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Conference Paper · January 2005

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# Bias Field Correction for MRI Images

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**Summary.** Bias field signal is a low-frequency and very smooth signal that corrupts MRI images specially those produced by old MRI (*Magnetic Resonance Imaging*) machines. Image processing algorithms such as segmentation, texture analysis or classification that use the graylevel values of image pixels will not produce satisfactory results. A pre-processing step is needed to correct for the bias field signal before submitting corrupted MRI images to such algorithms or the algorithms should be modified. In this report we discuss two approaches to deal with bias field corruption. The first approach can be used as a preprocessing step where the corrupted MRI image is restored by dividing it by an estimated bias field signal using a surface fitting approach. The second approach shows how to modify the fuzzy *c*-means algorithm so that it can be used to segment an MRI image corrupted by a bias field signal.

## 1 Introduction

A bias field is a low frequency smooth undesirable signal that corrupts MRI images because of the inhomogeneities in the magnetic fields of the MRI machine. Bias field blurs images and thus reduces the high frequency contents of the image such as edges and contours and changes the intensity values of image pixels so that the same tissue has different graylevel distribution across the image. A low level variation will not have great impact on clinical diagnosis. However it degrades the performance of image processing algorithms such as segmentation and classification or any algorithm that is based on the assumption of spatial invariance of the processed image. A preprocessing step is needed to correct for the effect of bias field before doing segmentation or classification. The aim of the paper is to show how to restore the corrupted image and how to modify a classical fuzzy *c*-means clustering algorithm for MRI images corrupted by bias field signal.

## 2 Methods to Remove the Bias Field Signal

Different methods have been used for bias field correction such as using pre-scanned images, high-pass filtering and homomorphic filtering [1]. In this report, we discuss two techniques, namely, estimating bias fields by parametric surface fitting, and an iterative removal of bias

field based on modifying the objective function of the fuzzy  $c$ -means algorithm. Experimental results show the effectiveness of these techniques.

## 2.1 The Parametric Surface Fitting Approach

A common practice for images that are unevenly illuminated is to divide the corrupted image by a background image represents an estimate of the variation in the illumination across the image. The same can be done for MRI images corrupted by bias field signal. The background image is normally estimated from the corrupted image by low pass filtering operation. Since it is very difficult to design an optimal low-pass filter that has sharp cut-off frequency and at the same time has no ripples in the pass-band and stop-band regions, the background image estimated this way has some noise introduced such as ripples in the image and ringing around the edges. To improve the quality of the background image, a two-dimensional surface equation is fitted to data points selected from the background image and then the fitted equation is used to generate the bias field signal. The bias field signal obtained this way is much smoother than the background image obtained using a low-pass filtering operation alone. Fitting the surface also averages out the noise introduced by the low-pass filtering. The form of the fitted surface equation and the criteria used for the fitting process have to be decided based on certain objectives.

In [2, 3] the *PA*rametric *BI*as field *C*orrection (PABIC) method is proposed. The surface equation to be fitted is chosen as the superposition of Legendre polynomials combined with a probabilistic parametric model for the tissue class statistics. The valley function, a nonlinear objective function, is used to find the parameters of the model. The procedure has no mechanism for controlling the overfitting and has large number of parameters to set a priori.

In this section we propose to fit much more simple surfaces than the Legendre polynomials to a background image and use the simple least-squares as an objective function. The steps of the algorithm are:

1. Extract a background image from the corrupted MRI image, for example, by smoothing the image with a Gaussian filter of a large bandwidth (about  $2/3$  the size of the MRI image) to filter out all the image details that correspond to high-frequency components.
2. Select few data points from the background image and save their coordinates and graylevel values into a matrix  $D = (x_i, y_i, g_i), i = 1, 2, \dots, n$ . It is recommended not to select points from the regions where there is no MRI signal since this regions has no bias field signal.
3. Select a parametric equation for the fitted surface. It is better to fit simple surfaces such as low order polynomial surfaces since they are very smooth and their parameters are very easy to estimate.
4. Estimate the parameters of the surface that best fits the data in matrix  $D$  by the method of nonlinear least-squares.
5. Use the fitted equation to generate an image of the bias field signal.
6. Divide the corrupted MRI image by the estimated bias field image in step 5.

