

EVALUATION OF THE IMPACT OF STRAIN-CORRECTION ON THE ORIENTATION OF CARDIAC DIFFUSION TENSORS WITH IN-VIVO AND EX-VIVO PORCINE HEARTS

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ABSTRACT

Purpose: To evaluate the importance of strain-correcting STEAM-EPI cardiac diffusion tensor imaging (cDTI).

Methods: Healthy pigs (N=11) were successfully scanned with a 3D cine DENSE and a STEAM-EPI DTI sequence at 3T during diastasis, peak systole, and strain sweet-spots in a mid-ventricular short-axis slice. The same DTI sequence was repeated ex-vivo after arresting the hearts in either a relaxed (KCl-induced) or contracted (BaCl₂-induced) state.

The DENSE data were used to strain-correct the in-vivo cDTI in diastole and systole. The orientation of the primary (HA) and secondary (E2A) diffusion eigenvectors was compared with and without strain-correction and to the strain-free ex-vivo data.

Results: Strain-correction reduces systolic E2A significantly when compared to without strain-correction and ex-vivo [median absolute E2A = 34.3° vs E2A = 57.1° (P=0.01), E2A = 60.5° (P = 0.006) respectively]. The systolic distribution of E2A without strain-correction is closer to the contracted ex-vivo distribution than with strain-correction, root mean square deviation of 0.027 vs 0.038.

Conclusion: The current strain-correction model amplifies the contribution of microscopic strain to diffusion resulting in an over-correction of E2A. Results show that a new model that considers cellular rearrangement is required.

Keywords: cardiac; diffusion tensor imaging; strain; microstructure; cardiomyocyte; sheetlets.

INTRODUCTION

Myocardial micro-architecture is remarkably complex. Cardiomyocytes exhibit a transmural helical organization with helix angles (HA) rotating smoothly from positive in the endocardium to negative in the epicardium[1–3]. Additionally, cardiomyocytes have a laminar organization, where sheets of cardiomyocytes are surrounded by collagen-lined shear layers, as found histologically in many explanted mammalian hearts[4–7]. These myolaminae play a major role in the radial thickening and longitudinal shortening during the heart cycle[8–12]. The collective rotation of sheetlets accommodated by shear layer slippage, driven by cardiomyocyte contraction, is the dominant contributor to the radial thickening and longitudinal shortening observed in-vivo. Much smaller contributions arise from sarcomere driven changes in cardiomyocyte shape[13]. Because myolaminae are discrete and exist only very locally, Hales et al. referred to them as *sheetlets*[14].

Cardiac Diffusion Tensor Imaging (cDTI) is an MR imaging technique that encodes the self-diffusion of water molecules in three dimensions. A diffusion tensor is calculated for each voxel and several diffusion related parameters can be extracted. The orientation of the tensor is closely linked to the voxels' microstructure. It has been shown that the principal direction of diffusion aligns with the cardiomyocyte long-axis, while the secondary and tertiary directions of diffusion provide cross-cardiomyocyte sheetlet-plane and sheetlet-normal directions respectively[15–20]. More recent ex-vivo cDTI studies have been performed with hearts in relaxed and contracted states, thus probing microstructural reorganization during contraction[14,21]. No substantial changes of HA were measured, but the sheetlet planes were found to rotate from almost perpendicular to the local myocardial wall in systole to more wall parallel in diastole, in agreement with current models of sheetlet rotation during cardiac contraction.

In-vivo cDTI has attracted renewed interest aided by new technical advancements in both hardware and pulse sequence design[22–26]. Dou et al. in 2002 reported in-vivo rotation of sheetlets towards a more radial conformation during systolic contraction in one healthy volunteer[27]. More recent studies confirm a similar pattern of sheetlet rotation in a cohort of healthy volunteers and abnormal sheetlet dynamics in cardiomyopathy patients[28–30].

Two common approaches exist for encoding diffusion in-vivo: a motion compensated spin-echo with the encoding lasting for only a few tens of milliseconds[24,26]; and a *monopolar* stimulated (STEAM) approach where diffusion is encoded over an entire cardiac cycle[31]. The spin-echo approach encodes diffusion in

a single heartbeat, although the diffusion encoding time is around two orders of magnitude shorter when compared with the STEAM approach, which results in probing smaller microstructural length scales and concomitantly higher measured diffusivities[32–34].

A STEAM approach takes full advantage of cardiac motion being periodic, with the diffusion encoding/decoding gradients applied when the heart is at the same position in successive cardiac cycles. This technique requires breath-holding or dedicated respiratory triggering. However, a well-known disadvantage of the STEAM approach is regularly debated: *cardiac strain sensitivity*. Even though the heart returns to its original position, measuring diffusion with a STEAM sequence requires consideration of the myocardium's strain history during the diffusion encoding period[35–37]. Recently we have successfully acquired in-vivo cDTI data on both healthy and cardiomyopathy patients with a monopolar STEAM echo-planar imaging (EPI) sequence with both intra and inter-center reproducibility[28,30,38,39], but questions about strain effects remained unanswered, in particular the effects on the measurement of sheetlet rotation between systole and diastole.

Myocardial strain throughout the cardiac cycle can be measured and subsequently apply a correction to the diffusion tensor data acquired in systole or diastole[29,36]. However, the current strain-correction model ignores sheetlet rotation as a major contributor to wall thickening, and therefore likely to “correct” the diffusion data for an exaggerated strain effect.

The objective of this study was to evaluate the effect of strain-correcting cDTI data by directly comparing in-vivo cDTI data with and without strain-correction according to the established model proposed by Reese et al.[36], with strain-free ex-vivo DTI data of the same porcine hearts arrested in a diastolic-like or systolic-like conformations.

METHODS

The porcine cDTI data analyzed here are part of a larger data set previously used to compare in-vivo, in-situ, and ex-vivo DTI scans with histology wherein no strain analysis or correction was applied [30]. Here, we report data from a subset in which 3D strain was acquired successfully. A shortened version of this work has been presented at SCMR 2017[40].

EXPERIMENTAL DESIGN

Animal procedures were approved by the National Heart, Lung, and Blood Institute Animal Care and Use Committee. Sixteen Yorkshire pigs (weight 30 to 35 kg) were studied. Anesthesia was induced with the use of atropine, butorphanol, ketamine, and xylazine and maintained with the use of inhaled sevoflurane and supplemental IV propofol, together with mechanical ventilation.

All imaging was performed at 3T (MAGNETOM Skyra, Siemens, Germany) using investigational prototype sequences, a phased array Siemens torso coil and spine array combination. The mean cardiac cycle length was 737 ± 82 ms.

Following initial scans, which included breath-hold retro-gated cines, the pigs were scanned with a multi-slice cine-DENSE sequence with 3D displacement encoding[41] covering the entire left-ventricle (LV) in order to obtain 3D strain tensors throughout the entire cardiac cycle. This was followed by cDTI acquisitions in one mid-ventricular slice at multiple time points throughout the cardiac cycle including diastasis and peak systole as determined from a short-axis cine in the same plane.

All the animals were subsequently euthanized under anesthesia in either a “diastolic like” state with an intravenous administration of KCl (4 meq / Kg) (N=8), or a “systolic like” state by intravenous administration of BaCl₂ (40 meq / Kg) (N=8). The hearts were excised and rinsed in normal saline. Preparation followed the protocols described by Kung et al.[18]. The coronary arteries were flushed, and the cardiac chambers filled with vinyl polysiloxane (Microsonic Inc. USA). The hearts were placed in a cylindrical container filled with a susceptibility matching fluid (Fomblin Y-LVAC 6-06, Solvay Solexis, USA) and were supported using open-cell foam. cDTI was then repeated in the static excised hearts for a mid-ventricular slice using the same sequence as used in-vivo. This slice was visually positioned to match the in-vivo slice as much as possible.

