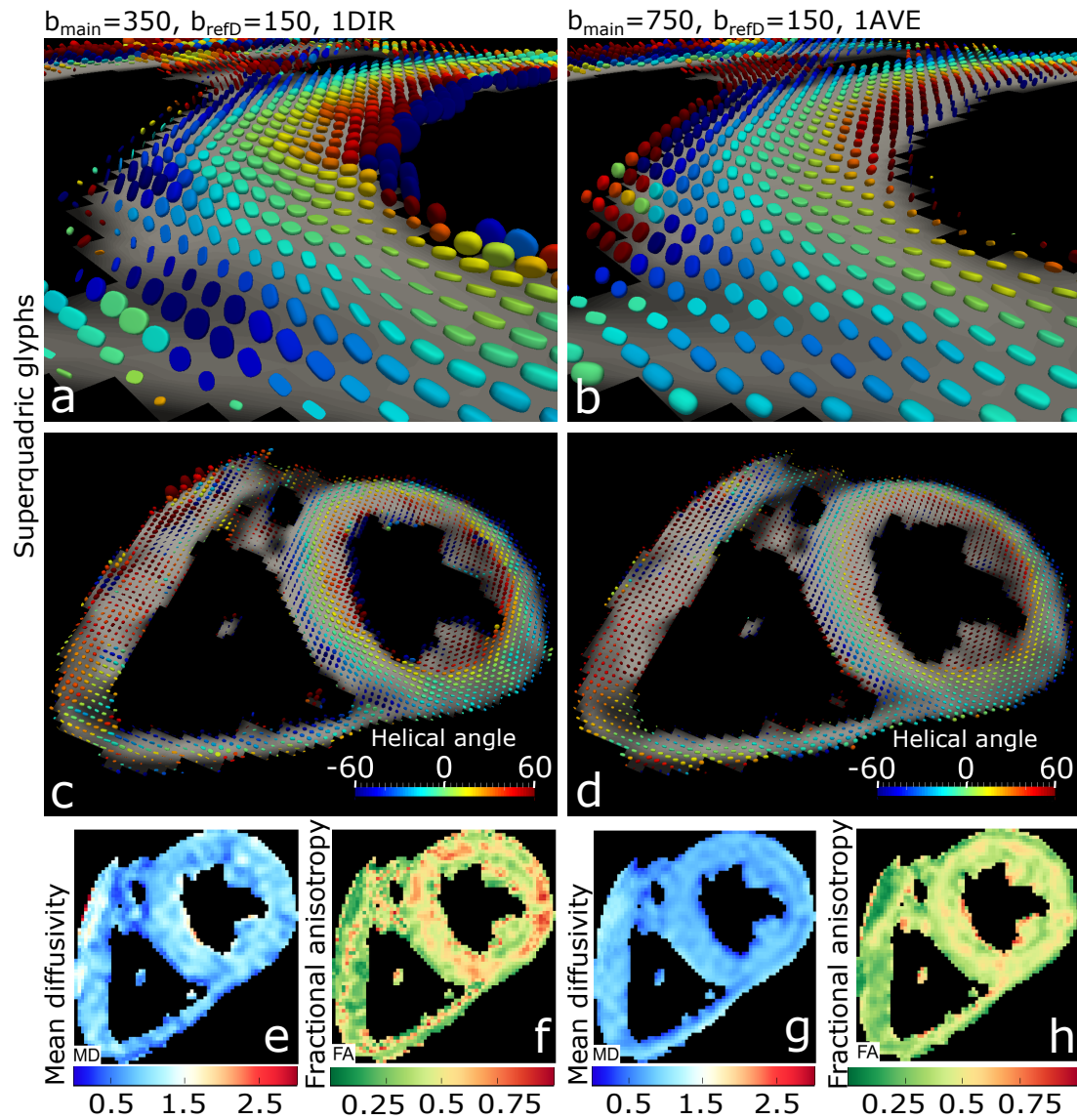


Figure 7: A comparison of the parameters closest to those used in our previous studies ( $b_{\text{main}}=350$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$  using 1DIR) in the left hand column (a, c, e and f) and the proposed new protocol ( $b_{\text{main}}=750$  and  $b_{\text{refD}}=150 \text{ s mm}^{-2}$  using 1AVE) in the right hand column (b, d, g, h). Superquadric glyphs describing the full diffusion tensor in the lateral wall (a and b) and the full myocardium (c and d) are coloured by helical angle. MD in units of  $\times 10^{-3} \text{ mm}^2 \text{ s}^{-1}$  (e and g) and FA (f and h) maps are also shown for each case. The b-values given are those prescribed (before heart rate correction) in units of  $\text{s mm}^{-2}$ .