Even though different surfaces can reasonably fit the data very well and it is not possible to tell which surface is most likely represents the actual bias field signal, however, in practice the bias signal estimated by fitting a smooth 2-dimensional

polynomial surface to a background image can be used effectively to restore the corrupted MRI image.

### How to Do the Surface Fitting?

Fitting of the surface is done by means of the Levenberg-Marquardt algorithm for nonlinear least squares fitting of a function  $f(x, y; a_1, \dots, a_m)$  of known form to  $n$  data points  $\{(x_1, y_1, g_1), \dots, (x_n, y_n, g_n)\}$ . For example, a polynomial surface of degree three can be fitted which has the following equation:  $f(x, y; \mathbf{a}) = a_1x^3 + a_2y^3 + a_3$ , where  $\mathbf{a} = \{a_1, a_2, a_3\}$  is the parameter vector that define the surface.

If we substitute the data points in the nonlinear function we get an overdetermined set of equations, i.e.,

$$\begin{cases} g_1 = f(x_1, y_1; a_1, a_2, \dots, a_m) \\ \vdots \\ g_n = f(x_n, y_n; a_1, a_2, \dots, a_m) \end{cases}$$

These equations can be solved to obtain the unknown parameter vector  $(a_1, a_2, \dots, a_m)$  by minimizing the sum of the squares of the differences between the data and the fitted function

$$Q(\mathbf{a}) = \frac{1}{2} \sum_{i=1}^n (g_i - f(x_i, y_i; a_1, a_2, \dots, a_m))^2 \quad (1)$$

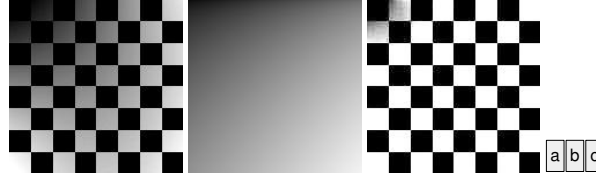
Let  $r_i(\mathbf{a}) = (g_i - f(x_i, y_i; a_1, a_2, \dots, a_m))$ , which is the residual vector of point  $i$ , then equation(1) can be written as:

$$Q(\mathbf{a}) = \frac{1}{2} \sum_{i=1}^n (r_i(\mathbf{a}))^2 \quad (2)$$

According to the Levenberg-Marquardt algorithm, Eq. 2 can be solved iteratively to find the values of the parameters vector  $(\mathbf{a})$  starting from an initial estimate of the parameter vector  $(\mathbf{a}_0)$  using:

$$\mathbf{a}_{i+1} = \mathbf{a}_i - (H + \lambda \text{diag}[H])^{-1} \nabla Q(\mathbf{a}_i) \quad (3)$$

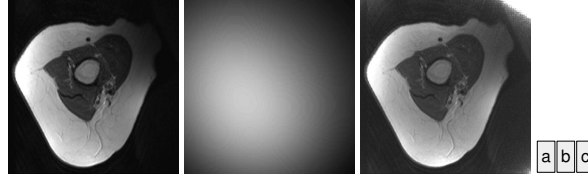
where  $H$  and  $\nabla Q(\mathbf{a}_i)$  are Hessian matrix and the gradient of Eq. 2 both evaluated at  $\mathbf{a}_i$ ,  $\text{diag}[H]$  is the diagonal elements of the Hessian matrix. At each iteration, the algorithm tests the value of the residual error  $Q(\mathbf{a})$  and adjusts  $\lambda$  accordingly (see [4] for more details). The result of applying surface fitting to a checker image corrupted by a bias field signal is shown in Fig. 1. The fitted surface is  $z = a + bx^n + cy^m$ . The estimated parameters are  $a = -3.6765$ ,  $b = 12.2149$ ,  $c = 0.6581$ ,  $n = 1$ ,  $m = 0.5$ . The fitted equation is used to generate the bias field image shown in Fig. 1b. Dividing the image in Fig. 1a by the generated bias field image in Fig. 1b results in the checker image in Fig. 1c. The improvement in SNR is 17.365dB.



