

# ACCURATE PARTIAL VOLUME ESTIMATION OF MR BRAIN TISSUES

ALAN WEE-CHUNG LIEW<sup>1</sup>, HONG YAN<sup>2,3</sup>

<sup>1</sup> Department of Computer Science and Engineering, The Chinese University of Hong Kong, Shatin, Hong Kong

<sup>2</sup> Department of Electronic Engineering, City University of Hong Kong, 83 Tat Chee Avenue, Kowloon Tong, Hong Kong

<sup>3</sup> School of Electrical and Information Engineering, University of Sydney, NSW 2006, Australia

E-mail: wcliew@cse.cuhk.edu.hk, h.yan@cityu.edu.hk

## Abstract:

Accurate estimation of tissue volume has important applications in brain diagnostic and morphologic studies. In this paper, we show how partial volume estimation of brain tissues from 3D MR brain images can be performed using the recently proposed adaptive spatial FCM algorithm. The efficacy of the proposed algorithm is demonstrated experimentally using simulated MR images with known ground truths.

## Keywords:

Magnetic resonance imaging; partial volume estimation; brain tissue segmentation

## 1. Introduction

Accurate segmentation of MR images of the brain is of interest in the study of many brain disorders [1], [2]. However, automatic MRI brain tissue classification has proven difficult since MR images are often degraded by various artifacts, notably the intensity non-uniformity (INU) artifact [3] and the partial volume averaging (PVA) artifact [4]. The INU artifact arises due to the inhomogeneity in the magnetic field or the non-uniform sensitivity in the receiver coil. PVA artifact occurs when multiple tissues are present in one voxel due to the limited resolution of the image. The intensity of a voxel affected by PVA is a weighted average of the intensities of the different tissues in the voxel, and fine anatomical structures are lost. PVA affects the accuracy of delineation and volume estimation of different tissue.

Various approaches have been proposed for partial volume (PV) estimation [4], [5], [6]. In these approaches, every voxel is assumed to be consisted of a mixture of pure tissue classes. The objective of PV estimation is then to determine the relative fraction of each tissue class that is present within every image voxel. This task is in contrast to tissue segmentation, where a voxel is classified to only one tissue type. Sophisticated statistical estimation techniques are often used to estimate the mixture parameters. In [7], the MRI brain tissue classes are modeled as finite Gaussian

mixtures with Markov random field regularization and a priori digital brain atlas initialization. The Gaussian mixture modeling of the tissue allows PV estimation to be performed during the segmentation process.

In [8], we proposed a novel algorithm called the adaptive spatial fuzzy C-means clustering (ASFCM) algorithm for 3D MR brain image segmentation. Our algorithm is able to accurately recover the bias field associated with the INU artifact, while giving very good segmentation results compares to several state-of-the-art algorithms. In this paper, we show that the soft segmentation framework used in our algorithm can also be used to perform accurate PV estimation of brain tissues.

## 2. Partial Volume Estimation

The ASFCM algorithm we proposed for 3D MR brain image segmentation has two novel features: (1) the incorporation of local spatial context into the clustering process, and (2) the suppression of the INU artifact in MR images via the simultaneous recovery of the bias field. We briefly outline the algorithm here, and interested readers are referred to [8] for details.

The cost function of the ASFCM algorithm is given by

$$J(U, v, w) = \sum_{\underline{x} \in I} \sum_{k=1}^c u_{k,\underline{x}}^m D_{k,\underline{x}} + \beta \eta(w_z(x, y)) + \gamma \varphi(w_z(x, y)) \quad (1)$$

subject to the constraint  $\sum_{k=1}^c u_{k,\underline{x}} = 1$ . The dissimilarity index  $D_{k,\underline{x}}$  measures the dissimilarity between the voxel  $s(\underline{x})$  and the  $k$ -th cluster centroid  $v_k$  as follow,

$$D_{k,\underline{x}} = \frac{1}{|\mathcal{N}_{\underline{x}}|} \sum_{y \in \mathcal{N}_{\underline{x}}} \left[ d_{k,\underline{x}}^2 \lambda_{\underline{x}y} + d_{k,y}^2 (1 - \lambda_{\underline{x}y}) \right] \quad (2)$$

where  $|\mathcal{N}_{\underline{x}}|$  is the cardinality of the neighborhood configuration, and the sigmoid weighting factor  $\lambda_{\underline{x}y}$ , with

