Modelling and Correcting Bias Field in MRI

Jesse Knight
School of Engineering, University of Guelph

***Abstract*— Bias field is a smoothly varying artifact in magnetic resonance imaging (MRI) which challenges many image analysis methods. Here we present a basic framework for characterizing and correcting the artifact. We assume that the multiplicative bias field image can be approximated by a parametric equation over the image volume. This equation is then fitted using the Levenberg-Marquardt algorithm. We illustrate this procedure on a synthetic brain MRI image.**

I. Introduction

Due to imperfections in the physics of acquisition, magnetic resonance imaging (MRI) suffers from a low frequency multiplicative artifact known as intensity inhomogeneity, or bias field [1]. While radiologists can often overlook the smoothly varying graylevel differences, this artifact challenges automated image analysis methods. As such, many methods have been proposed for correcting bias field before other image analysis algorithms are employed [1].

The aim of this paper is to illustrate the underlying model for most of bias field correction methods. In section II, we develop the model and note the required assumptions. In section III, we show how the parameters of the bias field model can be estimated. In section IV, we describe an toy application using a synthetic brain image, and in section V, we give the results. In section VI, we conclude the paper.

II. Bias Field Modelling

Consider a 3-dimensional volume $\mathcal{X}$ for imaging. The volume is divided into subvolumes x called voxels ("volume-pixels"), which are indexed by a vector $[\mathrm{x}_1, \mathrm{x}_2, \mathrm{x}_3] \in \mathbb{R}^3$.

Let us say that the imaged object in $\mathcal{X}$ comprises K tissue classes, which are indexed by k. We will denote the set of voxels containing tissue k as $\tilde{\mathcal{X}}_k$. This is a fuzzy set because many voxels contain a mixture of tissues. Let us further denote the set of voxels containing only a single tissue ("pure voxels") as $\mathcal{X}_k$, and the total number in each set as N_k.

A. Corruption Model

Now consider the ideal MRI signal $F(x)$, defined over $\mathcal{X}$. During acquisition, it is corrupted by a multiplicative bias field $B(x)$ and a random additive noise field $U(x)$, yielding the observed grayscale image $Y(x)$; we model this relationship as follows [1]:

$$Y(x) = F(x)B(x) + U(x).$$

For our purposes, we will neglect noise (i.e. $U(x) = 0$). To separate the multiplication, we take the logarithm of both sides of the above, yielding

$$\begin{aligned} \log\left[Y(x)\right] &= \log\left[F(x)B(x)\right] \\ \underbrace{\log\left[Y(x)\right]}_{y(x)} &= \underbrace{\log\left[F(x)\right]}_{f(x)} + \underbrace{\log\left[B(x)\right]}_{\beta(x)}. \end{aligned} \tag{1}$$

Now, in order to estimate the artifact image $\beta(x)$ given only the observed image $y(x)$, we make two assumptions:

1) The artifact image $\beta(x)$ can be approximated by a sum of M low order basis functions ψ, where the basis function ψ_j is parametrized by a vector of coefficients a_j. The sum is defined as
$$\beta(x) \approx \Psi(x, a) \coloneqq \sum_{j=1}^{M} \psi_j(x, a_j).$$
2) The ideal image signal in all pure voxels of this same tissue is the same. – i.e. $f(x_i) = f(x_j) = f_k$, $\forall\ x_i, x_j \in \mathcal{X}_k$.

Combining (1) and the second assumption, we observe that in pure tissue voxels $\mathcal{X}_k$, deviations from the ideal graylevel f_k must be attributable to the bias field:

$$\beta(x) = y(x) - f_k, \quad x \in \mathcal{X}_k.$$

Considering only these voxels, we can therefore estimate the parameters of the model equation Ψ. Specifically, we would like to minimize the squared differences between the parametric equation $\Psi(x, a)$ and the observed data $y(x) - f_k$, for all x in $\mathcal{X}_k$:

$$Q(a) = \sum_{x_i \in \mathcal{X}_k}^{N_k} \left[y(x_i) - f_k - \Psi(x_i, a)\right]^2. \tag{2}$$

Note that for real images, this minimization will be confounded in part by noise.

III. Model Fitting and Bias Removal

In this section, we describe how to estimate the parameters of the bias field model, and how to remove the artifact.