STRAIN IMAGING

A free breathing navigator-gated 2D multi-slice spiral cine DENSE imaging with 3D displacement encoding was performed with contiguous slices covering the entire LV. Sequence parameters included: in plane FOV 320 mm x 320 mm with a voxel size of 2.5 x 2.5 mm², slice-thickness 8 mm, flip-angle 10 degrees, time of repetition 14 ms, echo time 1.16 ms, temporal resolution 32 ms, displacement encoding frequency at 0.10 cycles/mm, 6 spiral interleaves.

While DENSE data was acquired to cover the entire LV only 5 slices were used for 3D strain calculation: two slices both above and below the chosen mid-ventricular slice of interest, the remaining slices were discarded. The DENSE data post-processing matrix was therefore 128 x 128 x 5 pixels.

3D strain and right stretch tensors were calculated from the DENSE data for the mid-ventricular slice throughout the cardiac cycle with MATLAB (Mathworks, Massachusetts, USA) based software developed at the University of Virginia[41,42]. The initial myocardial segmentation was performed semi-automatically using the open-source software *DENSEanalysis*[43,44].

The strain data were used for two purposes: firstly, to identify the two sweet-spot times in the cardiac cycle (Figure 1A); and secondly, to derive and register stretch tensors to the diffusion data to be corrected (Figure 1B) (see Supporting Information).

The components of strain along the local coordinates of the diffusion eigensystem was calculated at peak systole. Torsion was also calculated between the most basal and the most apical slice according to equation 2 from Rüssel et al.[45].

DIFFUSION TENSOR IMAGING

Breath-hold in-vivo DTI data was acquired in one mid-ventricular slice at 6 to 9 time points in the cardiac cycle. A STEAM-EPI sequence with a monopolar diffusion encoding scheme was used with the following b-values: $b_{ref} = 50 \text{ s/mm}^2$ (20 averages) in a single direction; $b = 500 \text{ s/mm}^2$ (20 averages) in 6 diffusion encoding directions; $b = 150 \text{ s/mm}^2$ and $b = 350 \text{ s/mm}^2$ in 6 directions (2 averages). Zonal excitation; fat saturation; diffusion weighting time 1 RR interval; echo time TE = 30 ms; BW = 1838 Hz/pixel; SENSE parallel imaging acceleration factor of 2; FOV = 320 mm x 120 mm; matrix = 160 x 60 pixels; EPI echo train length = 30 readouts; echo spacing = 0.65 ms; EPI readout duration = 19.5 ms; spatial resolution = 2x2x8 mm³

interpolated to $1 \times 1 \times 8 \text{ mm}^3$ by zero filling k-space. Ex-vivo DTI scans were performed with an identical protocol, with a repetition time set to 1400 ms (diffusion time 700 ms).

DTI data were analyzed from only four cardiac phases: diastasis, peak systole, and the two acquisitions closest to the sweet-spot times given by the circumferential strain curve.

The DTI data were post-processed with software developed in-house (MATLAB). The myocardium was manually segmented excluding the right ventricle, blood pool and papillary muscle. Three parameters related to the diffusion tensor orientation were extracted: two angles concerning the primary eigenvector: helix-angle (HA), and transverse angle (TA); and an angle related to the secondary eigenvector E2A[18,28] (Figure 2). In contrast to HA, TA and E2A demonstrate no obvious transmural organization, therefore for simplicity, the median absolute angle is represented without the polarity of the angle. However, for completeness the angle polarity is included in the DTI parameter maps and histograms. The mean diffusivity (MD) of the diffusion tensor was also calculated.

The diastolic and systolic diffusion tensor data were calculated with and without strain-correction, and compared to the sweet-spots and to the ex-vivo diffusion data of the same mid-ventricular slice.

Wilcoxon rank sum and Kruskal-Wallis (with follow-on pairwise comparisons) tests were used to assess differences. A *P*-value equal or lower than 0.01 was used for the follow-on pairwise comparisons to reduce the probability of type I errors when performing multiple comparisons. In an initial analysis, we failed to find any consistent significant differences between different sectors of the wall for DTI measures and have therefore kept our analysis global to reduce measurement noise.

RESULTS

Diffusion tensor data were successfully acquired for all pigs and 3D strain data were successfully extracted from the DENSE data for 11 of the original 16 pigs. The remaining five pigs had poor quality DENSE image data and/or phase-unwrapping issues. All subsequent analysis is therefore shown for 11 pigs only (6 with a diastolic arrest, 5 with a systolic arrest). The DTI acquisition trigger time closest to the calculated sweet-spot times was different by 24 ± 12 ms. Two DTI sweet-spot datasets (of 22) were excluded as the closest DTI trigger time differed by more than 40 ms. The mean heart-rate was 83 (10) bpm, and the LV ejection fraction was 0.49 (0.06) %.

STRAIN MEASUREMENTS

The mid-ventricular mean radial, circumferential, and longitudinal strain-time curves are shown in figure 3A. The measured mean (standard deviation) peak radial, circumferential and longitudinal strains were: $E_{rr}=0.21$ (0.06), $E_{cc}=-0.14$ (0.02), $E_{ll}=-0.11$ (0.01). The sweet-spots given by the E_{cc} curves are located at 24% (7%) and 74% (12%) of the RR interval time. Global torsion was 5.3 (1.5) degrees (figure 3B). The largest components of strain are aligned with the sheetlets (E_{ss} positive strain) and with the myocytes (E_{mm} negative strain). The shear components (E_{ms} , E_{mn} , and E_{sn}) are smaller at peak systole (figure 3C).

DIFFUSION TENSOR DATA

The measured DTI parameters are shown in table 1. There are significant differences between diastolic and systolic E2A values for in-vivo without and with strain-correction ($P<0.001$ and $P=0.005$ respectively) and for ex-vivo ($P=0.004$). Additionally there are significant differences for the in-vivo transverse angle without strain-correction ($P=0.015$), and for the ex-vivo HA range ($P=0.004:P=0.03$). No significant differences were found for any measure between sweet-spot 1 and sweet-spot 2. Mean diffusivity was found statistically different between diastole and systole for both with and without strain-correction ($P<0.01$ and $P=0.001$ respectively) but not for ex-vivo ($P=0.66$). MD is approximately 40% lower for the ex-vivo hearts compared to the in-vivo.

In addition to measuring changes from diastole to systole, we also compared the in-vivo results with and without strain-correction with the ex-vivo arrested hearts in the same corresponding state (bottom of table

1). Example maps showing the three DTI orientation measures in-vivo (both with and without strain-correction) and ex-vivo are shown in Figure 4 for two hearts, one arrested in a relaxed diastolic-like and one in a contracted systolic-like conformation. Visually HA and TA maps show a similar configuration between diastole and systole, and between without/with strain-correction and ex-vivo. E2A maps show pronounced differences between diastole and systole for the data without strain-correction, with strain-correction, and ex-vivo. E2A maps in diastole show low positive and negative angles while in systole they have high positive and negative angles. In both diastole and systole there is a significant difference in E2A between with and without strain-correction ($P=0.003$ and $P=0.01$ respectively). Ex-vivo E2As differ significantly from the respective systolic strain-corrected E2A ($P=0.006$) but less so from the diastolic non-strain-corrected E2A ($P=0.037$). Additional angular differences were found between the strain-corrected data and the ex-vivo data for the systolic endocardial HA mean values ($P<0.001$) and between the diastolic TA with and without strain-correction ($P=0.007$).

