Helix angle (HA) healthy statistical average technique for HA quantification in vivo cardiac diffusion tensor imaging

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Target audience: Scientists and clinicians working in the field of *in vivo* cardiac diffusion MRI.

Purpose: *In vivo* Cardiac Diffusion Tensor Imaging (cDTI) has great potential to depict the microstructure of the myocardium. Mean diffusivity (MD), fractional anisotropy (FA), and helix angle (HA) maps can be derived from *in vivo* cDTI datasets. Quantitative analysis of these parameters might help disease diagnosis. Previous work has assessed the reproducibility of *in vivo* cDTI in healthy volunteers [1]. However, HA is particularly difficult to quantify as it varies across the myocardial wall. To overcome this, we developed a method to quantify HA deviation from an average healthy map. This technique, together with quantitative FA and MD analysis, have been applied to healthy volunteer data by varying the number of averages to analyse the improvement of the accuracy of the data.

Methods:

The cDTI data of 10 healthy volunteers (mean age: 32) scanned at 3T (Siemens Skyra) during multiple breath-holds at end-systole with a diffusion-weighted STEAM single-shot EPI sequence [1] was used to generate a healthy statistical average LV HA (HSA_HA) map of basal, mid and apical slices. Imaging protocol: diffusion sensitivity b=350 s/mm^2 (6 directions), echo time 23 ms, spatial resolution 2.7x2.7x8 mm^3, three slices, and 8 averages. Automatic image registration with a cross-correlation algorithm [2] was used for averaging. Data was then post-processed to create FA, MD and HA maps. Each subject's HA map was divided into 24 myocardial segments and the superior right-ventricular insertion point aligned before inter-subject averaging of the range of helix-angles in each segment. Care was taken to remove papillary-muscle regions. The average range of helix-angles was then used to generate a HSA_HA map for each of the volunteers myocardial shape assuming an epi to endo linear slope of helix-angles as illustrated in higher spatial-resolution *ex vivo* human DTI scans [3-4]. These generated HSA_HA maps were used as reference maps to quantify deviation of fibre orientation, assessing the quality of the HA maps measured as the number of averages was increased from 1 to 8. The number of negative eigenvalues in the myocardium due to poor image quality were also calculated. All the analysis was performed with MATLAB.

Results

Figure 1a shows an example of a basal slice of one volunteer. Figure 1b shows the respective myocardial synthesised HSA_HA map. Figure 1c-e illustrates the calculated HA maps with 1, 4 and 8 averages respectively. With increasing numbers of averages, the maps resemble more and more the expected healthy pattern: endo/mid/epi with right-helix/circumferential/left-helix respectively. The pixel-by-pixel difference of HA from the HSA_HA is shown in figures 1f-h (myocardium only). Figure 2a shows the average difference from the HSA_HA map plotted as a function of the number of averages for all volunteers. After 5 averages HA difference changes at a rate lower than 5% per increased average (R^2 = 0.77). The same decreasing trend is seen for the number of negative eigenvalues, and FA (figures 2b-c) (R^2 = 0.60 and 0.51 respectively). The MD values (figure 2d) appear to have a weaker fit (R^2 = 0.14), not varying substantially with the number of averages, although its standard deviation decreases with the number of averages (result not shown).

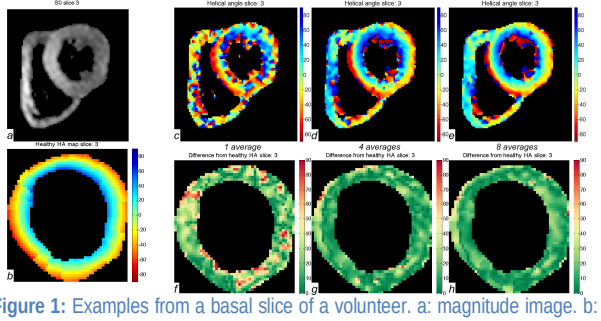

Figure 1: Examples from a basal slice of a volunteer. a: magnitude image. b: HSA_HA (myocardium only) (deg). c-e: HA maps when using 1, 4 and 8 averages respectively (deg). f-h: difference in degrees from the HSA_HA map for 1, 4 and 8 averages respectively (myocardium only).

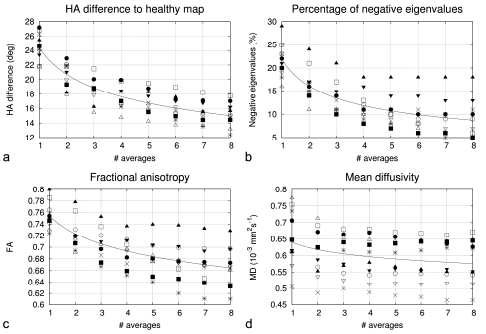

Figure 2: a: Myocardial average difference to HSA_HA map. b: percentage of negative eigenvalues. c-d: FA and MD average for all volunteers as a function of number of averages used respectively. The curve fits are calculated by: F(x)=ax^b.

Discussion

Synthesising a HSA_HA map from a dataset of 10 healthy volunteers, and matching the myocardial shape of the cDTI data being analysed, allows for a direct pixel-by-pixel comparison of the cardiac fibres' orientation *in vivo*. This atlas technique has previously been shown to be useful for *ex vivo* studies of the heart [4]. The *in vivo* nature of the method presented here tolerates comparisons at matching stages of the heart cycle, and will be useful for *in vivo* quantification of changes in disease hearts, such as periinfarcted regions and cardiomyopathies.

In this study the technique has been applied to determine the quality of the HA maps as a function of the number of averages acquired, showing an asymptotic increase in the quality of data, with changes in HA lower than 5% per increased average after 5 averages, although this number may increase in patients with more difficulty in breath-holding. The number of negative eigenvalues also decreases with the number of averages; this is most likely due to a more accurate measurement of the diffusion tensors. FA values decrease with the number of averages, a finding that agrees with previous work using numerical simulations [5]. In general MD values did not vary much with the number of averages, although an underestimation would be expected at low SNRs [5].

Conclusion

Here we have shown that a HSA_HA map synthesised to match each volunteer's myocardial shape allows for the quantification of fibre angle normality *in vivo*. This technique demonstrated that changes in HA (along with FA and MD) become relatively small with more than 5 averages when scanning healthy volunteers.

References [1] Nielles-Vallespin, et al., MRM (dahead of print)(2012). [2] Guizar-Sicairos et al., Opt Lett 33:156 (2008). [3] Rohmer, et al., Invest Radiol 42:777 (2007). [4] Lombaert et al., IEEE Trans Med Imag 31:1436 (2012). [5] Jones, et al., MRM 52:979 (2004).