A. Estimating f_k

First, we need to estimate the ideal signal f_k for each tissue, since it is unknown a priori. If we define the estimate $\hat{f}_k$ as the expected value (a.k.a. mean) of the ideal tissue signal,

$$f_k \coloneqq \mathbb{E}\left[\, f(x) \,\right], \quad x \in \mathcal{X}_k,$$

and assume that the mean of the log-transformed bias field $\beta(x)$ is zero, then we have

$$\left.\begin{aligned}\hat{f}_k &= \mathbb{E}\,[\,y(x)+\beta(x)\,]\\ &= \mathbb{E}\,[\,y(x)\,]+\mathbb{E}\,[\,\beta(x)\,]\\ &= \mathbb{E}\,[\,y(x)\,]+0\end{aligned}\right\}\ x\in\mathcal{X}_k$$
$$= \frac{1}{N_k}\sum_{x_i\,\in\,\mathcal{X}_k}^{N_k} y(x_i),$$

which is simply the average of the observed graylevels for the pure tissue k.

B. Identifying Pure Tissue Voxels

Second, we need to estimate the set of pure voxels $\mathcal{X}_k$. In fact, we should consider K different sets, corresponding to the K tissues in the image. This then entails a coarse image segmentation. However, we must construct conservative sets, which exclude non-pure voxels, because we cannot estimate their ideal signal.

Since this aspect is not the primary focus of the paper, further details are omitted here. It will suffice to conclude that we identify K sets of pure voxels $\{\mathcal{X}_1,\ldots,\mathcal{X}_K\}$ based on graylevel clustering. In each set, we then assume that all variation in graylevel is attributable to the bias field.

C. Least-Squares Model Fitting

Finally, we need to resolve the parameters a which minimize Q, yielding an estimate of the bias field

$$\hat{\beta}(x) = \Psi(x,a).$$

For now, we will return again to the single-tissue case, but the following process can (and should) be repeated for all tissues. The estimated bias images from each tissue $\hat{\beta}_k(x)$ can subsequently be averaged.

We assume the estimation problem for vector a can be solved iteratively, starting from a reasonable estimate $a[0]$. That is, we desire an update vector $\delta[n]$ such that the update

$$a[n+1] \;\leftarrow\; a[n]+\delta[n] \tag{3}$$

minimizes Q quasi-asymptotically.

To define δ (we omit the increment index $[n]$ for clarity), we begin by approximating changes in the parametric equation using its linearisation:

$$\Psi(x,a+\delta) \approx \Psi(x,a) + \underbrace{\frac{\partial\Psi(x,a)}{\partial a}}_{J}\delta, \tag{4}$$

where J denotes the Jacobian matrix of Ψ with respect to a:

$$J(x,a) = \begin{bmatrix} \frac{\partial\Psi(x_1,a_1)}{\partial a_1} & \cdots & \frac{\partial\Psi(x_1,a_M)}{\partial a_M}\\ \vdots & \ddots & \vdots\\ \frac{\partial\Psi(x_N,a_1)}{\partial a_1} & \cdots & \frac{\partial\Psi(x_N,a_M)}{\partial a_M}\end{bmatrix}.$$

We can then rewrite the energy function (2) including the desired increment δ,

$$Q(a+\delta) \approx \sum_{x_i\,\in\,\mathcal{X}_k}^{N_k}\big[y(x_i)-f_k-\Psi(x_i,a)-J(x_i,a)\delta\big]^2.$$

Now, to find δ which minimizes Q, we will set the derivative of $Q(a+\delta)$ with respect to δ to zero.

Before continuing, let us simplify notation by representing sets as vectors. We will also forgo denoting the tissue index k, since each tissue is treated independently. Let $\mathbf{y}$ be the vector of observed graylevels for the tissue, after subtracting the estimated ideal graylevel $\hat{f}_k$,

$$\begin{aligned}\mathbf{y} &= y(\mathcal{X}_k)-\hat{f}_k\\ &= \begin{bmatrix} y(x_1)-\hat{f}_k\\ \vdots\\ y(x_{N_k})-\hat{f}_k\end{bmatrix},\quad x\in\mathcal{X}_k.\end{aligned}$$

Similarly, we define $\mathbf{\Psi}$ as the vectorized values of $\Psi(\mathcal{X}_k,a)$, and $\mathbf{J}$ as the Jacobian of $\mathbf{\Psi}$.