The absolute median E2A values from Table 1 are also displayed in a scatter plot (Figure 5). The mobility of the individual myocardial median E2A values between diastole and systole for the in-vivo data without/with strain-correction, between the two sweet-spot times, and the respective arrested ex-vivo values are shown. A large rotation of E2 is seen in the non-strain-corrected data from a more wall parallel conformation in diastole (low angles), to a more wall-perpendicular conformation in systole (high angles). A similar effect is seen in the strain-corrected data, although the rotation is smaller. The biggest difference between in-vivo data with and without strain-correction is in the systolic phase where the strain-corrected E2A is significantly lower than the non-strain-corrected and the ex-vivo contracted systolic-like arrests [median absolute $E2A=34.3^\circ$ vs $E2A=57.1^\circ$ ($P=0.01$), $E2A=60.5^\circ$ ($P=0.006$) respectively]. As in Table 1, E2A is similar between the two sweet-spots.

Figure 6 and Figure 7 provide additional analysis of HA, TA and E2A. Figure 6 plots the mean transmural HA line profiles, and histograms of the myocardial distribution of HA values. There is a linear transmural progression of HA values in all cases, and a slightly wider distribution of HA values in the ex-vivo data. No clear transmural organization was found for TA and E2A. Figure 7 shows the distribution of TA and E2A values. There is no apparent difference between the TA with and without strain-correction in any of the plots, in contrast to the large differences in E2A. As observed in Figure 5, the systolic distributions of E2A angles without strain-correction appear more similar to the ex-vivo relaxed and contracted distributions than after strain-correction. The in-vivo systolic distribution appears to be the most different between with and

without strain-correction; while the distribution peaks at ± 90 degrees without strain-correction, the peak occurs at a much lower absolute angle of 25 degrees with strain-correction. The combined systolic and diastolic root mean square deviation of the in-vivo histograms without and with strain-correction to the ex-vivo histograms is 0.027 and 0.038 respectively. The in-vivo histograms without strain-correction are therefore closer to the ex-vivo.

DISCUSSION

In previous work we showed that in healthy human hearts there is a significant rotation of E2A as the heart contracts from diastole to systole, while HA remains relatively unchanged; however, the confounding contribution of strain to these results was unclear[28]. Subsequent pre-clinical studies have demonstrated a similar pattern of E2A rotation in a porcine model imaged in-vivo, and in-situ and ex-vivo in the absence of strain effects. The similarity of the in-vivo, in-situ and ex-vivo results enabled us to infer that that potential strain effects must be small, although no strain-correction was performed in our previous reports. In this work, we assessed the performance of the standard strain-correction model[35] by directly comparing in-vivo DTI data before and after strain-correction with ex-vivo strain-free data. We believe this to be the first study comparing in-vivo diffusion data with and without strain-correction with the same hearts after arrest. A previous study presented strain-corrected STEAM-EPI data acquired in peak-systole and diastole, demonstrating the effects of strain-correction[29]. However, these studies lacked a ground-truth which we have included in the form of ex-vivo DTI in the same hearts. We were therefore able to quantify the effect of strain on in-vivo cDTI and assess the performance of conventional strain-correction.

Several important results were found regarding tensor orientation. Changes in HA and TA throughout the cardiac cycle were small and these parameters were largely unaffected by strain-correction. Ex-vivo HA and TA values and distribution were similar to in-vivo, although the ex-vivo HA distribution was flatter than the in-vivo counterparts. It is noteworthy that our data showed very low transverse angles at all cardiac phases interrogated, indicating a highly coherent myocyte orientation. In contrast E2A varies as the heart contracts. Figure 5 and Figure 7 (lower panel) show that in-vivo E2A changed from predominantly low absolute angles in diastole to predominantly high absolute angles in systole without strain-correction. The same data with strain-correction showed a much smaller shift between systole and diastole, with the largest differences observed in systole when pre- and post-strain-correction data were compared. As expected, the distribution of E2A values at the two sweet-spots was similar, because the heart was in a similar configuration. When comparing without and with strain-correction data with the corresponding ex-vivo results, where no tissue strain history is present, the without strain-correction data more closely resembles the ex-vivo distributions of E2A. These results are consistent with a substantial rotation of E2 between diastole and systole, in keeping with current models of cardiac contraction due to rotation of sheetlets

with shear layer slippage. The current strain-correction model artefactually reduces measured E2A mobility. As the heart spends a longer proportion of the cardiac cycle in a relaxed rather than contracted state, the effect of strain-correction is most marked on data acquired at peak systole.

The change in distribution of E2A angles from diastole to systole was much more pronounced than that measured in a Langendorff perfused rat heart model from Hales et al.[14]. More work is needed to ascertain if this disparity is due to protocol differences, in particular the shorter diffusion mixing time of the spin-echo sequence used by Hales et al., or anatomical and physiological differences between the two species.

The in-vivo results presented here are consistent with those of Stoeck et al. in human hearts[29] and also with numerical simulations (see supporting figure S1 and supporting table S1). Strain-correcting the diffusion data significantly reduced E2A mobility, and brought systolic E2A values close to the sweet-spot values where strain effects are minimal. The observation that E2A mobility is reduced by strain-correction is not unexpected. Macroscopic tissue strain measured with MRI is intimately connected to cellular rearrangement and sheetlet shear, and therefore directly correlated with E2A mobility as measured by cDTI. As these measures are inextricably interconnected, correcting for macroscopic strain inevitably leads to altered E2A mobility.

The effects of strain-correction can be categorized according to three cardiac orthogonal coordinates. The diffusion tensor orientation measures are only affected by strain that has components along the same directions as the respective eigenvectors. For example, the primary eigenvector of diffusion, which defines HA, is commonly aligned close to the longitudinal-circumferential plane, with only small components in the radial direction. HA is therefore minimally affected by radial strain, commonly the direction with the greatest measured strain. Additionally, it was found that the effects of longitudinal and circumferential strain, which are typically of similar amplitude, have opposing effects on HA (see supporting table S2). This work therefore suggests that the global effect of strain and strain-correction on HA is small. By contrast, E2 is mainly affected by the cumulative effect of radial and longitudinal strains, resulting in E2 being affected more by strain-correction.

The strain-correction model established by Reese et al.[35] assumes the heart to be formed of a gelatin like material which is stretched and compressed at different stages of the cardiac cycle. If we are measuring

diffusion at peak systole, then while the diffusion is being encoded myocardial tissue initially shortens radially before contracting to its original position. The diffusion encoding in the radial direction is therefore enhanced by the history of material strain (Figure 8). Conversely if measuring diffusion in a diastolic state, then the material will be stretched in the radial direction before coming back to its original position, resulting in a reduction of the measured diffusion in the radial direction. Analogous strain effects will happen in the longitudinal and circumferential direction. This is the basis of the previously proposed strain-correction model: from the 3D stretch tensor history throughout the cardiac cycle, one can correct the measured 3D diffusion tensor to cancel these strain effects. However, this model assumes a uniform diffusivity throughout the cardiac cycle, with no barriers on the scales we measure diffusion on; additionally, it assumes that macroscopic cardiac deformation is a result of elastic material stretch only. It is now generally recognized that the majority of wall thickening, and longitudinal shortening, is not due to cardiomyocyte stretch but due to cellular reorganization and transmural shear moderated by its laminar organization. For this reason, it is thought that the previously proposed model may significantly overestimate the effects of microscopic cardiomyocyte strain based on the measured macroscopic tissue deformation.

