Chemical shift artifact correction by image processing in Spin-Echo imaging

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Introduction

In magnetic resonance imaging (MRI), the inherent differences in precessional frequencies between the water and fat protons (δ=3.25 ppm) are responsible for spatial misregistration. In conventional imaging, fat signal will be shifted in the frequency-encoding direction and consequently hippo and hyper signal intensity appears at the lipid-water interface (Fig. 3a). Numerous different techniques have been proposed to reduce or eliminate the chemical shift artifacts [1]. All the proposed techniques always constrain the acquisition process and a trade-off has to be found with the initial imaging goal. So far, there is no existing image processing method.

In this study, we propose a new image processing technique to correct chemical shift artifacts in Spin Echo (SE) MR images. It is based on a pre-scan image of the fat and enables the correction of any SE scheme sequence without any constraint on the sequence parameters.

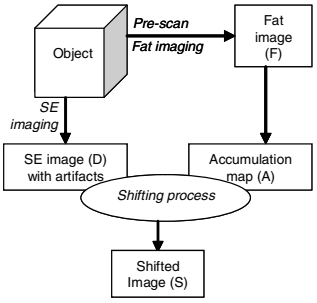


Figure 1: Shifting process.

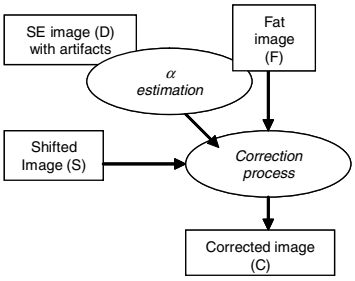


Figure 2: Correction process.

Proposed method

The first step of our method is the shifting process (Fig. 1) which shifts the fat signal at its true location. In fact, we consider the chemical shift artifact as inhomogeneities of the static magnetic field B_0 experienced by the fat protons [2]. Let $\Delta B(i,j)$ denotes the susceptibility-induced field gradients at the image position (i,j). The distortion along the x direction can be modeled by:

$$i' = i - \Delta B(i,j)/(Gx.\Delta x) \;;\; j' = j \qquad (1)$$

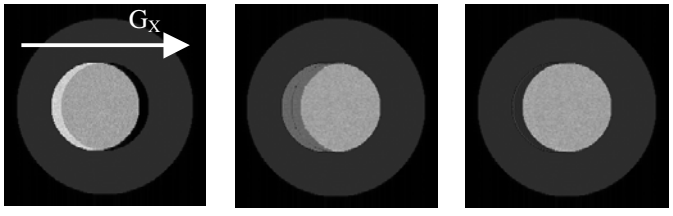
Where (i,j) and (i',j') refer to the true and distorted positions in the MR image, respectively, Gx is the readout gradient value, Δx the pixel size.

A pre-scan of the concerned object gives a fat image which specifies which pixels will be affected by the chemical shift artifact. Then, we build a $\Delta B(i,j)$ map as follows : $\Delta B(i,j)=0$ for a pixel without fat and $\Delta B(i,j)=\delta * B_0$ otherwise. An accumulation map, noted A, is built from the $\Delta B(i,j)$ map. This accumulation map represents the wrong encoding of the fat protons in the imaging process. The accumulation coefficient at each pixel location in the distorted image is computed iteratively according to (2), where d represents the fractional contribution calculated by (3).

$$\begin{aligned} A(i',j') &= A(i',j') + (1-d) \\ A(i'+1,j') &= A(i'+1,j') + d \end{aligned} \qquad (2) \qquad d = i' - Floor\{i'\} \qquad (3) \qquad S(i,j) = (1-d) * D(i',j') / A(i',j') + d * D(i'+1,j') / A(i'+1,j) \qquad (4)$$

From this accumulation map, the shifted image, noted S, is obtained iteratively by (4), where D is the distorted SE image. In the shifted image, fat signal recovers its true location (hippo intensity areas no longer exist) and two areas coming from the hyper intensity areas appear. Both areas have not their correct intensity (Fig. 3b).

Thus, the second step is the correction process (Fig. 2) that recovers the signal intensity of these areas located at the lipid-water interface. We define $\alpha = S_{DIS}/S_{FAT}$ where S_{FAT} is the non-zero pixel value in the proton density weighted fat image (F) and S_{DIS} the corresponding pixel value after chemical shift in the distorted image (D) with the condition that the signal has not been superposed to an other one. α is supposed to be constant and is calculated as the mean of all found values. Then, during the correction process, we directly estimate for each pixel of the higher frequency encoded area (among the two newly ones appeared during the shifting process) the true pixel value knowing α and the fat image pixel value by: $C(i,j) = \alpha * F(i,j)$ where C is the corrected image. Pixel values of the lower frequency encoded area are obtained by using the pixels values of the distorted image as follows: $C(i',j') = D(i',j') - \alpha * F(i,j)$. For the rest of the image, the corrected pixel values are the same than the shifted image ones: $C(i,j) = S(i,j)$.



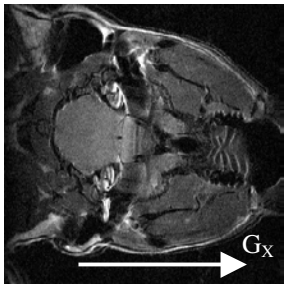
a) b) c)

Figure 3: a) Simulated SE image (TE=20ms, TR=400ms) with artifact. b) Shifted image. c) Corrected image.

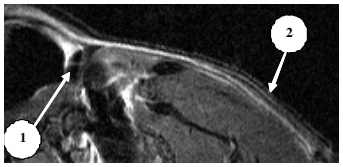
Results

The algorithm has been tested on several simulated images obtained with the MRI simulator SIMRI [3] with various combinations of MRI SE parameters and on real images at 1.5 T and 7 T. We present the correction of a 7T image of an object composed of a non-homogeneous fat circle surrounded by a water ring (Fig. 3) and of a mouse head image acquired at 7T (Fig. 4). We can see that under skin fat structures recover their locations and that the chemical shift artifact is well corrected.

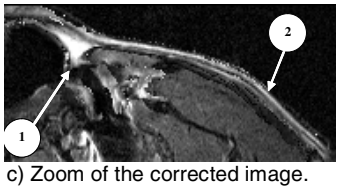
With the general evolution of MRI towards high field imaging, the proposed technique will be useful for the SE scheme based sequence imaging.



a) Full view of the SE artefacted image.



b) Zoom of the artefacted image.



c) Zoom of the corrected image.

Figure 4: Correction of a 256x256 SE image of a mouse head. TE=15ms , TR=1500ms , BW=25kHz.

References

[1] Kerviler et al., Biomed & Pharmacother 1998; 52 : 69-75.
[2] Belaroussi et al., ISMRM 2004; 2168.
[3] Benoit-Cattin et al., JMR 2005; 173 : 97-115.