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Simplified PCNN Based MR Images Grayscale Inhomogeneity Real-Time Calibration

Changtao He, Fangnian Lang, Hongliang Li and Haixu Wang
University of Electronic Science and Technology of China, Institute of Electronic Engineering, Chengdu, 611731, People's Republic China

Abstract: Grayscale inhomogeneities in Magnetic Resonance (MR) images can cause some difficulties in automated quantitative image processing and analysis. In order to remove such inhomogeneities in MR images, some researchers have employed various methods. In this study, we propose a novel bias field estimation method based on simplified Pulse Coupled Neural Network (PCNN). MR images pre-processing makes full use of PCNN's visual characteristics and provides an efficient iterative method for MR images bias field estimation. Finally, we use estimated bias field to reconstruct simulation images. The proposed method has been successfully applied to 3-Tesla MR images with desirable results. Compared to normal images, the proposed method is effective and self-adaptive to some different slice MR images which converges to the optimal solution at a fast rate.

Key words: MR images, grayscale inhomogeneity, pulse coupled neural network, grayscale calibration

INTRODUCTION

Magnetic resonance imaging is a powerful diagnostic technique which can provide high spatial resolution, slice selection at any orientation and excellent soft tissue contrast. However, automated quantitative analysis of MR images remains a difficult problem. One impediment to automated, quantitative MR image processing and analysis is the presence of low spatial frequency grayscale nonuniformities (Brinkmann *et al*., 1998). These inhomogeneities affect the measured gray level values so that pixels representing the same tissue class have different gray levels in different regions of the image. Without question, this increases the gray scale variances of the tissue classes and brings some difficulties for image segmentation and classification (Brinkmann *et al*., 1996).

Generally speaking, bias correction methods can be broadly categorized into two classes: prospective methods (Li *et al*., 2009; Wicks *et al*., 1993) and retrospective methods (Li *et al*., 2008; Pham and Prince, 1999a; Wells *et al*., 1996). The former can only correct some of the intensity inhomogeneity caused by MR scanner, however, they are no use for sources of inhomogeneity (Likar *et al*., 2001). The later can be applied to remove patient dependant effects. Moreover, segmentation-based methods that use fuzzy C-means clustering can be found by Pham and Prince (1999b), the usage of Markov random fields was considered by Rajapakse and Kruggel (1998). Other parameter optimization based methods were introduced by Guillemaud and Brady (1997), Wells *et al*. (1996). These methods can acquire a bias field at the cost of higher computation complexity and more time-consuming, this is very adverse for real-time image analysis. In this study, has proposed a novel MR image bias field estimation method based on simplified PCNN model, this method can obtain satisfied results, while avoiding the complex calculations at a fast rate.

SIMPLIFIED PCNN MODEL

The PCNN was originally presented by Eckhorn in order to explain the synchronous neuronal burst phenomena in the cat and other little mammals' visual cortex (Eckhorn *et al*., 1990). With the development of PCNN research, it has been widely applied in the image-processing realm. The model neuron consists of three parts: dendritic tree receptive field, the linking modulation field and the pulse generator field. Now, the common PCNN model that was applied to image processing is an improved model by Lindblad and Kinser (1998) on the basis of Eckhorn proposed original model (Lindblad and Kinser, 1998). In every computational iteration, this

Corresponding Author: Changtao He, University of Electronic Science and Technology of China, Institute of Electronic Engineering, Chengdu, 611731, People's Republic China

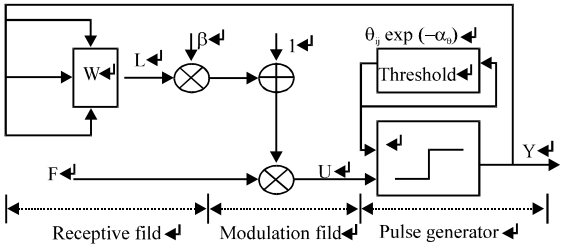

Fig. 1: Simplified PCNN neuron model

model parameters adjustment process is very inconvenient. So, in this study, we employ a simplified PCNN model, the single neuron model of simplified PCNN is shown as Fig. 1.

The mathematic expressions of this simplified PCNN system can be described as follows:

$$F_{ij} = I_{ij} \tag{1}$$

$$L_{ij}[n] = \sum w_{ijkl} Y_{kl}[n-1] \tag{2}$$

$$U_{ij}[n] = F_{ij}[n](1 + \beta L_{ij}[n]) \tag{3}$$

$$Y_{ij}[n] = \begin{cases} 1, & U_{ij}[n] > \theta_{ij}[n] \\ 0, & U_{ij}[n] \le \theta_{ij}[n] \end{cases} \tag{4}$$

$$\theta_{ij}[n] = \exp(-\alpha_\theta)\,\theta_{ij}[n-1] \tag{5}$$

where, F_{ij}, I_{ij}, L_{ij}, U_{ij}, θ_{ij} and Y_{ij} are the feeding input, external input stimulus (neuron corresponding pixel value), linking input, internal activity, dynamic threshold and output of the neuron ij, respectively; the linking coefficient w_{ijkl} among surrounding neurons is local gaussians; the constant β is the linking strength; α_θ is decay coefficient; n represent iterations. In addition, neuron neighborhood size is 3×3, each neuron can fire and create pulse only once during a pulsing cycle in the simplified model.