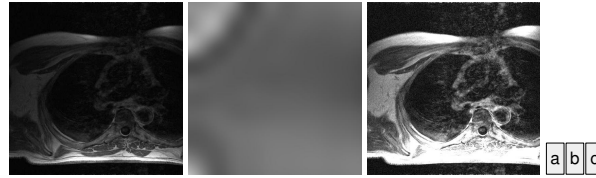
**Fig. 1.** (a) A checker image corrupted by a bias field signal. (b) Surface representing the bias field signal as estimated by the Levenberg-Marquardt algorithm. (c) The results of dividing image *a* by image *b*.

The result of applying surface fitting technique to a real biased MRI image is shown in Fig. 2. The fitted equation is  $z = a + bx + cx^2 + dy + ey^2 + fy^3$ . The estimated parameters are  $a = 9.2, b = 0.19, c = -0.023, d = 0.24, e = -0.061, f = 3.5$ . The improvement in SNR is 16.7306dB.

The method works well even for images that are highly corrupted by a bias field signal like the image in Fig. 3. The improvement in SNR for this case is 19.01dB.



**Fig. 2.** A bias field correction of MRI image. (a) The original biased image. (b) The estimated bias field by the Levenberg-Marquardt algorithm. (c) The corrected image.



**Fig. 3.** (a) A severely biased MRI image. (b) The estimated bias field by the Levenberg-Marquardt algorithm. (c) The corrected MRI image.

This technique works well for most biased MRI images; however, we have to specify beforehand the parametric form of the fitted surface. For example, we can fit: Quadratic surfaces, Polynomial surfaces, 2D Splines, etc. As a rule, it is better to fit low order polynomial surfaces because they take less time to calculate and approximate well the underlying bias field signal. Instead of fitting a pre-defined surface, it is also possible to fit a general non-parametric surface using neural networks, radial basis networks or support vector machines to the data points.

## 2.2 Segmentation of MRI Images by the Fuzzy $c$ -means Algorithm

Some image processing algorithms can be modified so that they can work with MRI images corrupted by bias field signal. For example, Wells [5] combined a classification algorithm and bias field correction in an iterative algorithm. In each iteration he estimates the bias field for each pixel then uses Bayes' theorem to guess the class of each pixel. Another similar approach was reported by Ripley [6].

The fuzzy  $c$ -means algorithm is an iterative algorithm proposed by Dunn [7] and modified by Bezdek [8] for clustering. It has also been used for segmentation. Here, we present a simple modification of the fuzzy  $c$ -means algorithm to segment field biased MRI images.

To segment an MRI into  $c$  segments using fuzzy  $c$ -means algorithm we minimize the following cost function

$$J_m(\mathcal{X}, U, v) = \sum_{i=1}^c \sum_{k=1}^N (u_{ik})^m d^2(v_i, x_k). \quad (4)$$

where the data points  $\mathcal{X} = \{x_1, x_2, \dots, x_N\}$  represent the MRI pixels stacked as a vector by lexicographic operation,  $U = \{u_1, u_2, \dots, u_c\}$  are the membership values taking values in the interval  $[0,1]$ .  $d(x, y)^2$  is a distance function which is mostly considered as the Euclidean distance.

Two constraints are usually used when optimizing Eq. 4, namely,

$$\begin{cases} \sum_{k=1}^N u_{ik} > 0; & \forall i \in \{1, \dots, c\} & (a) \\ \sum_{i=1}^c u_{ik} = 1; & \forall k \in \{1, \dots, N\} & (b) \end{cases} \quad (5)$$

The first constraint ensures that no cluster is empty. The second constraint forces the summation of the membership values for every single data point to be equal to one.

