# Water and Fat Separation using Standard SENSE Processing

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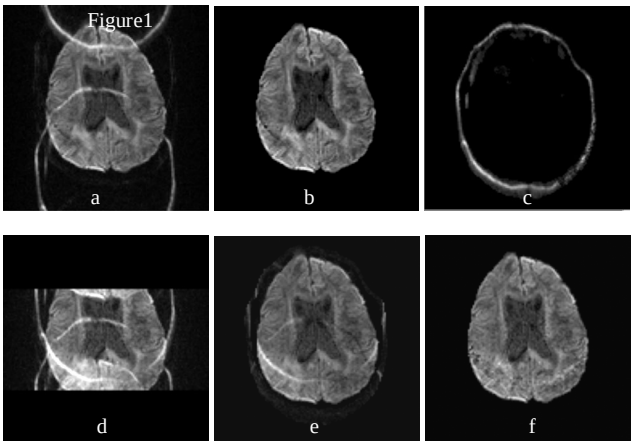
**Introduction:** If the receiver bandwidth is small, chemical shift leads to a spatial mis-registration of lipid and water signals. This is a common artefact in MRI, for example, in spin echo imaging where small bandwidths are desirable to increase signal to noise ratio (snr) chemical shifts in excess of 10 pixels are common. More extreme is echo planar imaging (EPI) where the length of the readout trajectory produces a small bandwidth in the "slow read" or "blip" direction. Partially parallel imaging (PPI) has been shown to reduce distortions in EPI, effectively increasing this bandwidth by reducing the total time required to cover the whole of the prescribed k-space[1]. However, the water fat shifts in EPI are still large. In this study we demonstrated how PPI can be used to produce separate fat and water images without modification to the acquisition unlike the recently proposed methods[2] and using standard SENSE[3] processing algorithms. The method can also be combined with SENSE speedup factors resulting in acceleration and water fat separation. Chemical shift artefacts are a known source of unfolding error in SENSE and are a particular problem for DTI because diffusion weighting suppresses signal in the brain whilst the immobile lipid signal remains high, potentially resulting in artefacts even when fat suppression is nominally good. The proposed method allows explicit handling of the chemical shift effects resulting in reconstructions which do not suffer from these artefacts. As presented prior knowledge of separate water and fat images is required, but these can then be used to process multiple images. The method is demonstrated with EPI data, combination with speedup is simulated.

**Background and Theory:** Typically a SENSE reference scan is a short TE/TR field echo to maximise snr and time efficiency. These scans have lipid shifts less than one pixel and in general can be used to successfully unfold images where water lipid shifts extend to several pixels, this robustness is due to the slowly varying nature of the coil sensitivities. However, where the water-fat water shift is large this reference data does not provide accurate sensitivity maps for the lipid content of the image, resulting in incorrect unfolding. This is seen most readily in single shot EPI where shifts of 10's of pixels are commonplace and hence reconstruction artefacts are readily seen. A solution to this artefact is to reconfigure the reference data prior to SENSE processing so that appropriate coil sensitivities are used for both water and lipid signals. In a fully sampled image, and referencing all image coordinates to the water signal, the signal intensity $S_1$ in a pixel where there is a superposition of lipid and water, imaged with a 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 fat has be shifted. This equation is the SENSE equation and with multiple coils the problem 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. The target data is then zero filled in the image domain to double its field of view and the data processed with standard SENSE algorithm for a speed up factor of two, the resultant image then can be cut into two images one containing water and the other lipid. Whilst the simple scheme described is effective it is not optimal as all pixels are considered to be two fold degenerate independent of the presence of lipid or not in the original data. This results in potential degradation of snr across the whole image due to g-factor effects. A better scheme is to generate separate water and lipid images using any of the available techniques, eg dixon[4], then the reference data can be constructed from these two images resulting in processing only where lipid is present. This data can be used as subsequent reference data for any number of acquisitions.

**Method:** To demonstrate the approach two fully encoded single shot EPI images were acquired with water saturation and then with lipid saturation. These were combined for use as sensitivity data for subsequent single shot diffusion weighted acquisitions. The lipid image was thresholded to exclude remaining water signal. SENSE accelerated data was simulated by decimation of k-space. The processing was performed with standard SENSE code set to an acceleration factor of 2 for the lipid removal and 4 for lipid removal and acceleration factor 2.




**Results:** Figure 1 a) shows the acquired single shot EPI diffusion weighted image (b=800) without fat suppression from a philips 3T system, the fat can be seen clearly and is shifted by 39.7 pixels from its true location, b) shows the resultant processed image where the fat has been removed, c) is the corresponding fat only image produced simultaneously with b). d) shows a simulated acceleration factor of two produced from the data shown in a).e) shows the unfolded image using standard SENSE reference data with the lipid ring clearly remaining in its original location and its aliased location. F) shows d processed with the proposed method showing correct unfolding, removal of lipid artefacts and (not shown) a separate lipid image, some g-factor artefact is seen.

**Discussion:** Here we have used fat and water suppression to acquire separate lipid and fat reference data. This provides an optimal snr solution. In the absence of such data a two step approach can be taken. A standard reference data set with minimal chemical shift artefact can be used (containing both lipid and water signal correctly located) to generate the duplicate sensitivity data. This produces a non snr optimal solution for the lipid only image. A threshold can then be applied to the lipid image to segment it and then this threshold applied to the original reference data to produce a lipid segmented image suitable for constructing the reference data. Equally, increasing the field of view of the reference data such that the lipid signal lies completely outside the brain also provides suitable reference data. The method has intriguing possibilities in non-EPI imaging where the lipid shift is orthogonal to the phase encode direction increasing the robustness of combining the method with acceleration due to geometric factors analogous to 2D SENSE[5]. In such a scenario the greater the chemical shift the less the g-factor affects the processed region and also the higher the intrinsic snr due to the smaller bandwidths. The method described provides a framework for accurate reconstruction in the presence of chemical shift producing paired lipid and water images without sequence modification.

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