Journal of Cardiovascular Magnetic Resonance

ORAL PRESENTATION

Open Access

Improving the accuracy of cardiac DTI by averaging the complex data

Andrew D Scott[1,2*], Sonia Nielles-Vallespin[3], Pedro Ferreira[1,2], Laura-Ann McGill[2,1], Dudley J Pennell[1,2],
David Firmin[1,2]

Background
When performing cardiac diffusion tensor imaging
(cDTI) multiple averages are typically acquired to com-
pensate 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 diffu-
sion weighting introduces a different, spatially varying
phase across each image. In this work we use simula-
tions 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 dif-
fusion weighted images of the left ventricle were calcu-
lated with b-values from $50\text{-}3000\,\text{smm}^{-2}$ 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, $500\text{-}2000\,\text{smm}^{-2}$, 12 averages, 6 direc-
tions, SENSE reconstruction (magnitude and phase
images) and $2.8\text{x}2.8\text{x}8\,\text{mm}^3$ resolution. In order to remove
motion-induced phase, each image (Real+Imaginary) was
filtered (pyramid mask in k-space, extent: ¼ 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 aniso-
tropy (FA) and helical angle (HA) for a range of
b-values. At low b-values, no benefit from complex aver-
aging is observed, but at high b-values $>1000\,\text{smm}^{-2}$, the
underestimation of MD and FA using magnitude aver-
aging ("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
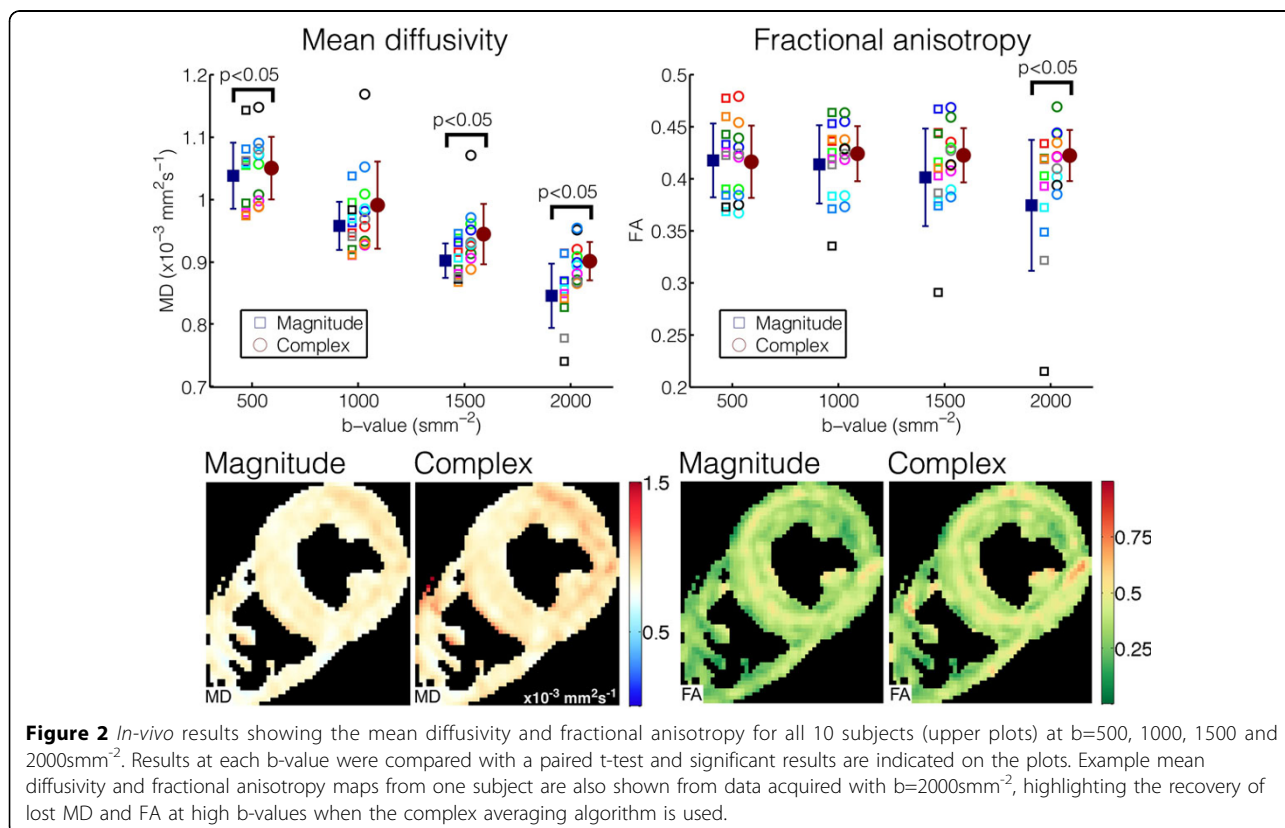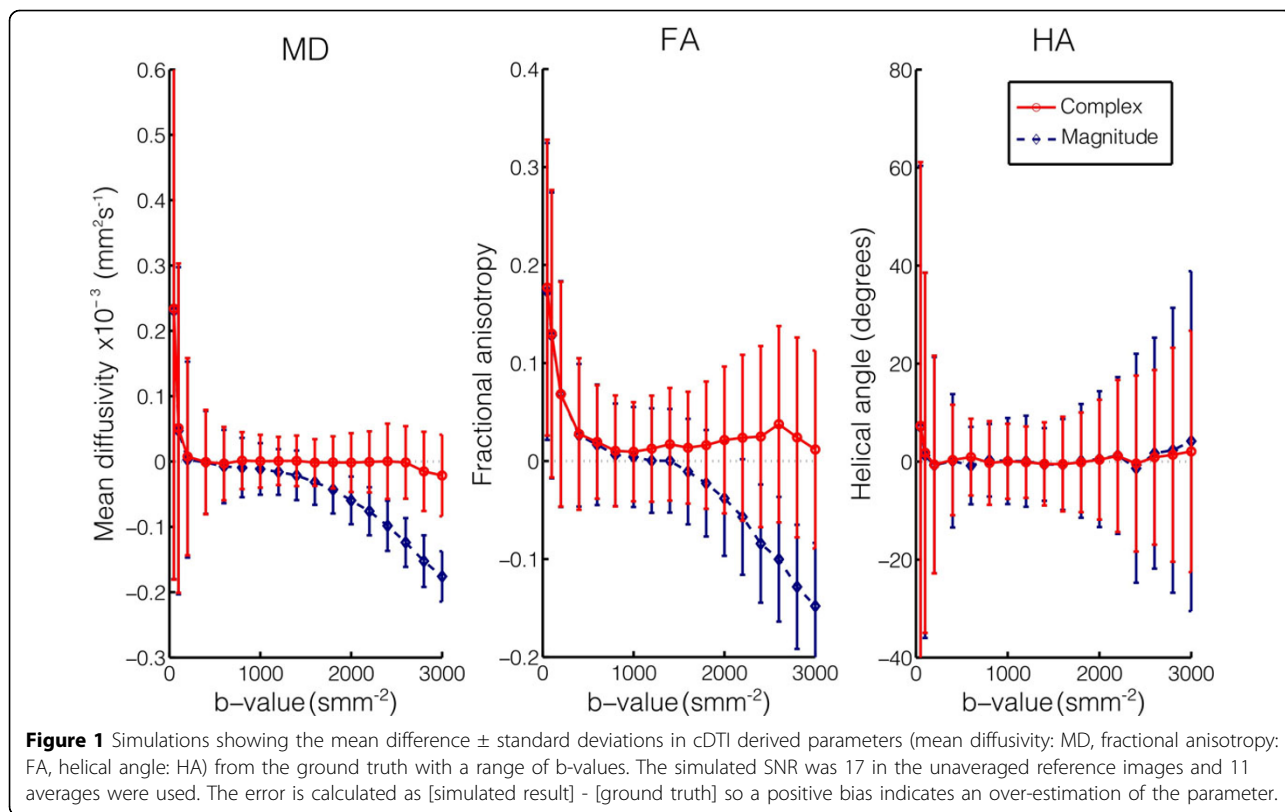at high b-values by using complex averaging.