The work by Sonnenblick et al. measured a reduction of 15% in the length of the cardiomyocyte sarcomere in the canine heart[13], which results in approximately 8% increase in radius for incompressible cardiomyocytes. The in-vivo median wall thickening in this study was approximately 28%. Assuming we have similar cardiomyocyte sarcomere length and radius changes in the porcine heart, then approximately 30% of the macroscopic wall thickening could be due to microscopic cardiomyocyte strain. Microstructural strain and reorganization of the tissue will therefore impact on the measured tensor, but the model required to describe this is highly complex and yet to be elucidated. In this paper, we mainly analyze tensor orientation, but there is an important rotational invariant measure that we should discuss: mean diffusivity. MD provides a measure of the mean square distance diffused by water molecules in a given time. With the STEAM sequence, diffusion is encoded over an entire heart cycle. Diffusivity measurements will depend on myocyte shape, strain and perfusion effects; all three vary throughout the cardiac cycle. Without strain-correction, MD decreases between diastole and systole (1.11 to $0.99 \times 10^{-3} \text{ mm}^2\text{s}^{-1}$, $p = 0.01$), and the opposite happens with strain-correction (1.00 to $1.14 \times 10^{-3} \text{ mm}^2\text{s}^{-1}$, $p = 0.001$). A similar result was found by Stoeck et al. in the human heart[29]. The measured ex-vivo diffusivities are approximately 40% lower, which is expected when diffusion measurements change from body temperature to room temperature. Importantly, there is no significant change in MD ex-vivo from diastole to systole ($P=0.66$), where no strain or perfusion effects are present.

We have simplified the TA and E2A analysis by calculating the median value from the absolute distribution, ignoring angle polarity. We believe this to be a valid simplification because the signed TA and E2A distributions from Figure 7 appear symmetric. The median value of absolute E2A is therefore a measure of sheetlet tilt relative to the local heart wall.

In this work, we assume that the ex-vivo arrested relaxed and contracted conformations approximate to diastole and systole in-vivo. Due to the lack of blood pressure loading, the arrested contracted heart wall thickness was found to be 140% of the in-vivo systolic wall thickness. Histology of these ex-vivo pig hearts after fixation was performed for another study and sheetlet and shear layer orientations were found to correlate to diffusion E2 orientation measured with DTI in both ex-vivo and in-vivo data[30]. We therefore believe that the ex-vivo contracted systolic-like state approximates the in-vivo conformation of the microstructure.

There are two important limitations to this work: the low number of animals studied, and the available spatial-resolution of current in-vivo MR measurements of strain and diffusion. Diffusion tensor estimation from a voxel containing a large number of cardiomyocytes and myolaminae can only be meaningful if there is coherence of the microstructure. Histology studies have observed two populations of counter sloping sheetlets and shear layers[18]; more advanced diffusion techniques will be required to interrogate these multiple populations[46]. The accuracy of radial and longitudinal strain is also affected by the low spatial resolution used in DENSE imaging. Porcine strain values measured in this work were found to be lower than typical values measured in humans, therefore the effects of strain-correction are expected to be greater in humans. DENSE cine imaging uses prospective ECG gating, and therefore the latest stages of the cardiac cycle may not be imaged. Some of the individual strain curves exhibit a late systolic peak (more than 60% of the RR-interval) which is not physiological and likely due to underestimation of the R-R interval and errors in the DENSE analysis. Microvascular perfusion will influence our diffusion measurements in-vivo, in particular mean diffusivity[47], although it does not seem to substantially impact principal eigenvector orientation significantly[48].

CONCLUSIONS

The currently accepted model of strain-correction for diffusion data obtained with a STEAM-EPI sequence does not significantly alter measures relating to the primary eigenvector (HA and TA). However, it has a considerable impact on the orientation of the secondary eigenvector (E2A). In-vivo E2A values without strain-correction approximate more closely to the strain-free ex-vivo values in a relaxed diastolic-like and contracted systolic-like states, than after strain-correction. A more complete model of dynamic myocardial microstructure is needed to enable accurate strain-correction taking into account cellular rearrangement and sheetlet shear.

FIGURE CAPTIONS

Figure 1 – A: diagram showing how the sweet-spot times are calculated. The sweet-spot times are defined when the measured strain equals its mean value. The mean LV circumferential strain-time curve was used, as the higher number of pixels along the circumferential direction are likely to make it more robust than the radial or longitudinal strain curves. B: flowchart showing how the strain-correction is applied to the diffusion tensors. D_{obs} is the diffusion tensor before strain-correction; $U(t)$ is the stretch tensor throughout an entire cardiac cycle Δ ; D is the diffusion tensor after strain-correction.

Figure 2 – Diagram showing the definitions of HA, TA and E2A. To calculate HA, E1 is projected in the local longitudinal-circumferential plane shown in blue (E1proj). The angle between E1 and E1proj defines TA. The angle of E1proj to the circumferential axis defines HA. HA is positive for a right-handed helix when viewed from the apex. TA is positive if it rotates clockwise from the longitudinal-circumferential plane and negative if it rotates counterclockwise, when looking along the circumferential axis direction. The projection of E1 is then used to define the plane perpendicular to it, known as the cross-cardiomyocyte plane shown in red. This plane contains two orthogonal directions: the radial direction and the wall tangent direction. The secondary eigenvector E2 is projected into this plane and the angle between E2proj and the wall-tangent direction defines E2A. E2A is positive if pointing towards the apex and negative if pointing towards the base.

Figure 3 – (A) Radial (Err), circumferential (Ecc), and longitudinal (Ell) strain curves normalized to the RR interval for the anterior, lateral, inferior and septum sectors. The thin lines represent the subjects' mean strain curves averaged over the LV slice of interest, and the thick lines represent the intersubject mean strain curve. (B) global torsion curves. (C) Strain tensor components along the diffusion tensor coordinate system at peak systole (mm – along myocytes, ss – along sheetlets, nn – along sheetlet-normal; shear components: ms – myocyte sheetlet, mn – myocyte sheetlet-normal, sn – sheetlet sheetlet-normal).

Figure 4 – Example DTI maps of tensor orientation measurements: HA, E2A, and TA for two hearts, one arrested in diastole (left) and one arrested in systole (right).

Figure 5 – Median absolute E2A values. The in-vivo values show the mobility of E2A from a diastolic to a systolic phase with and without strain-correction and at the two-time points closest to the sweet-spot times. The respective color-coded ex-vivo hearts are also shown for either a diastolic or systolic arrest.

Figure 6 – Top: mean transmural HA line profiles with intersubject interquartile range at the endocardium; mesocardium; epicardium. Line profiles are shown for diastole and systole with and without strain-correction, at the two sweet-spot times, and for the arrested ex-vivo hearts. The R^2 values are the adjusted

R^2 for a linear fit. Bottom: HA histograms of all myocardial voxels at diastole (with and without strain-correction), systole (with and without strain-correction), the two sweet-spots, and for the explanted hearts arrested in a diastolic/systolic like state. The histogram curves show the intersubject median and interquartile range; bin size is 10 degrees.

Figure 7 – TA (Top) and E2A (Bottom) histograms of all myocardial voxels at diastole (with and without strain-correction), systole (with and without strain-correction), the two sweet-spots, and for the explanted hearts arrested in a diastolic/systolic like state. The histogram curves show the intersubject median and interquartile range; bin size is 10 degrees.

Figure 8 – Simulation of the effects of an elastic stretch on a free diffusion cloud of particles. A stretch > 1 loop of the material during diffusion encoding will result in a reduction of the diffusivity along that direction. A stretch < 1 loop will have the opposite effect.

Supporting Figure S1 – Simulated diffusion tensors, and the respective HA, E2A and TA maps and histograms with and without strain-correction for a diastolic and systolic tensor conformation.

