

ORAL PRESENTATION

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Improving the accuracy of cardiac DTI by averaging the complex data

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Background

When performing cardiac diffusion tensor imaging (cDTI) multiple averages are typically acquired to compensate for the low signal to noise ratio of the individual images. However, the potential for reducing noise in low signal areas is not fully realized when the averaging is performed on the magnitude data[1]. Averaging the complex cDTI data is not straightforward as the diffusion weighting introduces a different, spatially varying phase across each image. In this work we use simulations to demonstrate the benefits available when using complex averaging and then develop an algorithm for performing complex averaging of *in-vivo* cDTI data, which accounts for the induced phase variations.

Methods

To compare the performance of magnitude and complex averaging in the presence of noise, simulated noisy diffusion weighted images of the left ventricle were calculated with b-values from 50-3000 mm^{-2} based on previously published *in-vivo* cDTI data[2]. Magnitude or complex averaging was performed before processing the images with the software we typically use for *in-vivo* cDTI data.

Additionally, *in-vivo* cDTI was performed on a Siemens Skyra in 10 subjects using the STEAM-EPI sequence[3] with 4 b-values, 500-2000 mm^{-2} , 12 averages, 6 directions, SENSE reconstruction (magnitude and phase images) and 2.8x2.8x8 mm^3 resolution. In order to remove motion-induced phase, each image (Real+Imaginary) was filtered (pyramid mask in k-space, extent: $\frac{1}{4}$ field-of-view [4]) and the phase of the low-resolution copy was

removed from the original images. The images were then processed as for the simulations.

Results

Figure 1 shows the results of simulations demonstrating the errors in mean diffusivity (MD), fractional anisotropy (FA) and helical angle (HA) for a range of b-values. At low b-values, no benefit from complex averaging is observed, but at high b-values $>1000\text{mm}^{-2}$, the underestimation of MD and FA using magnitude averaging ("squashing the peanut"[5]) can be compensated for by using complex averaging.

Figure 2 compares results obtained *in vivo*, processed with magnitude and complex averaging. As predicted by the simulations, FA and MD are increased when using complex averaging and changes in the parameter maps are evident.

Conclusions

Large b-values are required to avoid under-estimation of FA and MD in cDTI. We have demonstrated that the phase introduced by diffusion weighting *in vivo* can be corrected for within the reconstruction, allowing us to partially compensate for the noise-floor effects present at high b-values by using complex averaging.