BIAS FIELD ESTIMATION METHOD BASED ON SIMPLIFIED PCNN MODEL

The PCNN model has a strong biological background; it has many advantageous characteristics, which are similar to human vision. In the practical image processing, the neighboring neurons stimulate its neighboring neurons to be fired in succession and will yield a pulse wave propagating far away at activation areas. For image processing, those adjacent pixels with similar intensity will incline to synchronously fire. This is the reason that we select this model to estimate MR image bias field.

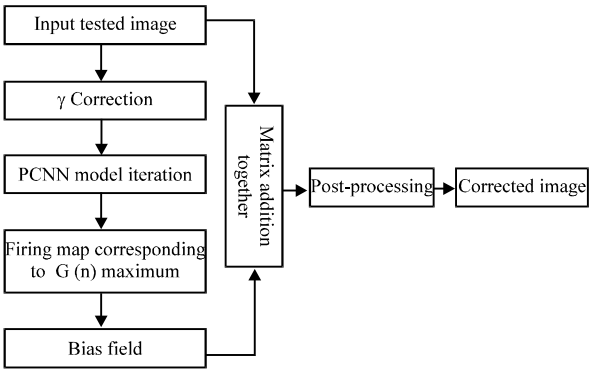

Fig. 2: The flowchart of the proposed method

Our main method is to use Pulse synchronization theory to realize clustering of Gray Matter (GM) and White Matter (WM) and adjust parameters of PCNN model to yield a satisfied result as bias field of tested image. Here, using time signature G (n) to determine whether end PCNN's iteration, we can obtain firing map corresponding to G (n) maximum as tested image's bias field. G (n) is computed as:

$$G(n) = \frac{\sum_{ij} Y_{ij}(n)}{N} \tag{6}$$

The method main process is shown in Fig. 2.

EXPERIMENTS AND RESULTS

Experiments for validating the correction method: Here, we tested the proposed correction method using two simulated MR T1-weighted images (Cocosco *et al*., 1997; Collins *et al*., 1998), one with 0% (normal image) and the other with 40% intensity non-uniformity. In Fig. 3 the recovery of the gray distribution can be observed by comparing the histograms of normal, non-uniform and corrected image. The corresponding Statistic histogram of crest value correction shows in Fig. 4.

Evaluation criteria: In order to demonstrate the proposed method's effectiveness, we must adopt some evaluation criteria to judge this method. Generally, the performance of a grayscale inhomogeneity correction method is commonly evaluated by comparing the coefficients of variations (CV) within the individual tissue classes in the original and corrected images. The CV which is invariant to the uniform multiplicative intensity transformation (Likar *et al*., 2001), is computed as follows:

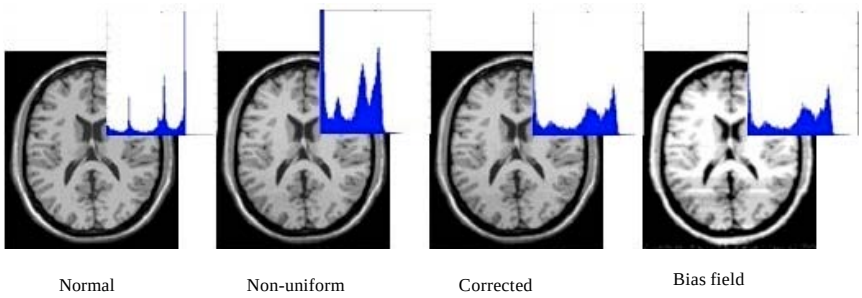

Fig. 3: Simulated normal, non-uniform (40% intensity inhomogeneity), corrected, bias field images and the corresponding histograms