TABLE TITLES AND CAPTIONS

Table 1 – Diffusion parameters

Top: Diffusion parameters in-vivo with and without strain-correction, at the in-vivo sweet-spots and at the ex-vivo arrested hearts. HA range is the mean angle range from endocardium to epicardium. TA and E2A are the median of the absolute values of all LV myocardial voxels. MD is the mean over all LV myocardial voxels. All values are shown as intersubject median [interquartile range]. * (red) - denotes a statistically significant difference when compared to the corresponding systolic or sweet-spot 2 value ($P < 0.05$).

Bottom: P values when comparing between in-vivo without and with strain-correction (sc) and ex-vivo arrested. HA range is the mean angle range from endocardium to epicardium. *(red) - denotes statistical difference ($P \leq 0.01$; P-value threshold with a Bonferroni correction for 3 multiple tests, conservatively rounded down to 0.01).

Supporting table S1 – Numerical simulations: effects of strain-correction on DTI parameters. HA range is the mean angle range from endocardium to epicardium. TA and E2A are the median of the absolute values of all myocardial voxels.

Supporting table S2 – Summary of the effects of each strain direction to HA range and E2A. TA is not considerably affected by any strain direction. ↗ = increase; ↘ = decrease; – = no considerable effect.

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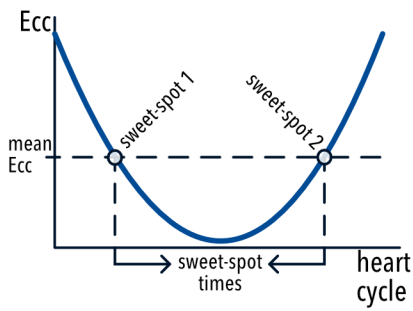
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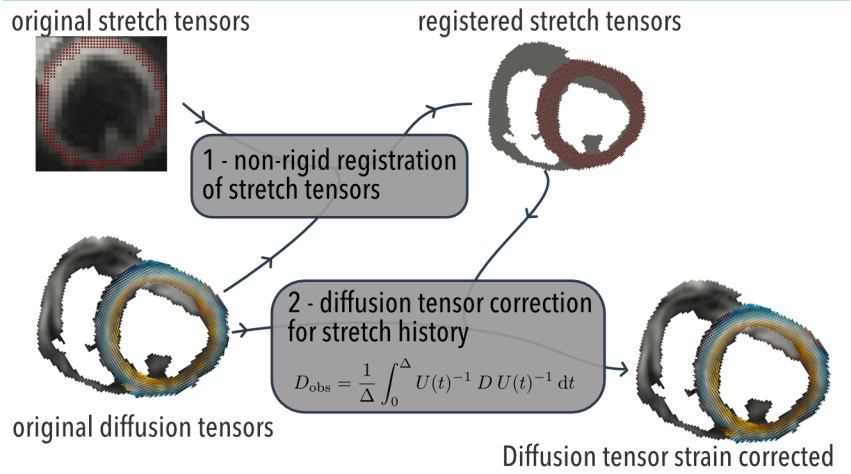
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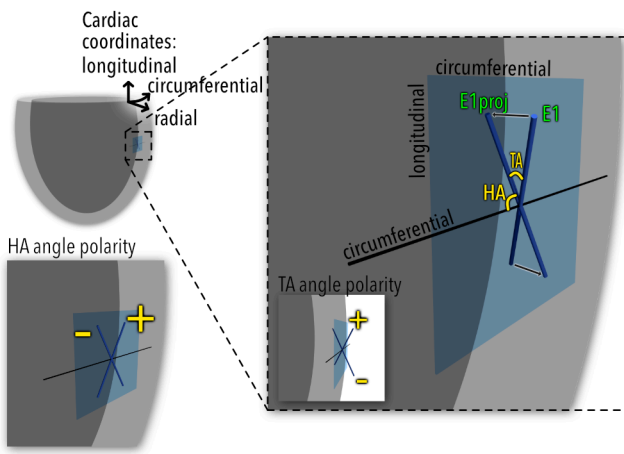
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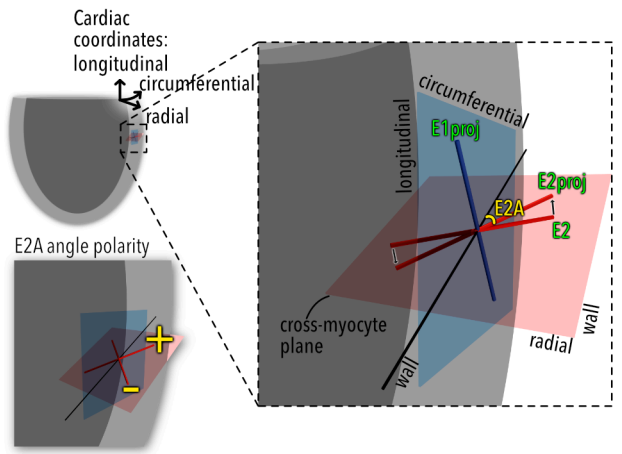
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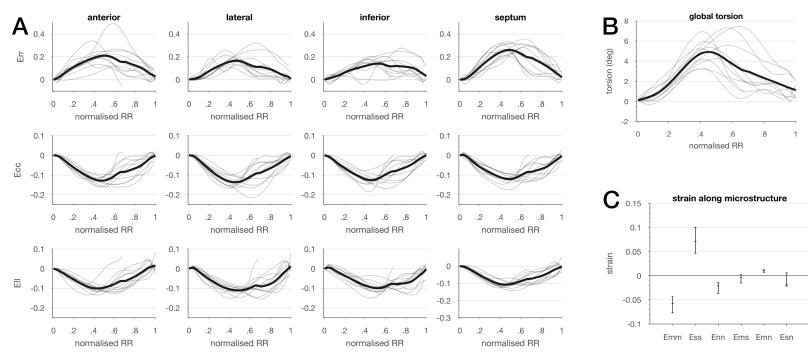