Rewriting the energy function using this notation, we have

$$\begin{aligned}Q(a+\delta) &\approx \|\mathbf{y}-\mathbf{\Psi}-\mathbf{J}\delta\|^2\\ &= [\mathbf{y}-\mathbf{\Psi}-\mathbf{J}\delta]^T[\mathbf{y}-\mathbf{\Psi}-\mathbf{J}\delta]\\ &= [\mathbf{y}-\mathbf{\Psi}]^T[\mathbf{y}-\mathbf{\Psi}]-2[\mathbf{y}-\mathbf{\Psi}]^T\mathbf{J}\delta+\delta^T\mathbf{J}^T\mathbf{J}\delta.\end{aligned}$$

Setting the derivative $dQ/d\delta$ to zero, we obtain

$$[\mathbf{J}^T\mathbf{J}]\delta = \mathbf{J}^T[\mathbf{y}-\mathbf{\Psi}].$$

Then, isolating for δ, we have

$$\begin{aligned}\delta &= [\mathbf{J}^T\mathbf{J}]^{-1}\mathbf{J}^T[\mathbf{y}-\mathbf{\Psi}]\\ &= [\mathbf{J}^T\mathbf{J}]^{-1}\mathbf{J}^TQ(a),\end{aligned}$$

which is the definition of an increment from the Gauss-Newton minimization algorithm.

This definition of δ would suffice were it not for poor convergence speed in nonlinear problems. As remedy, the Levenberg-Marquardt method proposes to hybridize this increment with the gradient descent increment, which is simply

$$\delta = \mathbf{J}^TQ(a).$$

Using Marquardt's contribution, the gradient descent increment δ is also adjusted by the curvature, using

$$\mathbf{J}^TQ(a) \;\;\rightarrow\;\; \mathrm{diag}(\mathbf{J}^T\mathbf{J})^{-1}\mathbf{J}^TQ(a),$$

so that directions of small gradient are traversed faster.

Finally, the hybridization employs a parameter λ to control the influence of gradient descent over the Gauss-Newton method, yielding

$$\begin{aligned}\delta &= [\mathbf{J}^T\mathbf{J}+\lambda\,\mathrm{diag}(\mathbf{J}^T\mathbf{J})]^{-1}\mathbf{J}^TQ(a),\\ &= [\mathbf{J}^T\mathbf{J}+\lambda\,\mathrm{diag}(\mathbf{J}^T\mathbf{J})]^{-1}\mathbf{J}^T[\mathbf{y}-\mathbf{\Psi}].\end{aligned} \tag{5}$$

Thus, we have derived a definition for δ which depends on a. Therefore, given a reasonable initialization of $a[0]$, we can iterate Equation (3) until some convergence criteria are met, yielding an estimate of the bias field $\hat{\beta}_k(x)$ for each tissue k. These estimates can then be averaged to give $\hat{\beta}(x)$.

D. Artifact Removal

For completeness, we conclude by showing how to remove the estimate bias image $\hat{\beta}(x)$ from the observed image $y(x)$, yielding the estimated ideal signal $\hat{F}(x)$ which we desire:

$$\hat{F}(x) = e^{\left(y(x) - \hat{\beta}(x)\right)}.$$

IV. Experiments

To demonstrate the methods presented, we apply a known bias field and additive noise to an ideal synthetic MRI image (from [2]), and estimate the bias field. We simplify the problem by defining and estimating the bias field using the same model – i.e. $\Psi(x, a)$ can equal $\beta(x)$ exactly. The model is a simple additive linear function in x:

$$\beta(x) = \Psi(x, a) = a_0 + a_1 \mathrm{x}_1 + a_2 \mathrm{x}_2 + a_3 \mathrm{x}_3. \qquad (6)$$

The experimental procedure is as follows:

