Correction of Dynamic Intensity Inhomogeneity in MR Images

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Abstract. In magnetic resonance imaging (MRI), image intensity inhomogeneity hampers the quantitative analysis, e.g. segmentation or registration. Intensity inhomogeneity is an effect perceived as a smooth variation in intensities across the image. This study provides an efficient, fully automated intensity inhomogeneity correction method that makes no a priori assumptions on the image intensity distribution and is able to correct intensity inhomogeneity with high dynamics. The proposed iterative framework enables incorporation of intensity as well as spatial image features, which are used to compute the force in each image point so that probability distribution of features will condense along the intensity feature. Extensive regularization of forces produces a smooth inhomogeneity correction estimate, which is gradually improved in each iteration. The method was tested on simulated and real MR images for which gold standard segmentations were available. The results showed that the method was successful on all images, having either none, lower or even highly dynamic intensity inhomogeneity.

Keywords: intensity inhomogeneity, shading, bias correction, MRI

1 Introduction

Image intensity inhomogeneity, also referred to as bias field, intensity nonuniformity or shading, is perceived as a smooth variation of intensity across the image. In MRI, intensity inhomogeneity may be induced by a number of factors, such as poor radio frequency coil uniformity, static field inhomogeneity, radio frequency penetration, gradient-driven eddy currents, and overall patient anatomy and position [1]. Intensity inhomogeneity correction is not trivial because it depends on the measured object and thus cannot be eliminated by scanner calibration. Therefore, intensity inhomogeneity has to be corrected retrospectively, which is a common pre-processing step in many automatic image analysis tasks, e.g. in segmentation and registration, especially if the quantitative analysis is the final goal.

The most intuitive approach for intensity inhomogeneity correction is image smoothing or homomorphic filtering [2, 3]. The methods of the kind are based on the assumption that intensity inhomogeneity is a low-frequency signal which can be suppressed by high-pass filters. However, since the imaged objects themselves usually contain low frequencies, filtering methods often fail to produce meaningful correction. Iterative optimisation that maximises the frequency content of the distribution of tissue intensity has been proposed in [4].

In [5] bias field is estimated by fitting splines to the intensities at points selected inside the anatomical structure of interest. Styner et al. [6] modelled each tissue by its mean intensity and standard deviation. A parametric bias field is fitted to the image by a non-linear energy minimisation process, which requires initialisation in the form of class means and standard deviations that have to be defined for each type of images. The information minimisation technique [7] has
proved to be a robust and accurate approach by which the bias field is modelled by polynomials and applied to acquired image in an optimisation process. The method based on fuzzy C-means [8] minimises the sum of the class membership function and the first and second order regularisation terms that ensure the smooth bias field. Other segmentation-based methods use expectation-minimisation algorithm to compute the bias field from the residue image by either spatial filtering [9] or by weighted least-squares fit of the polynomial bias model [10]. These methods interleave classification and bias field estimation [9] and also the estimation of class-conditional intensity distribution [10] but require initialisation, which is nontrivial and impractical. Besides, the assumption on normality of intensity distribution of individual tissues may often not be valid, especially when correcting pathological data.

In this paper we propose a novel, fully automated non-parametric bias correction method that makes no assumption on the distribution of image intensities. As most of the existing methods, the proposed method is based on intensity features but, to improve bias correction and to make it more dynamic, additional spatial image features are used. The term dynamic addresses increased local variability of the bias field, where the frequency ranges several times higher than usual. In the existing methods, bias fields are commonly modelled by polynomials [6, 7] or B-splines [4, 11, 12], which dynamics depends on polynomial order or node distances, respectively. Increasing the dynamics of the bias correction fields would require either higher polynomial orders or an increased number of nodes, which could lead to diminished accuracy or convergence problems and significantly increase computation times. To overcome these difficulties, we compute local estimations of intensity inhomogeneity (voxel forces) from a two-dimensional feature space in which intensity and spatial information are combined. Bias correction is obtained by spatial regularisation of the local estimates, which improves accuracy and robustness of local estimation, which reflects also in better convergence.

2 Method

Corruption of intensity homogeneity in MR imaging is a multiplicative phenomenon that is most commonly described by the following model:

\[ u(x) = v(x)s(x) + n(x) \]  

(1)

in which the acquired image \( u(x) \) is a combination of the uncorrupted image \( v(x) \), corrupted by the multiplicative bias field \( s(x) \), and statistically independent noise \( n(x) \). The problem of correction of intensity inhomogeneity is to estimate \( v(x) \), given the acquired image \( u(x) \). The proposed method is based on the assumptions that statistically independent noise \( n(x) \) can be neglected and \( s(x) \) is a smoothly varying function of location. A further assumption is the possibility to invert intensity homogeneity corruption, having only the intensity distribution of \( u(x) \).

The proposed method can be outlined in four steps:

S1. Calculate the probability distribution \( p(.) \) of image features.
S2. Estimate the forces that will condense \( p(.) \) along the intensity feature.
S3. Estimate the bias correction field.
S4. Perform partial correction. Stop if a predefined number of iterations is reached, otherwise go to S1.