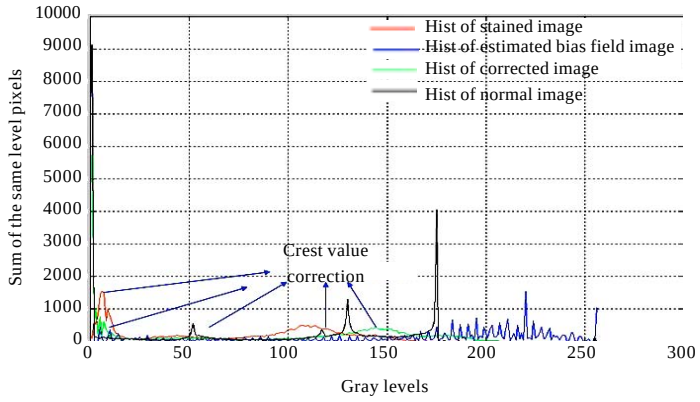

Fig. 4: Statistic histogram of crest value correction

$$cv(C) = \frac{\sigma(C)}{\mu(C)} \quad (7)$$

where, σ (C) and μ (C) are the standard deviation and mean intensity of class C, respectively. To reflect more overlap information between the intensity distributions of distinct tissue classes. We adopt the coefficient of joint variations (CJV) to estimate correction results of the proposed method in this study:

$$CJV(C_1, C_2) = \frac{\sigma(C_1) + \sigma(C_2)}{|\mu(C_1) - \mu(C_2)|} \quad (8)$$

Which is the sum of the standard deviations of two distinct classes; C_1 and C_2, the other parameters are same as the above. The CJV is invariant to the uniform linear and is more quantitative measure than the CV. The smaller of CJV index, the better of correction result.

Comparisons and analysis: To show the proposed method's robustness and self-adaption, we select additional 3T brain MR image as a real testing image, the experimental result is illustrated in Fig. 5, the corresponding histogram distributions can be seen in Fig. 6.

Table 1: Correction of simulated and real data of the testing image. CJV (GM, WM) in [%]

Image	Mod	Bias (%)	Normal	The proposed method	FCM
1-Normal (simulated)	T1	0%	8.5396	8.9301	8.9713
		40%	15.2113	8.6020	8.8643
1-Normal (real)	T1		8.3506	8.1748	8.2879

Comparing with classical fuzzy C-means clustering correction method by Pham and Prince (1999b), so-called FCM method. Quantitative evaluation of the proposed method, FCM method was performed by computing the CJV (GM,WM) of the gray and white matters for all images from the two experimental images. Table 1 includes the results of non-uniformity correction of the images from the above two images.

In general, the clustering result of FCM method is better than other clustering method. But, from

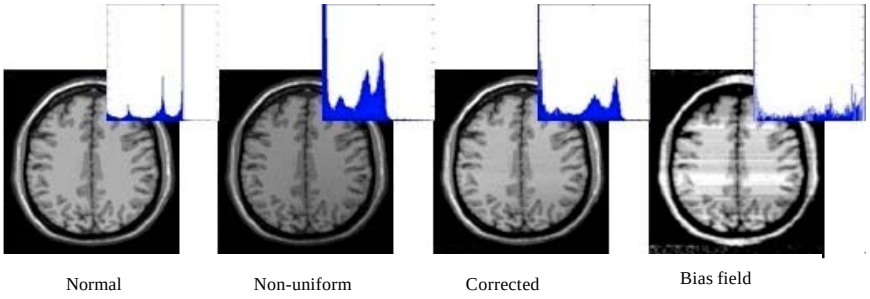

Fig. 5: Real normal, non-uniform, corrected, bias field images and the corresponding histograms

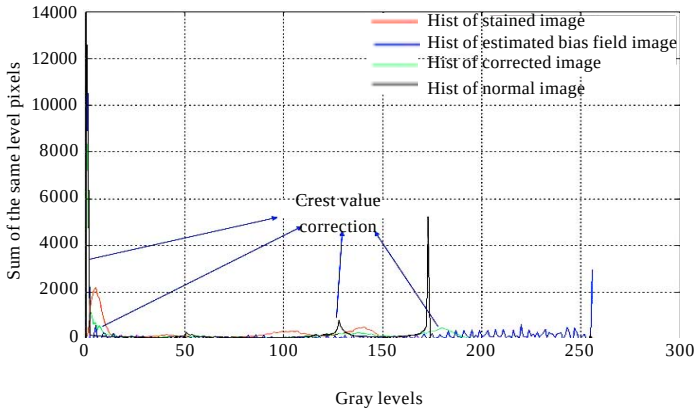

Fig. 6: Statistic histogram of crest value correction

the above data, the proposed method outperformed the FCM method in this study and was also faster than the FCM and other methods. To a simulated MR T1-weighted image, the average processing time of the proposed method is about 0.6 sec and usual clustering method is about 1.5 sec on the same processing platform.

CONCLUSION

A novel simplified PCNN model based is proposed which is used to correct intensity inhomogeneities in MRI and the iterative firing map of PCNN model as bias field which is corresponding to the time signature G (n) maximum. This method is simply and also very effective, it needn't acquire transcendental information of intensity non-uniform MR images and require no any assumptions and user interaction. The corrected results are very satisfied to simulated and real MR images at a fast rate, and I think this method is valuable tool in MR image analysis.

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