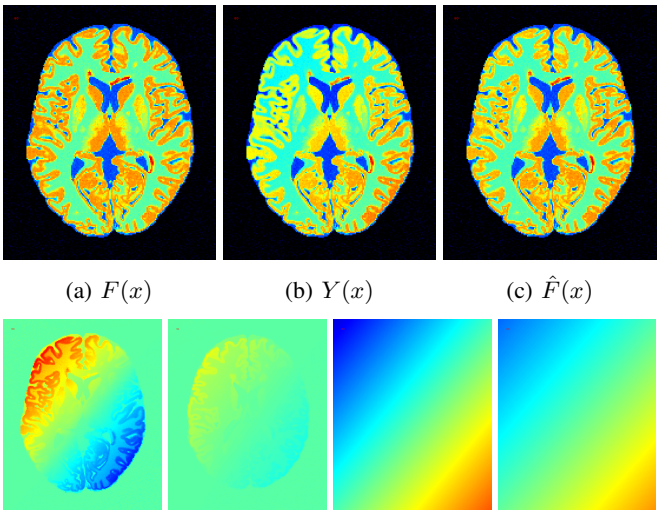
1) Define the true image $F(x)$, the true parameters a, and generate the true bias field image $\beta(x)$ using (6).
2) Create the "observed" image $Y(x) = F(x)B(x)$.
3) Perform a coarse image segmentation to define three sets of pure tissue voxels $\mathcal{X}_1, \mathcal{X}_2, \mathcal{X}_3$ (corresponding to gray matter, white matter, and cerebrospinal fluid).
4) For each tissue, estimate the bias field $\hat{\beta}_k(x)$, initializing $a[0] = [1\ \ 0\ \ 0\ \ 0]$.
5) Average the results for all tissues, and remove the estimated artifact $\hat{\beta}(x)$.
6) Compare the ideal and estimated bias field images, and the ideal and estimated anatomical images.

To generate $F(x)$, mean image graylevels were 0.6 for gray matter, 0.4 for white matter, 0.2 for cerebrospinal fluid, and 0.8 for an outlier lesion class (not used for bias field estimation). Normally-distributed noise was also added to the image with a standard deviation of 0.01. The true parameter vector a was defined as $a = [0.7\ \ 0.2\ \ 0.2\ \ 0.2]$.

V. Results

Since the given definition of Ψ results in an exact linearisation (4), it was not necessary to employ the Levenberg-Marquardt hybridization here. Setting $\lambda = 0$ resulted in convergence in one update.

The estimated vector $\hat{a}$ is given in Table I, where we see that the parameters are generally underestimated due to imperfect selection of pure tissue voxels $\mathcal{X}_k$. It is worth noting, however, that in any model with an "intercept" parameter a_0, the estimated value does not matter, since it equates to a global graylevel scaling, which does not affect the contrast in the image.



(a) $F(x)$ (b) $Y(x)$ (c) $\hat{F}(x)$

(d) $F(x) - Y(x)$ (e) $F(x) - \hat{F}(x)$ (f) $B(x)$ (g) $\hat{B}(x)$

Fig. 1: Synthetic MRI axial slices showing correction of a simulated bias field. The top row colour scale spans $[0, 1]$, the bias image colour scale spans $[0.7, 1.3]$, and the difference image colour scale spans $[-0.1, +0.1]$.

TABLE I: Applied and estimated bias field model parameters

	a_0	a_1	a_2	a_3
Applied	0.7	0.2	0.2	0.2
Estimated	−0.20	0.12	0.14	0.14

Lastly, Figure 1 depicts one slice from the original, bias-corrupted, and corrected images, as well as the the difference images, and the true and estimated bias field images. The visual results corroborate Table I, as the estimated artifact is less severe than the true artifact, but overall similar.

VI. Conclusions

We have presented a framework for modelling and estimating bias field in MR images. Two basic assumptions underpin the approach: 1) the artifact image can be approximated using a parametric equation; 2) graylevel variation in pure tissues is attributable to bias field.

Using these assumptions, we derive the least-squares update equation for an iterative estimation of model parameters. We then show how to remove the estimated artifact, and hopefully recover the uncorrupted image. Finally, we demonstrate the procedure on a simulated brain MRI.

References

[1] U. Vovk, F. Pernuš, and B. Likar, "A review of methods for correction of intensity inhomogeneity in MRI," *IEEE Transactions on Medical Imaging*, vol. 26, no. 3, pp. 405–421, Mar. 2007.

[2] D. Collins, "Design and construction of a realistic digital brain phantom," *IEEE Transactions on Medical Imaging*, vol. 17, no. 3, pp. 463–468, 1998.