

Model Independent Correction of Complex Intensity Inhomogeneities

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Introduction: MRI at high field strength suffers typically from pronounced signal intensity inhomogeneities. If arrays coil are used for signal reception the inhomogeneities show furthermore irregular pattern depending on slice positioning and coil application. Such inhomogeneities degrade image quality in general and impede image segmentation and quantification. Several previously published methods for inhomogeneity correction (1-3) developed mainly for brain applications perform suboptimally for high field abdominal investigation. This was also found for a method based on the experimentally determined coil sensitivities implemented on the used scanner. The aim of the present work was the development of an image data based method for model-free removal of complex signal inhomogeneity patterns for threshold based image segmentation.

Material and Methods: The signal intensity in MRI $I(x)$ can be described by the following equation (neglecting flow, diffusion.. etc.):

$$I(x) = k * S(x) * \sin(\alpha(B_{1+}(x))) * R(T_1(x), T_2(x), f(B_{1+}(x))) + \text{noise}(x) \quad [1]$$

where k represent a general constant, $S(x)$ the coil reception sensitivity distribution, $\alpha(B_{1+}(x))$ the spatially varying excitation flip angle and $R(T_1 \dots)$ the relaxation term. The $B_{1+}(x)$ influence in the relaxation term can be neglected for a sufficiently long TR. This applies also for the noise for typical SNR. In that case the signal inhomogeneity can be described by a single term $g(x) = k * S(x) * \sin(\alpha(B_{1+}(x)))$ with the final signal model $I(x) = g(x) * R(T_{1,2}(x))$. To restore a homogeneous image a function $c(x) = 1/g(x)$ must be determined. For image segments a linear estimate for $c(x)$ can be found by minimizing the functional $F(c(x)) = N(c(x) * I(x))$, where $N(c(x) * I(x))$ is the negentropy (4). In the present work 2D-spline functions were used to model the correction field $g(x)$ for the whole image. Optimization was performed by a simplex algorithm in a multi-grid approach. The negentropy was efficiently calculated from the histogram of the corrected and standardized image. The start values for optimization were found by homomorphic filtering. The program was implemented in IDL on a standard PC. Simulations were performed to optimize the grids and to study the minimization procedure. In-vivo analysis was performed with TSE images (TR/TE=1000/53) acquired at 1.5T (n=12) and 3T (n=3).

Results: The result of the proposed procedure is shown in Fig 1. Threshold based segmentation of adipose tissue in the original images would not work as the peaks from the different tissues are not separable in the original histograms (red histogram). After inhomogeneity correction a clearly separated distinct fat peak exists (green histograms). The visual analysis of possible disease related signal changes is also generally improved (e.g. spine). The slice dependent varying correction functions were adequately modelled by 2D-spline functions with equally spaced nodes at a final grid distance of (image matrix)/8. Additionally to the regular grid inside the body supplementary nodes were positioned at the boundary of the body. With the current implementation the processing of one slice lasts approximately 45s. According to the simulation results homomorphic filtering turned out to be a recommendable preprocessing step for choosing the starting guess for $c(x)$.

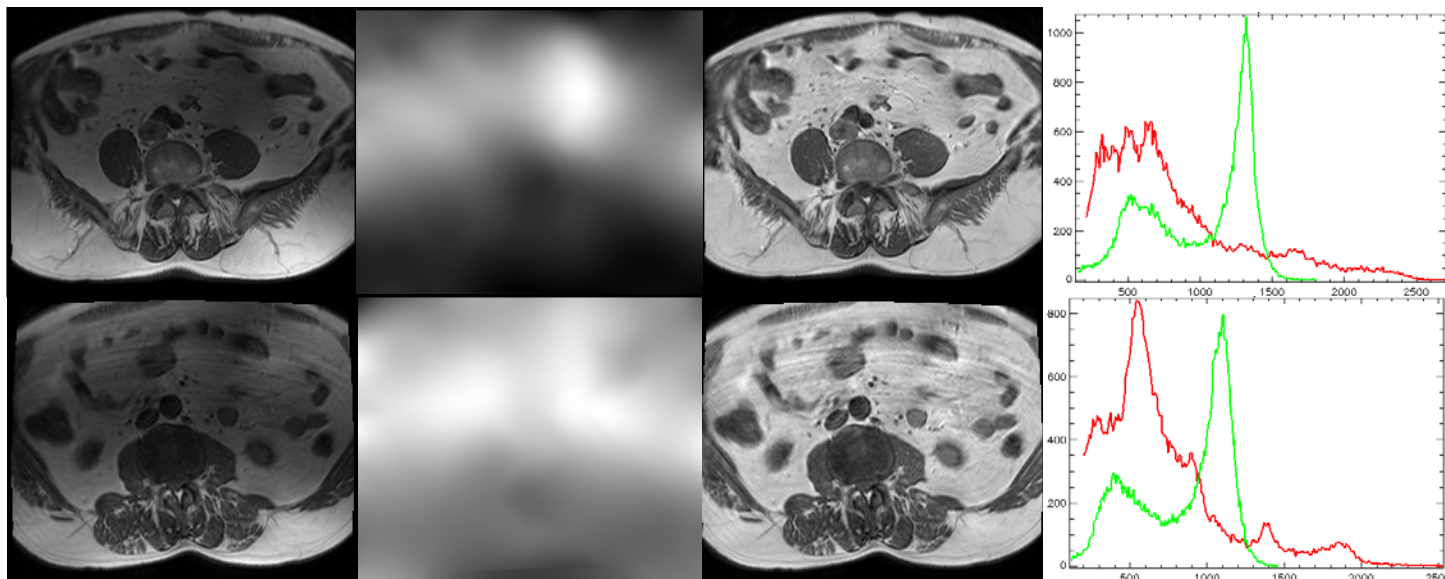


Fig. 1. Two representative cross sections from a scan at 3T using a coil array for signal reception. The first column shows the original images, the second the correction function $c(x)$, the third the restored images and in the fourth column the histograms of original (red) and corrected image (green) are shown (without background).

Discussion: The method was found to be robust with the used image data and the applied simplex algorithm for multi-scale optimization. The current processing duration of less than a minute is acceptable for image segmentation. A significant reduction of the processing should be possible with the implementation of the procedure in C or a similar programming language. Further improvement should be possible with a dedicated optimization procedure and an appropriate down sampling of the images. Additional investigations will be performed for different image contrasts and normalization of different slices.

References: 1. Sledg JH et al., *IEEE Trans. Med. Imag.* **17**: 87–97. (1998), 2. Brinkmann BH et al. *IEEE Trans. Med. Imag.* **17**: 161–171. (1998), 3. Cohen MS et al. *Hum. Brain Mapp.* **10**: 204–211. (2000), 4. Yang GZ et al., *MAGMA* 2002, 14:39-44 (2002)