Automated lipid artefact removal for DTI using multiple coils

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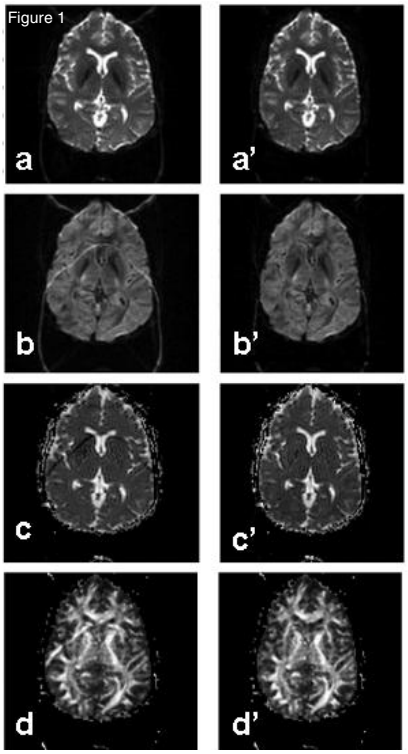
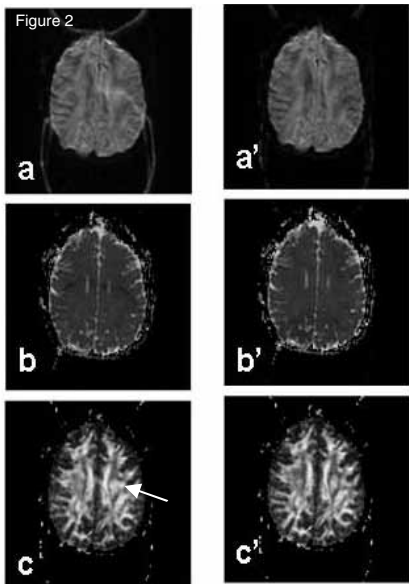
Introduction: Diffusion Tensor Imaging (DTI) is extremely sensitive to imperfect fat suppression as the immobile lipid protons signal is largely unaffected by the diffusion gradients whilst signal in the rest of the brain is suppressed. In addition any distortions which result from eddy currents can produce high apparent FA in lipid-containing voxels. In our experience imperfect fat suppression at 3T is not uncommon. Lipid signal separation in EPI using multiple coils without sequence modification has been demonstrated as a proof of principle [1] In this study we develop further this method to be practically implemental and robust. We apply the method to DTI and demonstrate that errors introduced by lipid contamination can be eliminated entirely from apparent diffusion coefficient (ADC) maps and fractional anisotropy (FA) maps, both of which are extremely sensitive to it. The method has been developed such that it requires no additional information other than the standard coil reference scan. We have performed a small study of 4 subjects to test the robustness of the method. In all subjects a non fat suppressed dataset was acquired alongside a fat suppressed data set and the two processed identically with pixels for correction being automatically detected and corrected a needed.

Theory: In a fully sampled image the signal intensity S_1 in a pixel where there is a superposition of lipid and water, imaged with surface coil C_1 can be written as $S_1=C_{11}x_1+C_{12}x_2$ where x_1 and x_2 are the signal intensities of water and lipid, C_{11} represents the sensitivity of coil 1 to pixel location 1 (the "true" signal location) and C_{12} the sensitivity of coil 1 at the position from which the lipid has been shifted. This equation is the SENSE equation [2] and with multiple coils can be solved. The difference in position between the locations of x_1 and x_2 is not necessarily half a field of view as in traditional SENSE with factor two pixel degeneracy but this can be made to be the case by constructing new reference data from two copies of the reference data, doubling the effective field of view and then shifting one by the known lipid shift. This reconstruction, whilst correct, is sub-optimal as pixels which do not contain a superposition of water and lipid are processed resulting in possible SNR degradation (due to g-factor). To reconstruct with optimal SNR the pixels containing a superposition of lipid and water are identified and only these pixels reconstructed via the PPI algorithm. To identify these pixels a data consistency measure is used [3][4] The individual coil images are divided by their respective coil sensitivities, this renders all images from all coils identical to within noise, except where data is not consistent with the coil sensitivity profile. The lipid signal, having originated from a location different to the one it appears in the image is not consistent with the coils sensitivity and so appears with different signal intensity in each coil image. A map of the range of pixel intensities across all coils reveals those pixels containing superimposed lipid and water, these are identified by a threshold.

Method: Standard SENSE reference data was acquired. These scans have lipid shifts less than one pixel and can be used to successfully unfold images where water lipid shifts extend to several pixels without further processing. The data is reconstructed with a standard SENSE algorithm using reference data as described. Following this processing ADC maps and FA maps are produced in the usual way. The imaging protocol used was single shot EPI with 6 diffusion directions b=800 with a single average, all data was taken using a Philips 3T Intera.



Results: All processed data has no observable remaining lipid signal. Both data where lipid suppression was used and where it was not were processed in the same way. If the suppression was good then no fat pixels were identified in the data consistency test and no further processing performed. This was the case in 2 of the 4 fat suppressed datasets. The figures show example data from two different subjects pre and post correction. Figure 1, with no fat suppression and figure 2, with failed fat suppression. Figure 1 a shows the acquired b=0 image without fat suppression, the fat can be seen clearly and is shifted by 39.7 pixels from its true location, a' shows the resultant processed image where the lipid has been removed. b and b' show one of the 6 directions of diffusion weighting pre and post processing, c and c' show the associated ADC maps and d and d' the FA maps. All show successful removal of lipid signal with no remaining artefact. Figure 2 shows an example where fat suppression partially failed and has been repaired using the method described. a and a' show b=800 single direction images, b and b' show ADC maps and c and c' show FA maps. The effect on the FA maps are subtle in this example, and as such, potentially more malignant, as the elevated FA in regions of artefact is not obviously discernable and may be mistaken for anatomy. (arrows show region of artificially elevated FA)



Discussion: Regional failure of lipid suppression is not uncommon in DTI. This work presents a practical method for recovery of such images using PPI methods combined with a data consistency measure used to identify problem pixels. The method is robust provided the coil sensitivity data represents the sensitivity of the coils to the lipid containing area, susceptibility distortions do not present a major impediment to the method due to the slowly varying nature of the coil profiles. However artefacts can be provoked by seeking to remove lipid signal originating from highly distorted regions of the brain. This was not seen in data from this standard DTI protocol. Where distortion is large we have found that registration of the reference data to the lipid ring (obtained from the consistency measure) provides robust reference data even in these areas. The process is automated and if fat suppression is good no correction is applied.

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References: [1] Larkman et al Proc. Intl. Soc. Mag. Reson. Med. 13 (2005) 505.[2] Pruessmann et al Magn Reson Med. 1999 Nov;42(5):952-62. [3] Atkinson et al Magn Reson Med. 2004 Oct;52(4):825-30 [4] Winkelmann R et al Magn Reson Med. 2005 Oct;54(4):1002-9