Parametric Method for Correction of Intensity Inhomogeneity in MRI Data

Alexei A. Samsonov[1,3], Ross T. Whitaker[2,3], Eugene G. Kholmovski[1,4], Chris R. Johnson[2,3]

[1]Department of Physics, University of Utah, Salt Lake City, Utah, USA; [2]School of Computing, University of Utah, Salt Lake City, Utah, USA; [3]Scientific Computing and Imaging Institute, University of Utah, Salt Lake City, Utah, USA; [4]MIRL, University of Utah, Salt Lake City, Utah, USA

Intensity inhomogeneity is one of the main obstacles for MRI data post-processing. The problem requires retrospective correction due to the strong dependence of the inhomogeneity on patient anatomy and the accompanying acquisition protocol. We have developed a new method for correcting the inhomogeneities using a polynomial estimation of the bias field. The method minimizes the composite energy function to find parameters of the polynomial model. The energy function is then designed to provide a robust estimation of the bias field by combining measures from histogram analysis and local gradient estimation. The method was validated on a wide range of MRI data obtained with coils of different types and under different acquisition protocols.

Introduction

Intensity inhomogeneity in MRI data arises from multiple sources, for example, non-uniform coil excitation/reception profiles and RF wave attenuation of tissue. Such contributions can be approximated by smoothly varying the multiplicative gain field $G(r)$, or in the log domain, by an additive bias field $B(r)$:

$$I = I_0 \cdot G(\boldsymbol{r}) + n, \quad \log(I) \approx \log(I_0) + B(\boldsymbol{r}) \quad (1)$$

where I is MRI data corrupted by the gain field G, and n is additive Rician noise. The existing methods for correction of the bias often require expert supervision, the presence of large homogeneous regions of tissues [1] or rely on global optimization criteria that may lead to local minima [2]. In the paper, we present a fast and robust method for correction of MRI data intensity inhomogeneity. Our new method relies both on local and global characteristics of the data providing a reliable estimation of the underlying bias field.

Method

We start by modeling the smoothly varying bias field $B(r)$ by Legendre polynomials of degree l (3D case):

$$B(r,\boldsymbol{p}) = \sum_{i=0}^{l} \sum_{j=0}^{l-i} \sum_{k=0}^{l-i-j} p_{ijk} P_i(x_1) P_j(x_2) P_k(x_3) \quad (2)$$

The estimation of polynomial model parameters is accomplished by minimization of the following energy function:

$$E(\boldsymbol{p}) = -\sum_{i=1}^{N_{bins}} h_i^2(\boldsymbol{p}) + \lambda \sum_{i=1}^{N_p} \sum_{j=1}^{3} \omega_{ij} \left(\frac{\partial \log(I)}{\partial x_j} - \frac{\partial B(\boldsymbol{p})}{\partial x_j} \right)^2, \quad (3)$$

where h is a histogram of data corrected by the current estimation of the bias field, ω_{ij} are weights reflecting the error in gradient estimation [1], and λ is chosen to balance relative significance of each term for a particular class of correction problems. The first, so-called "global" term of (3) is the energy of the histogram power spectrum. Distribution of data corrupted by an independent additive bias field can be approximated by the convolution of the distribution of initial data and the bias field distribution. The corruption by the bias field leads to the degradation of the high frequency content in the histogram [3]. We choose to restore the frequency content by maximizing the energy of its power spectrum. The second, so-called "local" term of (3) is essentially a data consistency constraint. The term holds everywhere except for tissue boundaries and partial volume pixels [1]. Significant gradients that could be assigned to the tissue boundaries are eliminated by thresholding. Then partial volume pixels are excluded by a morphological erosion operation with small structuring element. The estimation of the "local" term requires preprocessing. We choose to use anisotropic diffusion filtering [4] for denoising purposes. Using such a filtering allows effective noise elimination while preserving smooth trends.

Results

The method was tested on a number of datasets acquired on a 1.5T MR scanner (GE SIGNA, GE Medical Systems, Milwaukee, WI) with different acquisition protocols using volume and surface coils. Figure 1 presents results of correction of a PD-weighted $256 \times 256 \times 16$ dataset acquired by the head coil. The correction time using a 2nd order polynomial was less than 2 minutes. Segmentation of initial data by thresholding underestimated the gray matter in the brain (Fig. 1-d), while thresholding on the corrected volume produced a reliable segmentation of the tissue (Fig. 1-e). Figure 2 demonstrates results of correction of a "sum-of-square" image from a 4-coil phased array. The correction was done on a 256×256 slice using a 4th order 2D Legendre polynomial.

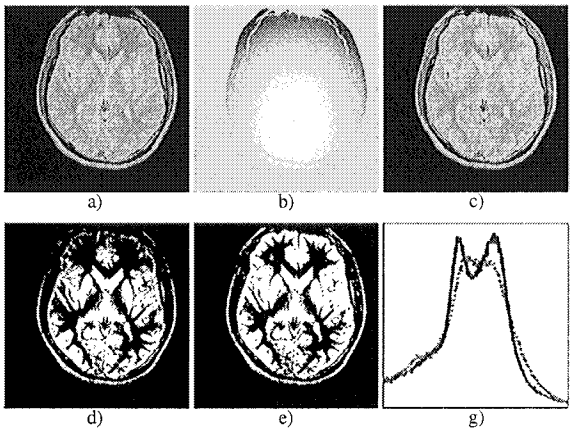

Figure 1. Correction of head coil data. a) initial slice b) estimated bias field (2nd order Legendre polynomial), c) corrected slice, d) gray matter segmentation of initial slice, e) gray matter segmentation of corrected slice, f) histograms of initial (dotted) and corrected (solid) data

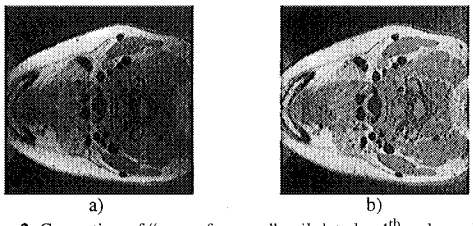

Figure 2. Correction of "sum-of-square" coil data by 4th order polynomial. a) initial slice, b) corrected slice

Discussion

The developed method provides reliable estimation of the intensity inhomogeneities in MRI data. The proposed energy function combines both global and local criteria ensuring a robust and fast optimization process. Both terms are complimentary. Using only the "global" term of the energy function may potentially lead to incorrect identification of minima, especially in the cases when polynomial model is a modest approximation of underlying bias field. Parameters required by the algorithm in most cases could be chosen automatically [4]. The correction times are dependant on the number of parameters of model used, the dataset size and the degree of subsampling in estimation of both local and global terms and vary from 1 to 5 minutes using a mid range PC.

Acknowledgements

This work was supported in part by NIH BISTI grant 1P20HL68566-01.

References

[1] Vokurka EA, Thacker NA, et al., JMRI, 10:550-565 (1999)
[2] Likar B, Viergever MA, et al., MICCAI'00, 1935:375-384 (2000)
[3] Sled JG, Zijdenbos AP, et al., IEEE TMI, 17(1):87-97(1998)
[4] Gerig G, Kubler O, et al., IEEE TMI, 11(2), pp. 221-232 (1992)