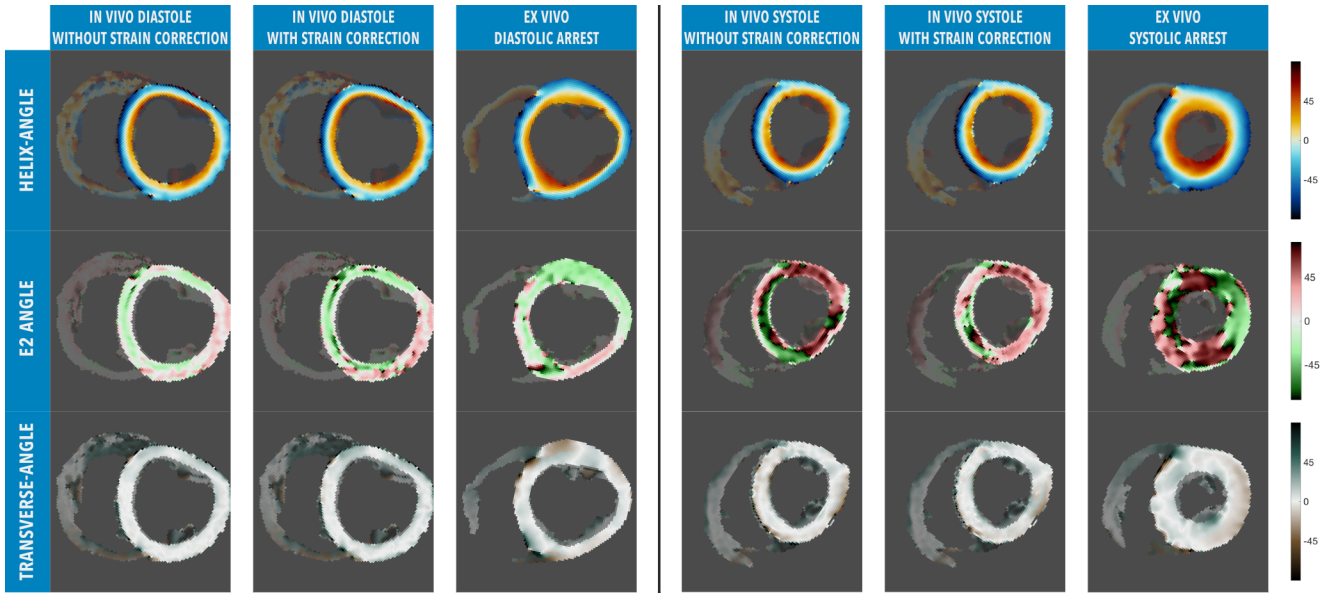
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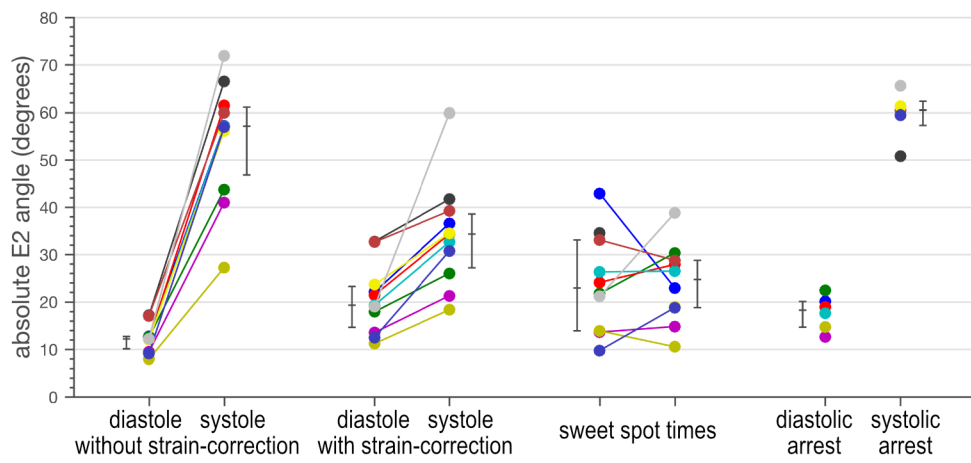


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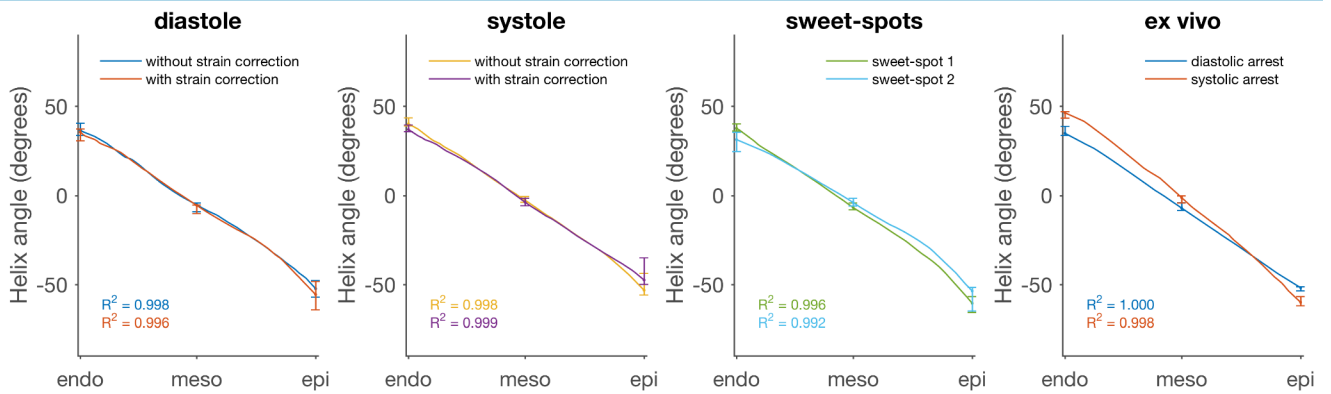




