A Unifying Framework for Inhomogeneity Correction and Partial Volume Segmentation of Brain MR Images

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***Abstract* --- We propose a unifying framework for fully automated inhomogeneity correction and partial volume (PV) segmentation of multi-spectral brain magnetic resonance (MR) images. The MR data is modeled as a stochastic process with an inherent effect of smoothly varying intensity or bias field. Unlike the conventional hard segmentation methods with a unique label for each voxel, a new PV model is developed in which the percentage of each voxel belonging to each class is considered in establishing the maximum *a posteriori* (MAP) framework. A new Markov random field (MRF) model is built to reflect the spatial information for the tissue mixture. The MAP solution is calculated by the iterative expectation-maximization (EM) strategy that interleaves PV segmentation with estimations of class parameters and bias field distribution. Experimental studies on clinical MR brain datasets are performed. The results demonstrate that our unifying framework can substantially improve the performance as both bias field and PV effects have been taken into account.**

I. INTRODUCTION

To facilitate diagnosis of brain disorders, automatic and accurate segmentation of magnetic resonance (MR) images is the key prerequisite toward quantifying the volume of different tissues, i.e., white matter (WM), gray matter (GM), and cerebral spinal fluid (CSF). A number of methods have been proposed for fully-automatic segmentation of MR images in the past decades [1]-[6]. These methods model the image intensity distribution as a multivariate likelihood function. A Markov random field (MRF) *priori* is built to specify the neighborhood tissue correlation and manage the noise artifacts, therefore resulting in a robust maximum *a posteriori* (MAP) probability performance. However, these intensity-based methods belong to a category of hard segmentation, in which each voxel is classified as a single tissue type. In MR imaging, due to the limited spatial resolution of medical imaging equipment and the complex anatomic structures in the brain, the tissue border voxels are usually composed of two or more tissue types, which are called partial volume (PV) effects [7]–[10]. Therefore, segmenting each voxel as a mixel with different tissue percentages is theoretically attractive and clinical desired to minimize the PV effects among the tissue boundaries.

Another problem for automated MR image segmentation is the intensity corruption with a smooth bias field, called inhomogeneity effect. This effect is due to the non-uniformity in the radio-frequency (RF) field during MR data acquisition [11]-[12]. Several methods address this problem by charactering the inhomogeneity effect as a component of the lowest frequency of image, where an assumption is made that anatomical information has much higher spatial frequencies than that of the inhomogeneity [13]-[14]. They assume that the frequency spectrum of the bias field is separable from the tissue structures. However, recent literatures found that a good image segmentation also helps the estimation of bias field [15]-[17].

In this paper, we present a unifying framework for fully automated inhomogeneity correction and PV segmentation of MR Brain Images. It takes into account the following effects that commonly appear in MR imaging:

1) The MR data is modeled as a stochastic process with an inherent effect of smoothly varying intensity inhomogeneity.
2) A new PV model is built in establishing the MAP segmentation scheme.
3) Noise artifacts are minimized by *a priori* MRF penalty or constraint indicating neighborhood correlation for tissue mixture.

By integrating all these effects simultaneously into our framework, we aim to develop an accurate and fully automatic segmentation algorithm. The MAP solution is calculated by the iterative expectation-maximization (EM) strategy [18] that interleaves PV segmentation with estimations of class parameters and bias field distribution. The initial estimation of the parameters for the unifying framework is given by the self-adaptive vector quantization method [19]. Experimental results on clinical datasets are presented.

This work was supported in part by the National Institutes of Health (grant #CA82402), the National Multiple Sclerosis Society (grant #RG3042-A-2) and the City University of New York PSC-CUNY Award Program.

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II. METHODS

Let Γ and S be two sets: $\Gamma = \{1, 2, \ldots, K\}$ and $S = \{1, 2, \ldots, N\}$, where K is the total number of tissue classes and N is the total number of voxels in the acquired image. Let $\boldsymbol{Y}$ be a set of random variables, which represent the observed image intensities $Y = \{y_1, \cdots, y_i, \cdots y_N \,|\, i \in S\}$, and M be a set of vectors $M = \{m_1, \cdots, m_i, \cdots, m_N \,|\, i \in S\}$ with the following properties of (a) $m_i = (m_{i1}, \ldots, m_{ik})$, $k \in \Gamma$, and (b) $\sum_{k=1}^{K} m_{ik} = 1$, $0 \le m_{ik} \le 1$, where m_{ik} reflects the fraction of tissue type k inside voxel i. Each voxel value y_i in the observed image is considered as the following random process:

$$y_i = \sum_{k=1}^{K} m_{ik}\mu_k + \varepsilon_i \qquad (1)$$

where μ_k is the observed mean value of tissue type or class k when it fully fills in a voxel; m_{ik} can be defined as the probability of voxel i belonging to class k; and ε_i is assumed as Gaussian noise associated with the observation y_i at voxel i with its mean being zero and variance of ν_i. For the multi-spectral MR images, ν_i becomes a covariance matrix Σ_i.

