Improved Navigator Based Diffusion Tensor MRI of the Human Heart in vivo

Pedro Ferreira[1], Sonia Nielles-Vallespin[2], Peter Gatehouse[1], Ranil de Silva[1], Jennifer Keegan[1], Peter Speier[3], Thorsten Feiweier[3], Timothy Reese[4], Tevfik Ismail[1], Andrew Scott[1], Choukri Mekkaoui[4], David Sosnovik[4], and David Firmin[1]

[1]BRU, Royal Brompton Hospital, London, United Kingdom, [2]National Heart Lung and Blood Institute (NHLBI), National Institutes of Health (NIH), Bethesda, Maryland, United States, [3]MR Application & Workflow Development, Siemens, Erlangen, Germany, [4]Martinos Center for Biomedical Imaging, Massachusetts General Hospital, Charlestown, Massachusetts, United States

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

Purpose: Cardiac Diffusion Tensor Imaging (cDTI) provides a non-invasive approach for the depiction of myocardial fibre architecture. *In vivo* cDTI remains extremely challenging due to a mixture of cardiac and respiratory motion. Several techniques have been used to compensate for respiratory motion: multiple breath-holds (>36 per patient), synchronised breathing, and retrospective navigators based on image cross-correlation [1-4]. In previous work a prospective navigator technique (NAV) has been implemented and compared to breath-hold (BH) acquisitions [5]. Statistically significant differences were found between BH and NAV techniques for helix-angle (HA) values. Further interrogation of the data suggested that the inconsistent HA patterns were found in NAV data sets in which a small fraction (up to 10%) of the diffusion-weighted frames had signal voids in some part of the LV, as shown in Figure 1. Inspection of the navigator plots showed that most of the frames with signal voids were correlated with those frames that were accepted immediately after deep inspiration. The purpose of this work was to improve the robustness of the NAV technique, making it comparable to the BH, and therefore allow the technique to be broadly applied to patients with cardiovascular disease.

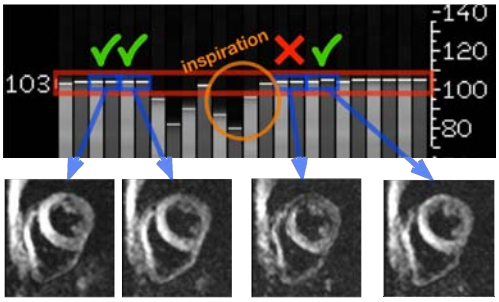

Figure 1. Sensitivity to bulk motion of navigator acquisitions after a deep inspiration. The third frame, which follows an inspiration, was accepted by the navigator but contains image artefacts due to bulk motion.

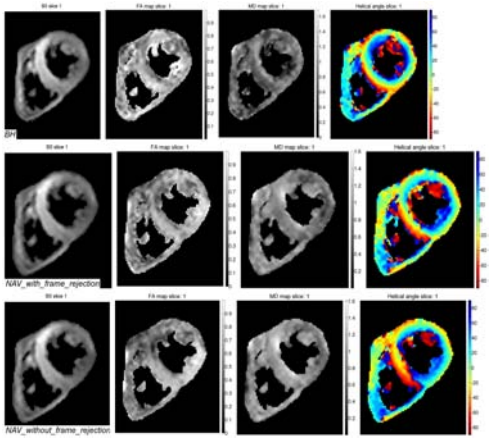

Figure 2. From left to right: averaged b0 image, FA, MD, and HA map. Top to bottom: BH, NAVnew, NAVold.

Materials and Methods: A stimulated-echo single-shot-EPI sequence with zonal excitation and parallel imaging was used, together with a modification of the crossed slice prospective-navigator technique combined with a biofeedback mechanism as described in Nielles-Vallespin et al. (2012) [5]. To prevent bulk respiratory motion artefacts the first and second heartbeat have to be within 1mm of each other as well as being inside the navigator acceptance window. 7 volunteers were scanned, with both BH and NAV techniques. Protocol parameters: 6 diffusion encoding directions, b=350s/mm^2, TR=900-1100ms, TE=23ms, BW=2442Hz/pixel, fat saturation, spatial resolution=2.7×2.7×8mm^3, 1 slice, 8 averages. Post-processing was enhanced by firstly adding an interface where bad frames where rejected based on a visual analysis, and secondly by using an automatic image registration cross-correlation algorithm [6] prior to averaging. The cDTI data was then processed to create fractional anisotropy (FA), mean diffusivity (MD) and HA maps in the myocardial region. A comparison (paired sample t-test) of the BH was then made between the two sets of NAV data: NAVold (without frame rejection and image registration) and NAVnew (with frame rejection and image registration). We specifically looked at the average myocardial FA and MD value, and the HA difference to a statistically averaged HA map from 10 healthy volunteers. Care was taken to not include papillary muscle in the quantitation.

Results: A subject's averaged b0 image, FA, MD, and HA maps are shown in Figure 2 for the three datasets. A paired t-test of the results of all volunteers between BH and NAVold shows significant difference in the mean FA (p=0.014), and mean MD (p=0.0036) but no significant difference in the mean HA difference maps (p=0.25). No statistical difference was found between BH and NAVnew: FA (p=0.14), MD (p=0.074), and HA difference (p=0.21) (Figure 3).

Discussion

Here we showed for the first time that a free-breathing navigator based approach to cDTI produces high quality *in vivo* images, comparable to that of the BH protocol. Investigations into the effect of more robust accept/reject algorithms, balancing different diffusion directions between averages, and intelligent automatic frame rejection methods are currently ongoing. The ability to perform free breathing DTI will be critical if the use of DTI is to be extended to patients with cardiovascular disease and limited breath-hold capacity. This could prove to be a powerful tool to characterise the structural remodelling and fibre disarray patterns of diseases such as myocardial infarction and cardiomyopathies, improving the capability of cardiac MRI for diagnosis and therapy follow-up.

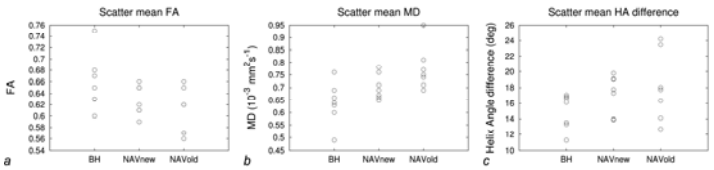

Figure 3. Scatter plots of the mean FA, mean MD, and mean HA difference.

Conclusion

Free-breathing navigator based approach to cardiac DTI, coupled with robust post-processing is capable of producing high quality *in vivo* images, comparable to that of the BH protocol.

References

[1] Edelman RR. et al. MRM 32:423 (1994). [2] Reese et al. MRM 34:786 (1995). [3] Dou J et al. MRM 50:107 (2003). [4] Wu et al. Circulation 114:1036 (2006). [5] Nielles-Vallespin, et al., MRM (ahead of print) (2012). [6] Guizar-Sicairos et al., Opt Lett 33:156 (2008).