Substituting back the Euclidean distance function in Eq. 4,

$$J_m(\mathcal{X}, U, v) = \sum_{i=1}^c \sum_{k=1}^N (u_{ik})^m \|x_k - v_i\|^2. \quad (6)$$

The mathematical model for a biased MRI image is

$$y_k = x_k B_k. \quad (7)$$

In the last equation  $y_k$ ,  $x_k$ ,  $B_k$  are the corrupted image, the original image and the bias field signal stacked columnwise, respectively. If we substitute back Eq. 7 in Eq. 6 we obtain

$$J_m(Y, U, B, v) = \sum_{i=1}^c \sum_{k=1}^N (u_{ik})^m \left\| \frac{y_k}{B_k} - v_i \right\|^2. \quad (8)$$

To optimize Eq. 8, use the Lagrange multipliers method and the constraints in Eq. 5

$$J_m(Y, U, B, v) = \sum_{i=1}^c \sum_{k=1}^N (u_{ik})^m \left\| \frac{y_k}{B_k} - v_i \right\|^2 + \lambda \left( 1 - \sum_{i=1}^c u_{ik} \right). \quad (9)$$

Equation(9) is solved by taking the derivative of  $J_m(Y, U, B, v)$  with respect to  $U, B_k, v_i, \lambda$  and setting the result equal to zero

$$\frac{\delta J_m(\cdot)}{\delta \lambda} = 0, \quad \frac{\delta J_m(\cdot)}{\delta U_{ik}} = 0, \quad \frac{\delta J_m(\cdot)}{\delta v_i} = 0 \text{ and } \frac{\delta J_m(\cdot)}{\delta B_k} = 0.$$

After carrying out all the necessary calculation, eliminating  $\lambda$  by substituting it back, we arrive at the following three equations:

$$U_{ik} = \frac{1}{\sum_{j=1}^c \left( \left\| \frac{y_k}{B_k} - v_i \right\|^2 / \left\| \frac{y_k}{B_k} - v_j \right\|^2 \right)^{\frac{1}{m-1}}}, \quad (10)$$

$$v_i = \left( \sum_{k=1}^N (u_{ik})^m \frac{y_k}{B_k} \right) / \sum_{k=1}^N (u_{ik})^m, \quad (11)$$

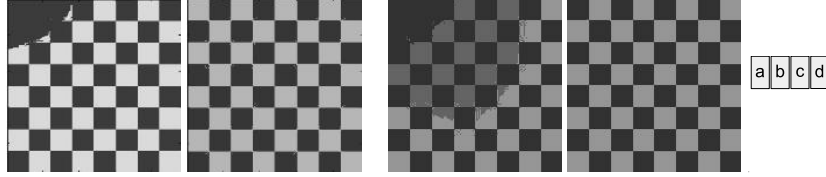
$$B_k = \left( \sum_{i=1}^c (u_{ik})^m y_k \right) / \sum_{i=1}^c (u_{ik})^m v_i. \quad (12)$$

These three equations(10-12) are used iteratively to calculate the membership matrix ( $U$ ), the prototype of each cluster ( $v_i$ ) and the bias field signal ( $B_k$ ), respectively. The following algorithm shows how to apply the fuzzy  $c$ -means algorithm to a biased MRI image:

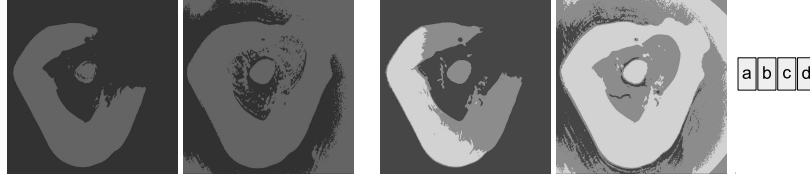
1. Set the fuzziness index to a constant (empirically  $m = 1.5$ ), the number of clusters  $c$  and the size of the spatial constraint window used to average the membership matrix.
2. Estimate an initial bias field signal  $B_0$  from the corrupted MRI image by smoothing it with a low-pass Gaussian filter.
3. Calculate the membership matrix  $U_{ik}$  using Eq. 10.
4. For each pixel take the average of the membership matrix around a window of size  $3 \times 3$  or  $5 \times 5$ . Normalize the membership matrix so for each image pixel the summation of the membership values corresponding to different clusters equals to one as in Eq. 5b.
5. Calculate the prototype centers  $v_i$  using Eq.11 and estimate the bias field  $B_k$  using equation (12).
6. Test if the difference between the norm of the previous calculated membership matrix and the norm of the current membership matrix  $\|U_l\| - \|U_{l+1}\|$  is less than a pre-specified error or if the algorithm exceeds certain number of iterations then exit, otherwise iterate again.