A. Inhomogeneity Model and PV segmentation

To correct for bias field inhomogeneities during classification, we propose a MAP algorithm with a bias field β estimation step. According to the MAP criterion,

$$P(M, \beta \,|\, Y) \propto P(Y \,|\, M, \beta) P(M) P(\beta) \qquad (2)$$

where M and β are independent. It is also assumed that for $m \in M$, the random variables y_i are conditionally independent and follow a Gaussian distribution with parameters $\Phi\ \{\mu_k, \Sigma_i, k \in \Gamma, i \in S\}$. That is,

$$P(Y \,|\, M, \beta) = \prod_{i=1}^{N} p(y_i \,|\, m_i, \beta_i)$$

$$= \prod_{i=1}^{N} \left(\frac{1}{2\pi}\right)^{\frac{r}{2}} |\Sigma_i|^{\frac{1}{2}} \exp\left[-\frac{1}{2}(y_i - \beta_i \mu^T m_i)^T \Sigma_i^{-1} (y_i - \beta_i \mu^T m_i)\right] \qquad (3)$$

The prior distribution of mixture M can be derived from the MRF model of

$$p(m_i) = \frac{1}{Z} \exp\left(-\alpha \sum_{j \in N_i} \kappa_j \left\| m_i - m_j \right\|^2\right) \qquad (4)$$

where N_i denotes the neighborhood of voxel i. The bias field β can be expressed as

$$p(\beta_i) = \frac{1}{Z'} \exp\left[-\lambda_1 \sum_{k=1}^{R} (D_k * \beta)_i^2 - \lambda_2 \sum_{k=1}^{R} \sum_{j=1}^{R} (D_k * D_j * \beta)_i^2\right] \qquad (5)$$

where D_k and D_j are the standard forward finite difference operators along the different directions. The symbol * denotes the one-dimensional (1D) discrete convolution operators. The parameters λ_1 and λ_2 control the first- and second-order regularization terms of the bias field.

The iterated conditional modes (ICM) is utilized to maximize equation (2). That is, the MAP estimation is equivalent to minimizing the posterior energy function

$$U = \frac{1}{2}[y_i - \beta_i \mu^T m_i]^T \Sigma_i^{-1} [y_i - \beta_i \mu^T m_i] + \alpha \sum_{j \in N_i} \kappa_j \left\| m_i - m_j \right\|^2 + \lambda_1 \sum_{k=1}^{R} (D_k * \beta)_i^2 + \lambda_2 \sum_{k=1}^{R} \sum_{j=1}^{R} (D_k * D_j * \beta)_i^2 \qquad (6)$$

Given estimated bias field β, the energy function U in equation (6) has a quadratic property. So, we can rewrite it as follows to obtain the PV segmentation.

$$U = \frac{1}{2} m_i^T A m_i + b^T m_i + C \qquad (7)$$

$$A = [\beta_i^2 \mu \Sigma_i^{-1} \mu^T + 2\alpha \sum_{j \in N_i} \kappa_j I] \qquad (8)$$

$$b^T = -\beta_i y_i^T \Sigma_i^{-1} \mu^T - 2\alpha \sum_{j \in N_i} \kappa_j m_j^T \qquad (9)$$

where C is a constant and I is an identity matrix. On the other hand, given the estimation of m_i, the bias field can be estimated as

$$\beta_i m_i^T \mu \mu^T m_i + \lambda_1 (\beta ** H_1)^2 + \lambda_2 (\beta ** H_2)^2 = y_i \mu^T m_i \qquad (10)$$

An accurate estimation of the model parameter set Φ is necessary for the above bias field estimation and PV segmentation. In the next section, we employ the EM algorithm to estimate the model parameters Φ.

B. Parameter Estimation

Let x_{ik} be the contribution of tissue type k to the observation y_i with $y_i = \sum_{k=1}^{K} x_{ik}$. The conditional probability of x_{ik} given parameter set Φ is distributed as normal $N(\beta_i m_{ik} \mu_k, m_{ik} \sigma_k)$. This function implies that variance σ_i over the whole volume image is smooth and has the property of $\sigma_i = \sum_{k=1}^{K} m_{ik} \sigma_k$.