The above steps are described in more detail in the following sections. Fig. 1 shows the outputs of steps 1 to 4 for a MRI PD image.

Figure 1. Clockwise: simulated PD image, feature space of intensities \((i)\) and second derivatives \((d)\), forces in image domain (bright and dark pixels indicate different magnitudes of positive and negative forces), and bias correction field.

2.1 Probability Distribution Calculation

Probability distribution of image features \( p(i,d) \) is determined by binning the intensities \((i)\) and the corresponding second spatial derivatives \((d)\) into a discrete two-dimensional feature space. The second derivatives are obtained by convolving the original image by the Laplacian operator, which was implemented as a \(3\times3\) kernel and applied separately for each slice.

The purpose of using additional image features in a form of second derivatives is to additionally separate tissue...
clusters in the feature space. This is especially important when image intensities are not sufficiently discriminating features, i.e. when intensity distributions of distinct tissues overlap significantly. This adverse and unfortunately quite frequent phenomenon in MRI is the main source of error in segmentation and inhomogeneity correction methods.

2.2 Force Estimation

To condense probability distribution \( p(i,d) \) of each distinct tissue of \( u(x) \), we derive intensity correction force \( F_x \) for each image point \( x \). The force \( F_x \) should accordingly correspond to the extent to which the intensity of \( x \) should be brightened or darkened. For this purpose, we use a global energy, say \( E \), measuring the probability distribution dispersion in a form of Shannon entropy \( H \):

\[
E = H(u(x)) = - \sum_{i,d} p(i,d) \ln p(i,d).
\]

(2)

The entropy \( H \) is usually computed as above by summation of the uncertainties \( \ln p(i,d) \) in the feature space domain but since we are seeking a contribution of each image point \( x \) to the global entropy, we will compute the entropy alternatively by summation of the uncertainties over the image domain of a size \( X \):

\[
E = H(u(x)) = - \frac{1}{X} \sum_{i,d} \ln p(i(x),d(x)).
\]

(3)

We can now derive point energy, say \( E_x \), which is the contribution of each image point \( x \) to the global energy \( E \):

\[
E_x = - \frac{1}{X} \ln p(i(x),d(x)).
\]

(4)

\( E_x \) is, therefore, the contribution of image point \( x \) to the dispersion of probability distribution \( p(i,d) \). The corresponding point force \( F_x \), that will condense the probability distribution \( p(i,d) \) along the intensity feature \( i \), can thus be obtained by partial derivation of \( E_x \) over the intensity:

\[
F_x = - \frac{\partial E}{\partial i} = \frac{1}{X} \frac{\partial}{\partial i} \left( \ln p(i(x),d(x)) \right).
\]

(5)

Forces \( F_x \) are computed by the Sobel operator in the feature space for all feature pairs \((i,d)\) and then mapped to the points with corresponding features in the image space. The obtained forces can be interpreted as votes for point intensity changes that would result in a less disperse probability distribution. Next, we will use these forces to obtain a smooth estimation of the bias correction field.

2.3 Bias Correction Estimation

To control the speed of the iterative bias correction and to make it independent of the shape of feature probability distributions, point forces \( F_x \) are first normalized in magnitude. The normalized forces are then regularized in the image domain by a Gaussian kernel \( g \). This yields a smooth field of normalized forces that are used to derive an estimation of the multiplicative bias correction field \( s^{-1}(x) \):

\[
s^{-1}(x) = 1 + \left( f \frac{F_x}{\mu(|F_x|)} \right) \ast g
\]

(6)

where \( \mu(|F_x|) \) denotes the mean absolute force, \( f \) a predefined magnitude of forces, and \( \ast \) the convolution. Smoothness of the bias correction field \( s^{-1}(x) \) is determined by the standard deviation \( \sigma_g \) of the Gaussian kernel \( g \). To reduce the high computational cost of convolution, sub-sampling by a factor of 3 in each dimension was implemented. This resulted in a significant acceleration and insignificant performance deterioration since the bias field does not contain high frequencies.

2.4 Partial Correction

Partial bias correction is performed in each iteration, say \( n^{th} \), by applying the bias correction field \( s^{-1}(x) \) to the input image \( u_n(x) \) so that mean intensity \( \mu(u_n(x)) \) (brightness) and standard deviation \( \sigma(u_n(x)) \) (contrast) of the input image are preserved:

\[
u_n(x) = u_n(x)s^{-1}(x) \frac{\sigma(u_n(x))}{\sigma(u_n(x))s^{-1}(x)},
\]

(7)

\[
u_n(x) \Leftarrow u_n(x) + \mu(u_n(x)) - \mu(u_n(x)).
\]

(8)

The extend of partial correction depends on the predefined magnitude of force \( f \) and the standard deviation \( \sigma_g \) that controls the regularization, i.e. the smoothness of the bias correction field.
3 Results

Removal of the background in MRI images is essential in nearly all inhomogeneity correction methods because the background represents air voxels that are not corrupted by the multiplicative bias field and would therefore hamper inhomogeneity correction of the neighbouring tissue voxels. To mask out dark air voxels, we remove all voxels with intensities smaller than the predefined intensity threshold, which is the simplest and most commonly used approach [7, 4, 10].