At each iteration the algorithm estimates a new approximation of the bias field signal and uses it to update the prototype centers and the membership matrix. The modified algorithm is sensitive to the number of iterations. If we iterate for long time, the algorithm is not guaranteed to converge. To overcome the convergence problem, a spatial constraint are imposed which forces neighbor pixels to be classified to the same class. This can be seen in step 4 of the algorithm where the membership matrix  $U_{ik}$  is averaged before calculating the prototype centers  $v_i$ .

The results of applying the classical  $c$ -means algorithm and the modified algorithm to the biased checker image and the biased MRI image are shown in Fig. 4 and Fig. 5, respectively.



**Fig. 4.** The results of clustering using the classical and the modified fuzzy  $c$ -means algorithms. (a,b) Two-class clustering using the classical fuzzy  $c$ -means algorithm and the modified one, respectively. (c,d) Three-class clustering using the classical and the modified fuzzy  $c$ -means algorithm, respectively.



**Fig. 5.** The results of applying the classical fuzzy  $c$ -means algorithm and the modified fuzzy  $c$ -means algorithm on a field biased MRI image. The first set (a) and (b) are the result of two classes clustering using the classical and the modified  $c$ -means algorithms, respectively. The second set (c) and (d) are the result of three classes clustering using the classical and the modified  $c$ -means algorithms respectively. Notice how the modified algorithm better detected the boundaries in both cases.

### 3 Conclusion

The bias field signal signal changes the intensity values of the MRI image pixels and it should be reduced before doing segmentation or classification. Removal of the bias field is an ill-posed problem and some implicit or explicit assumptions



should be made to obtain an approximate solution. For the surface fitting approach the assumption made here is the smoothness of the bias field signal. The least squares fits the smoothest surface to a given data points by averaging out the residual errors. For the modified fuzzy  $c$ -means algorithm, the objective is the minimization of the distances between the cluster centers and the data points. Including the bias field in the objective function of the fuzzy  $c$ -means algorithm disturbs the convergence of the algorithm. The solution adopted here is averaging the membership values of the neighborhood pixels which forces them to be clustered to the same class.

## 4 Acknowledgements

Thank to the *Universitaire ziekenhuis (UZA)*, department of *Magnetic Resonance Imaging* for providing the MRI images used in this research.

## References

1. B.H. Brinkmann et al. Optimized homomorphic unsharp masking for MR grayscale inhomogeneity correction. *IEEE Trans. Med. Imag.*, (17):161–171, 1998.
2. Gabor Szekely et al. Parametric estimate of intensity inhomogeneities applied to MRI. *IEEE Trans. on Medical Imaging*, 19(3):153–165, March 2000.
3. C. Brechbuhler, G. Gerig and G. Szekely. Compensation of spatial inhomogeneity in MRI based on a parametric bias estimate. In *Proceedings of the Fourth International Conference on Visualization in Biomedical Computing*, Hamburg, Germany, 1996.
4. William H. Press et al. *Numerical Recipes in C++*. Cambridge University Press, second edition, 2002.
5. W.M. Wells III et al. Statistical intensity correction and segmentation of MRI data. In *proceedings of the SPIE: Visualization in Biomedical Computing 1994*, October 1994.
6. Brian D. Ripley and Jonathan Marchini. Statistical considerations in magnetic resonance imaging of brain function. Technical report, SCIA99 conference, Kangerlussuaq, Greenland, June 1999.
7. J.C. Dunn. A fuzzy relative of the ISODATA process and its use in detecting compact well-separated clusters. *J. cybern.*, 3(3):32–57, 1974.
8. James C. Bezdek et al. *Pattern Recognition with Fuzzy Objective Function Algorithms*. New York: Plenum Press., 1981.