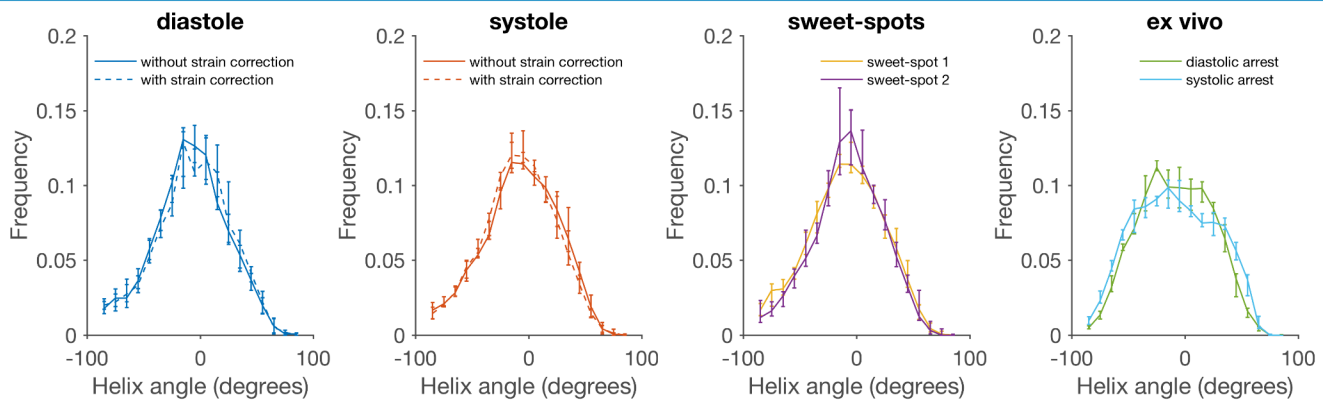




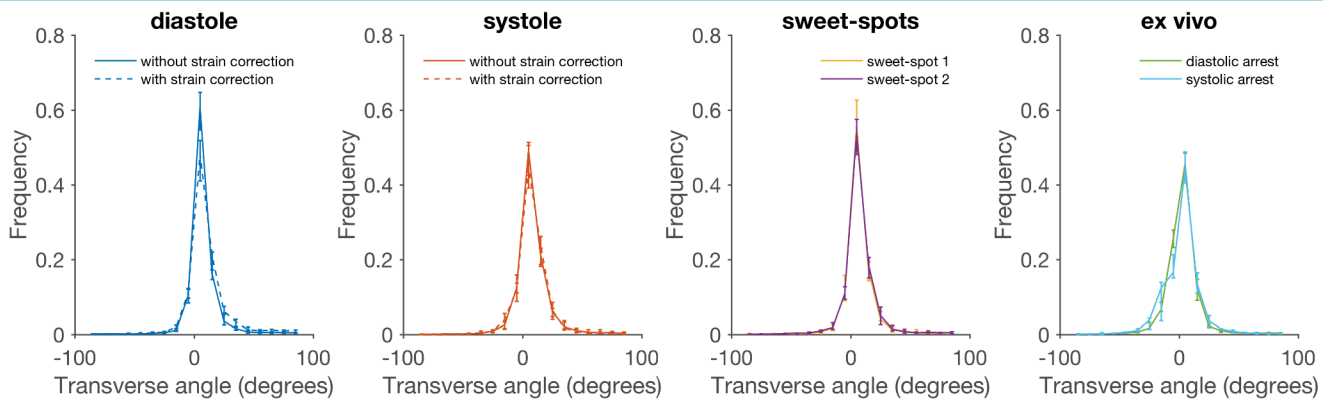
TRANSMURAL HELIX-ANGLE



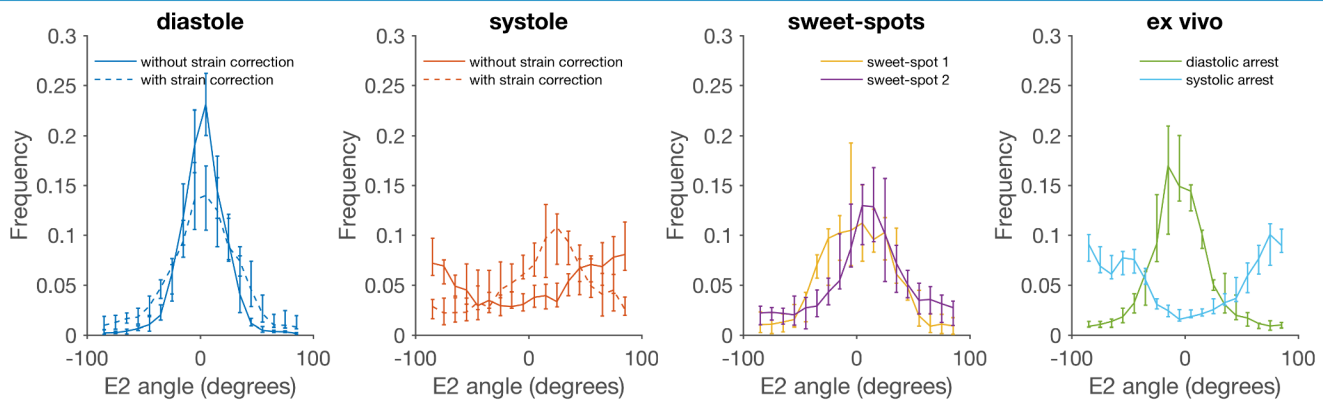
HELIX-ANGLE HISTOGRAMS

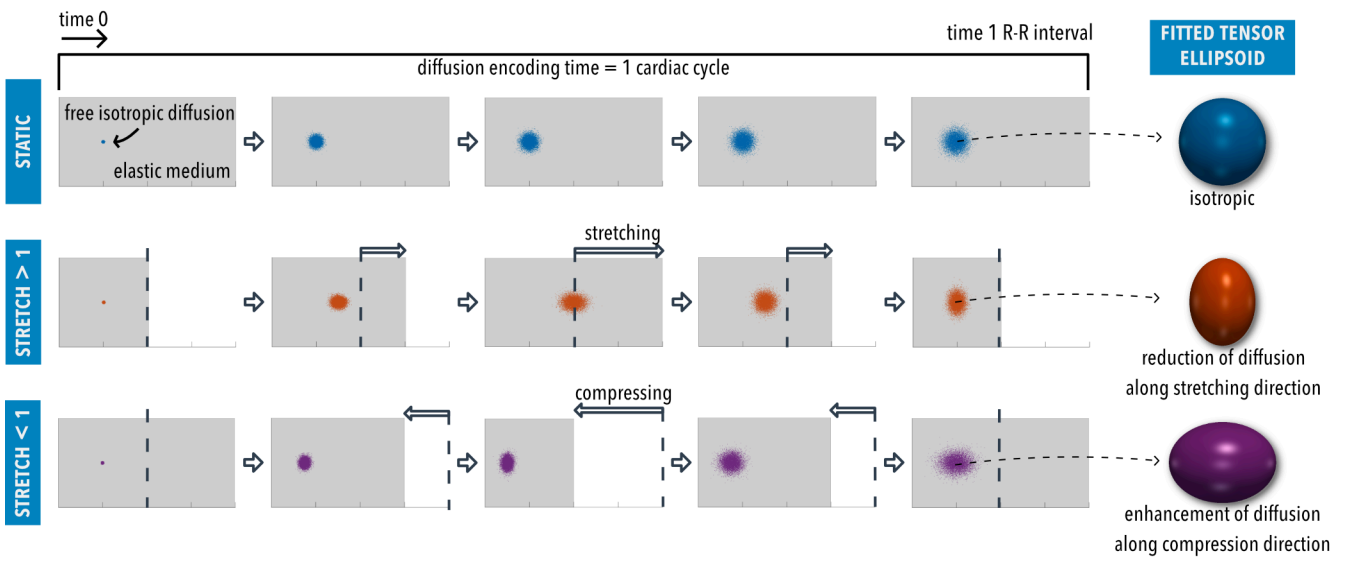


E1 TRANSVERSE ANGLE HISTOGRAMS



E2 ANGLE HISTOGRAMS





	without strain-correction		with strain-correction		sweet-spots		ex vivo arrests	
	diastole	systole	diastole	systole	sweet-spot 1	sweet-spot 2	diastole	systole
HA range (deg)	[36.9[6.9]: - 52.4[9.3]] (P=0.14:P=0.58)	[40.3[4.7]: - 53.3[11.8]] -	[35.7[6.7]: - 55.7[16.0]] (P=0.79:P=0.39)	[37.2[3.9]: - 47.5[15.1]] -	[37.8[4.0]: - 60.6[9.0]] (P=0.34:P=0.92)	[31.4[10.9]: - 53.7[13.3]] -	[35.0*[5.0]: - 51.8*[2.1]] (P=0.004:P=0.03)	[46.5[3.7]: - 60.1[5.2]] -
absolute E2A (deg)	12.2* [2.6] (P<0.001)	57.1 [14.2] -	19.3* [8.64] (P=0.005)	34.3 [11.4] -	22.9 [19.2] (P=0.91)	24.7 [10.0] -	18.2* [5.42] (P=0.004)	60.5 [5.05] -
absolute TA (deg)	6.08* [1.46] (P=0.015)	7.45 [2.94] -	8.3 [2.38] (P=0.89)	8.67 [1.85] -	6.42 [2.17] (P=0.18)	7.25 [1.29] -	5.92 [0.56] (P=0.13)	7.62 [2.34] -
MD (10 ⁻³ mm ² s ⁻¹)	1.11* [0.07] (P=0.010)	0.99 [0.12] -	1.00* [0.08] (P=0.001)	1.14 [0.07] -	1.05 [0.12] (P=0.31)	1.10 [0.19] -	0.61[0.09] (P=0.66)	0.66[0.11] -

Between groups comparison (Kruskal-Wallis with follow-on pairwise comparisons)

		without sc vs with sc	without sc vs ex-vivo	with sc vs ex-vivo
diastole	HA range (deg)	P=0.98:P=0.72	P=0.59:P=0.99	P=0.48:P=0.77
	absolute E2A (deg)	P=0.003	P=0.037	P=0.94
	absolute TA (deg)	P=0.007	P=0.99	P=0.044
systole	HA range (deg)	P=0.26:P=0.72	P=0.047:P=0.57	P<0.001:P=0.23
	absolute E2A (deg)	P=0.01	P=0.74	P=0.006
	absolute TA (deg)	P=0.91	P=0.76	P=0.56

Table 1 – Diffusion parameters

Top: Diffusion parameters in-vivo with and without strain-correction, at the in-vivo sweet-spots and at the ex vivo arrested hearts. HA range is the mean angle range from endocardium to epicardium. TA and E2A are the median of the absolute values of all LV myocardial voxels. MD is the mean over all LV myocardial voxels. All values are shown as intersubject median [interquartile range]. * (red) - denotes a statistically significant difference when compared to the corresponding systolic or sweet-spot 2 value (P<0.05).

Bottom: P values when comparing between in-vivo without and with strain-correction (sc) and ex-vivo arrested. HA range is the mean angle range from endocardium to epicardium. *(red) - denotes statistical difference (P<=0.01; P-value threshold with a Bonferroni correction for 3 multiple tests, conservatively rounded down to 0.01).