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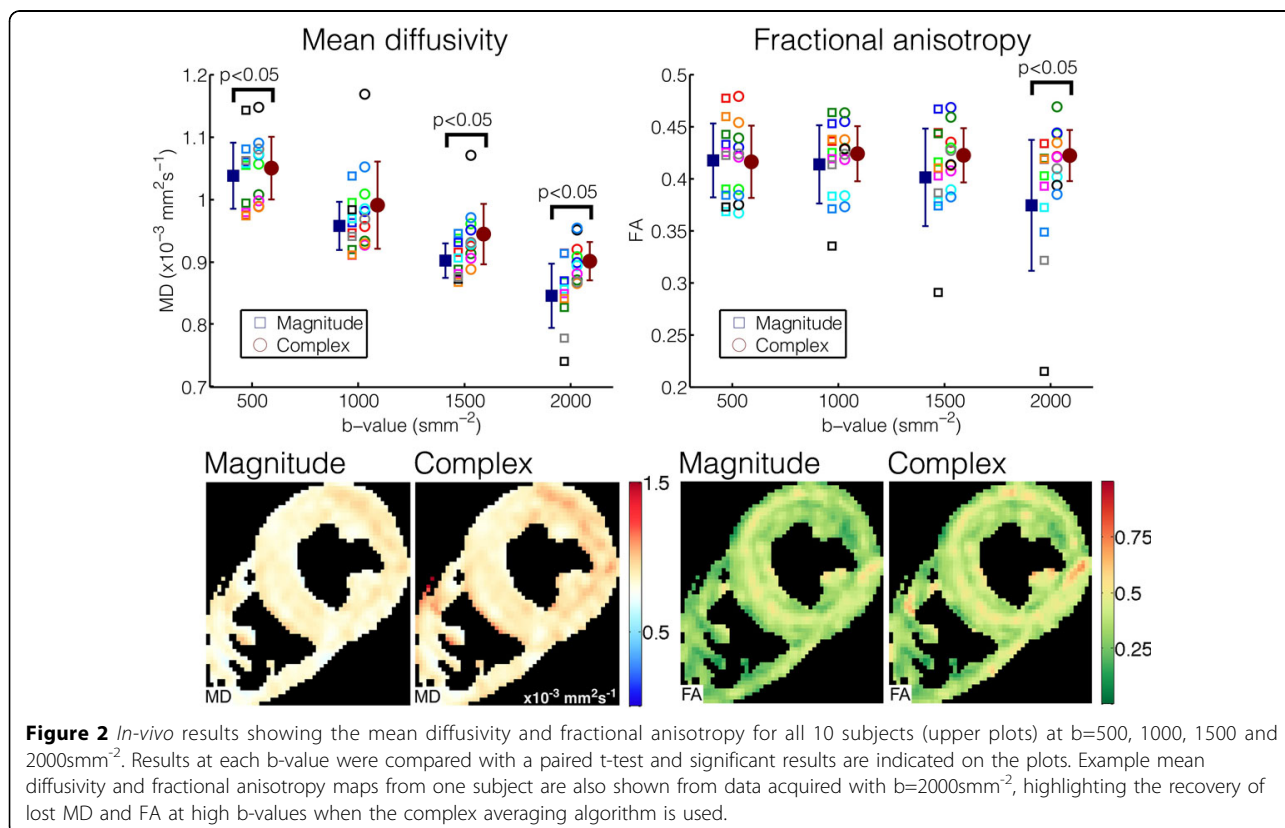
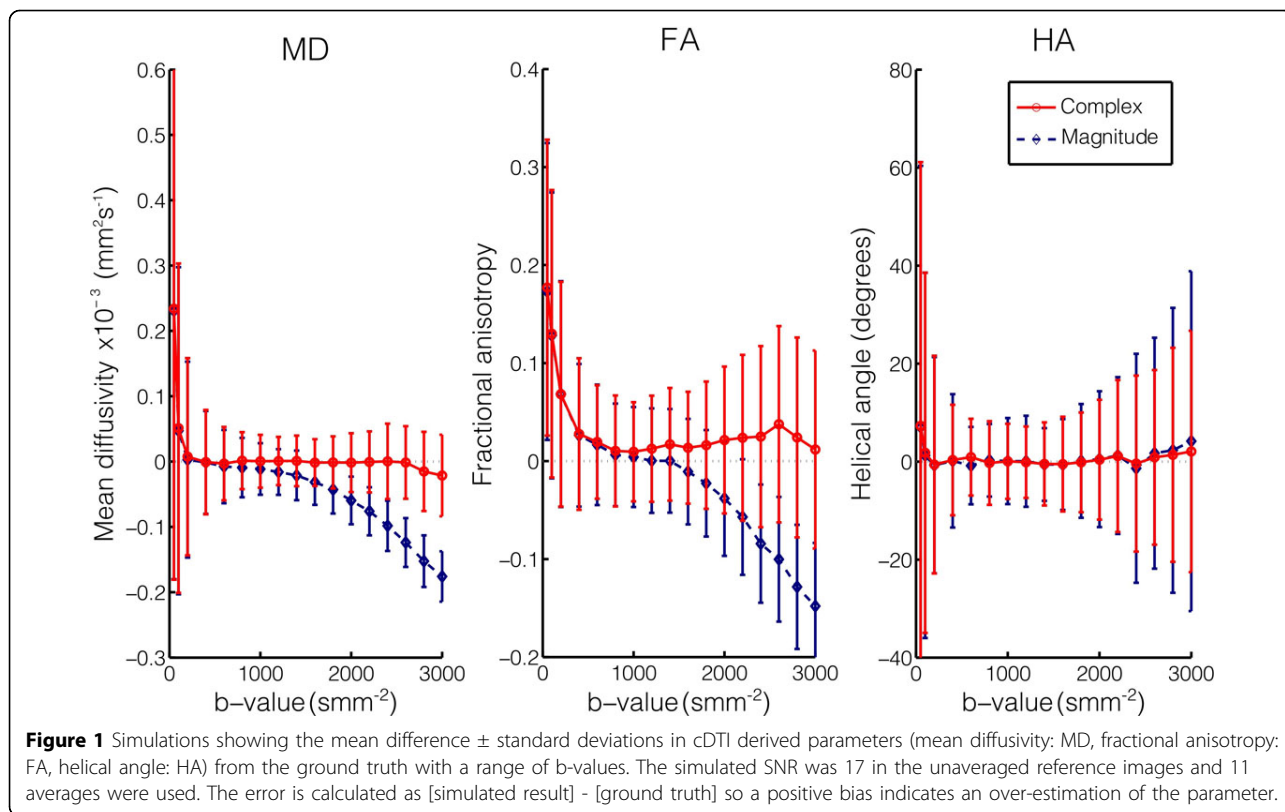
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