To demonstrate and evaluate the performance of the proposed method, we applied it to several simulated and real magnetic resonance images of the human brain.

In the first set of images, variations of the digital brain phantom acquired from the BrainWeb-MRI Simulator [13] were considered: six pairs of volumes with 3% Gaussian noise, including T1-, T2- and PD-weighted MR images, normal and multiple sclerosis (MS) cases (T1, T2 and PD indicate pulse sequence types set on a MR scanner machine). Each pair comprised inhomogeneity free volume and corresponding corrupted version with 40% intensity inhomogeneity. The resolutions were 181×217×181 voxels, sized 1×1×1 mm³.

In the second set of images, extra bias fields with more dynamics were added to all the images from the first set. Bias fields were generated by cubic B-spline interpolation between equally spaced nodes at every 50 voxels in each direction. Node values (multiplication factors) were randomly distributed on the interval between 0.8 and 1.2.

The third set consisted of six volumes (T1, T2 and PD), three of a normal volunteer (256×256×25 voxels, 8bit) and three of a tumour patient (256×256×20 voxels, 8bit, slice thickness of 5mm, in plane resolution of 1×1 mm²). 

Volumes of the second set were used to show the capability of our method to successfully cope with bias fields, which have a high degree of dynamics. Changing the size of the regularization kernel has a direct impact on the estimated fields. Reducing the kernel size makes the fields more locally flexible, but loses a part of its regularization functionality. The effect of regularization of the kernel size on the shape of the reconstructed bias field is shown in Fig. 2. Image (a) indicates the position of the bias field profiles shown on the images (b) and (c). Solid lines indicate the generated bias field and dashed lines the corresponding reconstruction after inhomogeneity correction. Standard deviations of the regularization kernels were set to 30 pixels in case (b) and to 90 pixels in case (c). In the first case high correlation between the applied and reconstructed bias fields was found, while in the second case the correlation was poor due to too high regularization.

\[
c_{jv}(GM, WM) = \frac{\sigma(GM) + \sigma(WM)}{|\mu(GM) - \mu(WM)|},
\]

Figure 2. Image (a) shows the profile position, (b) and (c) the applied (solid curve) and reconstructed bias field (dashed curve) for the regularization of 30 and 90 mm, respectively.

Quantitative evaluation was performed by computing the coefficient of joint variations \(c_{jv}\) [7] between grey (GM) and white matter (WM) of the brain for which gold standard segmentations were available. \(c_{jv}\) is computed from standard deviations \(\sigma\) and mean values \(\mu\) of the voxel intensities belonging to the two matters:

\[
c_{jv}(GM, WM) = \frac{\sigma(GM) + \sigma(WM)}{|\mu(GM) - \mu(WM)|}.
\]

The measurement is independent of the changes in contrast and brightness and measures the intensity inhomogeneity in the sense of minimizing the intensity overlapping between two tissues.

In Table 1, results of inhomogeneity correction in the first set of images are given. The four columns describe the volume properties (modality, bias field and pathology) and starting, final and ideal \(c_{jv}\) values. The method successfully corrected the first six volumes and
Correction of Dynamic Intensity Inhomogeneity in MR Images

The results of inhomogeneity correction in the second set of images are given in Table 2. The proposed method successfully corrected the inhomogeneities with high dynamics. Final \( c_jv \) values did not match the ideal ones as perfectly as in the first set, because the induced bias fields could not be exactly reconstructed by Gaussian convolution. Nevertheless, the results of inhomogeneity corrections are very close to ideal.

Table 3 shows results on real MR volumes of the third set. The volumes without intensity inhomogeneity were not known so that the extent of the achieved correction cannot be determined. The last column states the relative change of \( c_jv \) value, where it can be seen that improvement was achieved in all volumes.

The algorithm was implemented in Matlab 5.3 where each correction took approximately 60 seconds on a Pentium IV 1.4GHz computer. Figure 3 shows the \( c_jv \) values of every iteration slowly approaching their final values.

The proposed fully automated bias correction method makes no assumption on the distribution of image intensities and provides non-parametric correction. No \textit{a priori} knowledge, such as digital brain atlases or reference points, is needed. Spatial image features are incorporated in addition to the commonly used intensity features, which give the method enough information to successfully correct even highly dynamic bias fields.

The performance depends on the overlap between the probability distributions of image features, which should be small. The proposed correction framework, however, enables straightforward incorporation of additional image features that could yield an additional discriminative power and improve the correction performance on the images of poor quality. Examples of additional features would be digital brain atlas or any complementary modality providing helpful information.

The method was implemented on MR images, but it could also be used on any type of images with multiplicative nature (Eq. (1)) of the homogeneity corruption process.
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References


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