SUPPORTING INFORMATION

STRAIN CORRECTION

The right stretch tensor $\mathbf{U}(t)$ throughout the cardiac cycle was calculated from the strain tensor data $\mathbf{E}(t)$:

$$\mathbf{U}(t) = \sqrt{2\mathbf{E}(t) + \mathbf{I}} \quad (1)$$

where \mathbf{I} is the identity matrix.

Just like the diffusion tensors, the stretch tensors are positive-definite. In order to register the stretch tensors to the diffusion tensors and maintain the positive-definiteness a log-Euclidean metric[1] was used with a non-rigid demon registration[2]. This registration step was performed for the diffusion data measured (\mathbf{D}_{obs}) at diastasis and peak systole.

To perform strain-correction, the stretch tensors are integrated over an entire cardiac cycle Δ with the initial integration time $t=0$ at the same cardiac phase as the diffusion data to be corrected:

$$\mathbf{D}_{obs} = \frac{1}{\Delta} \int_0^{\Delta} \mathbf{U}(t)^{-1} \mathbf{D} \mathbf{U}(t) dt \quad (2)$$

\mathbf{D}_{obs} is the diffusion tensor without strain-correction and \mathbf{D} is the diffusion tensor with strain-correction. The equation above needs to be solved for \mathbf{D} as described by Reese et al.[3].

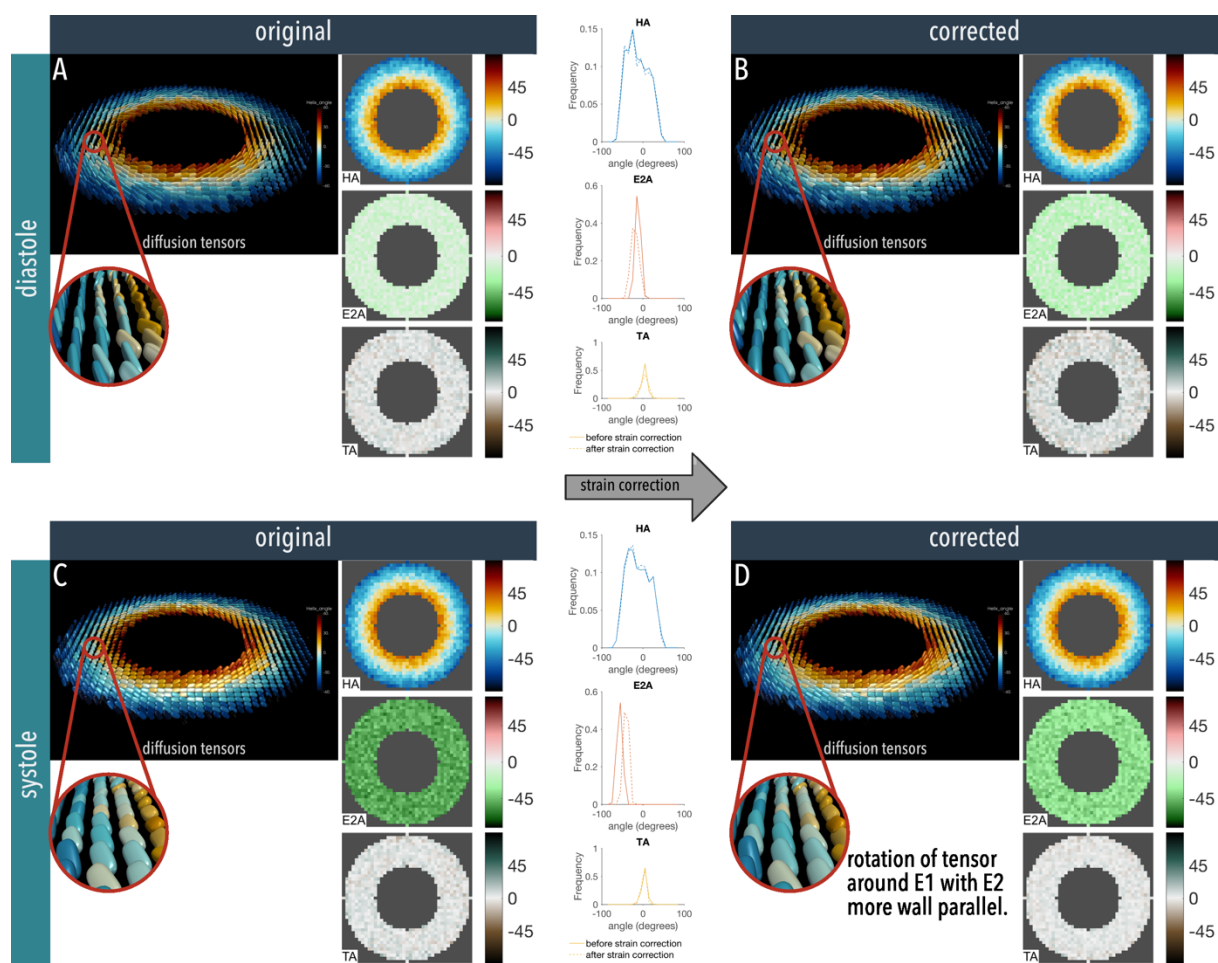
NUMERICAL SIMULATIONS

Stretch tensors and diffusion tensors were simulated by using the median eigenvalues and the median HA and E2A from all the measured in-vivo data. A hollow disc was used to simulate the myocardium of the LV in a mid-slice. The tensor shape is given by the eigenvalues, and the tensor orientation by the transmural HA distribution with a homogenous E2A. Tensor directional noise was introduced by 3D rotating the diffusion tensors with a distribution of pseudorandom angles between [-10, 10] degrees. This introduced some tensor orientation uncertainty without changing the tensor shape.

The average strain curves from figure 3 were used to simulate stretch tensors throughout the cardiac cycle with eigenvectors aligned with the local cardiac coordinates (radial, circumferential, longitudinal). The effects of strain-correcting the diffusion tensors were then analyzed for an average diastolic and systolic conformation.

The numerically simulated diffusion tensors are shown in supporting figure S1. The values and the effects of strain-correction agree well with the animal data. E2A is the most affected parameter, especially in systole. This effect can be seen as a rotation of the diffusion tensors around E1, with E2 towards a more wall parallel orientation with strain-correction (from panel C to panel D). HA and TA remain very similar throughout. The effects of the simulated strain-correction are summarized in supporting table S1.

Supporting table S2 shows the effects of each strain direction individually to HA and E2A. TA is not considerably affected by any strain direction.



Supporting Figure S1 - Simulated diffusion tensors, and the respective HA, E2A and TA maps and histograms with and without strain-correction for a diastolic and systolic tensor conformation.

	diastole			systole		
	input		output	input		output
HA range (deg)	[-48.6 31.9]	~	[-49.7 32.8]	[-49 34.2]	~	[-48.5 33.4]
absolute E2A (deg)	12.2	↗	20.0	56.6	↘	40.7
absolute TA (deg)	5.4	↗	7.3	5.6	↘	4.2

Supporting table S1 - Numerical simulations: effects of strain-correction on DTI parameters. HA range is the mean angle range from endocardium to epicardium. TA and E2A are the median of the absolute values of all myocardial voxels.

	diastole			systole		
	Err	Ecc	Ell	Err	Ecc	Ell
HA range (deg)	–	↗	↘	–	↘	↗
absolute E2A (deg)	↗	–	↗	↘	–	↘

Supporting table S2 – Summary of the effects of each strain direction to HA range and E2A. TA is not considerably affected by any strain direction. ↗ = increase; ↘ = decrease; – = no considerable effect.

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