Funding

Authors' details
[1]Cardiovascular Biomedical Research Unit, The Royal Brompton Hospital,
London, UK. [2]National Heart and Lung Insitute, Imperial College, London, UK.

[1]Cardiovascular Biomedical Research Unit, The Royal Brompton Hospital,
London, UK
Full list of author information is available at the end of the article

BioMed Central

Figure 1 Simulations showing the mean difference ± standard deviations in cDTI derived parameters (mean diffusivity: MD, fractional anisotropy: FA, helical angle: HA) from the ground truth with a range of b-values. The simulated SNR was 17 in the unaveraged reference images and 11 averages were used. The error is calculated as [simulated result] - [ground truth] so a positive bias indicates an over-estimation of the parameter.

Figure 2 *In-vivo* results showing the mean diffusivity and fractional anisotropy for all 10 subjects (upper plots) at b=500, 1000, 1500 and 2000smm^{-2}. Results at each b-value were compared with a paired t-test and significant results are indicated on the plots. Example mean diffusivity and fractional anisotropy maps from one subject are also shown from data acquired with b=2000smm^{-2}, highlighting the recovery of lost MD and FA at high b-values when the complex averaging algorithm is used.

[3]Division of Transmural Research - National Heart Lung and Blood Institute, National Institutes of Health, Bethesda, MD, USA.

References

1. Skare: *ISMRM* 2009, 1409.
2. Scott: *MRM* 2014, DOI:10.1002/mrm.25418.
3. Nielles-Vallespin: *MRM* 2012, DOI:10.1002/mrm.24488.
4. Pipe: *MRM* 2002, DOI:10.1002/mrm.10014.
5. Jones: *MRM* 2004, DOI:10.1002/mrm.20033.