The EM algorithm seeks a solution for the model parameters Φ by interleaved Expectation and Maximization steps in an iterative manner. Then, we obtain, at each iteration t,

$$\mu_k^{(t+1)} = \frac{\sum_i x_{ik}^{(t)}}{\sum_i \beta_i m_{ik}} \quad (11)$$

$$\sigma_k^{(t+1)} = \frac{1}{N}\sum_i \frac{(x_{ik}^{2(t)} - 2m_{ik}\beta_i\mu_k^{(t+1)}x_{ik}^{(t)} + m_{ik}^2\beta_i^2\mu_k^{(t+1)2})}{\beta_i m_{ik}} \quad (12)$$

which x_{ik} and x_{ik}^2 are given by:

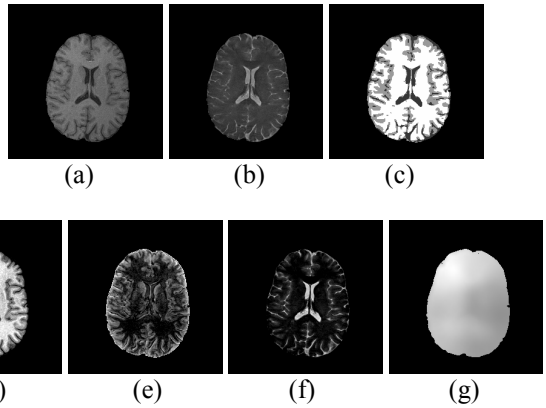
$$x_{ik}^{(t)} = \beta_i m_{ik}\mu_k^{(t)} + \frac{m_{ik}\sigma_k^{(t)}}{\sum_{j=1}^K m_{ij}\sigma_j^{(t)}} \cdot (y_i - \sum_{j=1}^K m_{ij}\beta_i\mu_j^{(t)}) \quad (13)$$

$$x_{ik}^{2(t)} = x_{ik}^{(t)2} + \beta_i m_{ik}\sigma_k^{(t)} \frac{\sum_{j\neq k}^K m_{ij}\sigma_j^{(t)}}{\sum_{j=1}^K m_{ij}\sigma_j^{(t)}} \quad (14)$$

III. EXPERIMENTAL RESULTS

Six patients were recruited (age range 20-55 years old) in this study. MRI sessions were performed using a 1.5 Tesla Philips Edge whole-body scanner with a body coil as the transmitter and a birdcage head coil as the receiver. A 3D SPGR sequence was employed to acquire T_1-weighted axial images covering the whole brain with 30° flip angle, T_E = 5 ms, T_R = 30 ms, 1.5 mm slice thickness, 24 cm field-of-view (FOV), and 256x256 matrix size. A 3D EXPRESS sequence with fat suppression was used to collect T_2-weighted axial images with the same acquisition location and parameters, except for T_E = 95 ms, T_R = 4000 ms, and ETL = 136. These two scans were performed sequentially with the subject lying in the same position in the coil. The multi-spectral images were registered well in the spatial domain. The total MR data acquisition time was less than 40 minutes.

The self-adaptive vector quantization method was applied first to remove the skull and scalp and extract the corresponding brain mask. In the meantime, the initial model parameters have also obtained. Following that, we applied the unifying framework for PV segmentation and bias field estimation. We compared our new framework with conventional MAP-MRF hard segmentation method. Figure 1(a) and 1(b) show the T_1- and T_2-weighted images. Figure 1(c) shows the hard segmentation results from conventional MAP-MRF. Figure 1(d)-(f) show the PV segmentation results with inclusion of bias field correction for brain tissues of white matter (WM), gray matter (GM), and cerebral spinal fluid (CSF). Figure 1(g) shows the corresponding bias field estimation by our framework. It is shown that our new method reflects more accurate anatomic information among different tissue boundaries.



(a) (b) (c) (d) (e) (f) (g)

IV. DISCUSSION AND CONCLUSIONS

We have developed a unifying framework for fully automated inhomogeneity correction and PV segmentation of MR brain Images. The initial estimation of the parameters for the unifying framework is given by the self-adaptive vector quantization scheme. The iterative convergence is guaranteed by the MRF model. Studies on clinical datasets showed its potential in performing accurate segmentation. Further evaluations by a large number of clinical datasets for correlation studies are under progress.

ACKNOWLEDGMENT

The authors wish to thank Dr. Wei Huang and Dr. Alina Tudorica for the acquisition of the MR images.

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