Segmentation of Gray- and White Matter on MR Brain Images in Multiple Sclerosis

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Introduction: Accurate classification of gray matter (GM) and white matter (WM) is an important step in the estimation of atrophy of these two tissues in Multiple Sclerosis (MS). However, even when the slice thickness is relatively small, the partial volume averaging between different tissues often results in false classifications and affects the estimated volumes. In order to minimize this problem, a technique based on partial volume averaging along with the bias field correction is presented to improve the classification of GM and WM in MS.

Image Acquisition: MR brain images of 14 clinically definite relapsing remitting MS subjects with median age 44 yrs (range: 23-49 yrs) were acquired on a 3T Philips intera scanner with a quaser gradient system with a sense factor of 2. As a part of the protocol, dual FSE images with TE1/TE2/TR=7.2/90/6800 ms, contiguous and interleaved 3mm slices, and FLAIR images with TR=10000 ms, TI=2600 ms and TE=80 ms, matrix 256x256 with a field of view 240 mm x 240 mm were acquired.

Methods: Prior to segmentations, MR images were preprocessed that included co-registration of FLAIR with FSE images, RF correction, anisotropic diffusion filtration, removal of extrameningeal tissues, and intensity normalization. The dual FSE and FLAIR images were segmented into parenchyma, CSF, and lesions using a Parzen window classifier [1]. The parenchyma was segmented into GM and WM using FSE images iteratively with the bias field correction based on the methods described in [2, 3]. In order to account for the partial volume averaging, we assume L to represent the set of predefined labels into which the whole parenchyma needs to be classified. It is assumed that the observed intensity at voxel i, given class labels x, follows multivariate Gaussian distribution with parameters $\theta(x_i = j) = (\mu_j, \Sigma_j)$,

$$p(y_i \mid x_i) = g(y_i; \theta(x_i)) = \frac{1}{(2\pi)^{n/2}\left|\Sigma_j\right|^{1/2}} \exp\left\{-\frac{1}{2}(y_i - \mu_j)^T \Sigma^{-1}(y_i - \mu_j)\right\},$$

where, $\mu_j = \alpha\mu_g + (1-\alpha)\mu_w$ and $\Sigma_j = \alpha\Sigma_g + (1-\alpha)\Sigma_w$, α and $(1-\alpha)$ are the fractions corresponding to GM and WM tissues present in class j. Parameters μ_g, μ_w, Σ_g, and Σ_w represent the mean vectors and covariance matrices corresponding to GM and WM classes. Class labels were estimated using a *maximum a posteriori* principle,

$$\hat{x} = \arg\max_x \; p(y \mid x)\, p(x).$$

A Markov Random Field (MRF) model was considered for the class labels with prior probability $p(x) = \exp(-U(x))/Z$, where Z is a normalizing constant. An expectation maximization (EM) algorithm proposed by Leemput et al. [2] was implemented to estimate the class labels. The expectation step calculates the conditional expectation $Q(\theta|\theta^{(m)}) = E[\log p(y, x|\theta)|y, \theta^{(m)}]$ and maximization step maximizes the function $Q(\theta|\theta^{(m)})$ which provides the estimation for x as $\theta^{(m+1)} = \arg\max_\theta Q(\theta|\theta^{(m)})$.

In the presence of bias, given the class labels x, it is assumed that the observed intensity y_i at voxel i follows the Gaussian distribution, $p(y_i|x_i, b) = g(y_i - b_i; \theta(x_i))$. Bias field was estimated using a *maximum a posteriori* principle proposed by Wells et al. [3].

$$\hat{b} = \arg\max_b \; p(y \mid b)\, p(b),$$

where the intensity distribution is modeled as Gaussian mixture given the bias field, $p(y_i|b) = \sum_{j\in L}\{g(y_i - b_i; \theta(j))P(j)\}$. Finally, the class labels were classified as GM or WM based on the largest proportion of these tissues present in these classes. False lesion classifications were minimized followed by lesion delineation using fuzzy-connectivity [1].

Results and Discussion: Figure 1 shows the short echo FSE (proton density or PD) (A), long echo FSE or T2 (B), and FLAIR (C) images. Initially the whole brain was segmented into cerebrospinal fluid (CSF), parenchyma and lesions (D). Parenchyma was further segmented into GM and WM (E) using the method described in [1, 4] followed by the minimization of false lesion classifications and lesion delineation using fuzzy connectivity [1]. Segmentation of parenchyma into GM and WM, after accounting for the partial volume averaging as described above, is shown in Fig. 1F. Fig. 2 shows the section of cerebellum from the same subject. For the segmentation of GM and WM, (m+1), where m is odd, class labels with tissue fractions α = 0, 1/m, 2/m, …, (m-2)/m, (m-1)/m, 1 were considered. In the final classification, the class labels with α = 0, 1/m, …, (m-1)/2m were classified as WM and those with α = (m+1)/2m, …, (m-1)/m, 1 were classified as GM. As can be seen in this figure, without taking the partial volume averaging into account, part of the WM was classified as GM (E). However, the above procedure considerably reduced this false classification (F). The average volumes of GM and WM in 14 subjects without including the partial volume averaging effects were 566.13 cc and 404.46 cc respectively, and the corresponding volumes following the correction were 495.89 cc and 470.27 cc.

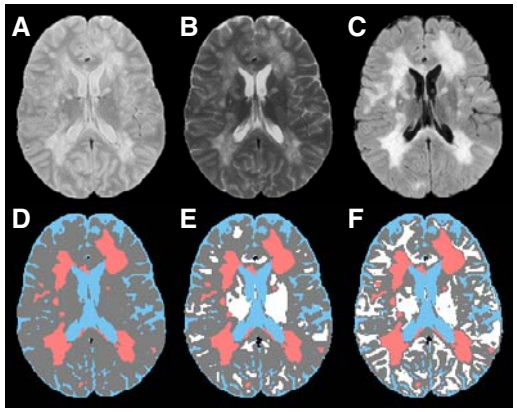

Fig. 1: A-C: PD, T2, FLAIR, of a MS brain. D: Segmented image: CSF (blue), Parenchyma (gray), and Lesions (salmon). E: Segmented image: CSF (blue), GM (gray), WM (white) and Lesions (salmon) using method described by Sajja et al. [1]. F: Segmented image: CSF (blue), GM (gray), WM (white) and Lesions (salmon) based on present methodology (m=3).

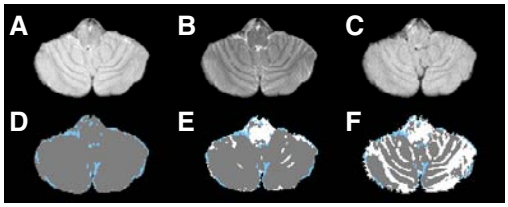

Fig. 2: Same as Fig. 1

Conclusions: We have presented a method for improving the segmentation of GM and WM by taking partial volume averaging into consideration. This method should result in more accurate estimation of GM and WM volumes.

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