range between zero and one, controls the degree of influence of the neighboring voxels  $s(\underline{y}) \in \mathcal{N}_{\underline{x}}$  on the center voxel  $s(\underline{x})$ . Through this novel dissimilarity index, local spatial context is utilized in the clustering process. When there is no INU, the distance  $d_{k,\underline{x}}^2$  between  $s(\underline{x})$  and  $v_k$  is given by the Euclidean distance. When INU is present, the MR data is compensated for the bias field by letting  $d_{k,\underline{x}}^2 = \|s(\underline{x})/\tilde{b}(\underline{x}) - v_k\|^2$ , where  $\tilde{b}(\underline{x})$  is the estimate for the unknown bias field. In [8], we proposed to estimate the bias field  $\tilde{b}(\underline{x})$  in the log domain, such that  $d_{k,\underline{x}}^2 = \|\hat{s}(\underline{x}) - w(\underline{x}) - \hat{v}_k\|^2$ , where  $w(\underline{x})$  is the log bias field,  $\hat{s}(\underline{x}) = \log s(\underline{x})$  and  $\hat{v}_k = \log v_k$ . The 3D log bias field  $w(\underline{x})$  is modeled as a stack of coupled 2D cubic  $B$ -spline surfaces  $\{w_z(x, y)\}$ . The two regularizing terms,

$$\eta(w_z(x, y)) = \iint \left\{ \left[ \frac{\partial^2 w_z(x, y)}{\partial x^2} \right]^2 + 2 \left[ \frac{\partial^2 w_z(x, y)}{\partial x \partial y} \right]^2 + \left[ \frac{\partial^2 w_z(x, y)}{\partial y^2} \right]^2 \right\} dx dy \quad (3)$$

$$\varphi(w_z(x, y)) = \iint \left[ \frac{\partial^2 w_z(x, y)}{\partial z^2} \right]^2 dx dy \quad (4)$$

are used to impose intra- and inter-slice continuity of the bias field. Through iterative update of the ASFCM variables, we can reach a local minimum of the objective function. The final segmentation is obtained by a hard thresholding operation on the membership maps. The ASFCM algorithm is able to perform a soft segmentation of the MR images, where the tissue membership value indicates the contribution of each tissue to a voxel. Thus, it would be possible to perform PV estimation using the returned membership values.

We model the PVA artifact as  $s(x) = \sum_{k=1}^c t_k(x)g_k(x)$ , with constraints  $\sum_{k=1}^c t_k(x) = 1$ ,  $t_k(x) \geq 0$ . Here,  $t_k(x)$  is the contribution of tissue  $k$  at location  $x$ ,  $g_k(x)$  is the true intensity of tissue  $k$  at location  $x$ , and  $c$  is the number of tissue classes. Hence, the centroids and membership values returned by the ASFCM algorithm could be interpreted as correspond to  $g_k(x)$  and  $t_k(x)$ , respectively.

In 3D volume segmentation, the interface between two tissues forms a surface, whereas the interface between three tissues forms a curve. PVA is therefore much more probable

between two tissue types, especially for highly convoluted brain tissues. In addition, the anatomical structure of the brain tissues indicates that PVA most frequently occurs between GM/WM interface and CSF/GM interface, and also between WM/CSF at the interface between the corpus callosum and lateral ventricles [9]. We therefore assume that PVA exists between two tissue types. We modify the final membership values returned by the ASFCM algorithm by setting, at each voxel location, the smallest membership value to zero, and proportionately scale the remaining two membership values such that they add up to one. This simple post-processing step on the membership maps is able to give very good PV estimation as our simulation results show next.

### 3. Experiments

For evaluation purpose, we perform PV estimation on the simulated MR brain image obtained from BrainWeb (<http://www.bic.mni.mcgill.ca/brainweb>) [10]. The simulated MR brain image has the following settings:  $T_1$  modality, ICBM protocol, slices thickness of 1 mm ( $1 \text{ mm}^3$  voxels), 3% noise level and 40% INU. The fuzzy tissue models for gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF) from BrainWeb are used as ground truths. The voxel value in the fuzzy tissue models reflects the proportion of tissue present in that voxel and ranges between zero and one.

The second to fifth row of Figure 1 shows the results of soft segmentation for GM, WM, and CSF from our algorithm, the FCM algorithm, and the EM-MRF algorithm [7] without and with MRF regularization, respectively. By comparing to the ground truth at the first row, it is clear that our algorithm can estimate the PV much more accurately than the other three algorithms. The PV estimations given by the FCM algorithm suffer from INU artifact and noise, whereas the PV estimations given by the EM-MRF algorithm either do not model the PVA accurate enough or suffer from perimeter shading. The perimeter shading is particularly noticeable in the GM PV estimation given by the EM-MRF algorithm with MRF regularization, and the CSF PV estimation given by the EM-MRF algorithm with and without MRF regularization.

For quantitative evaluation, we calculated the root mean square error (RMSE) in the PV estimation, as shown in Table 1. The RMSE for each tissue class is given by the square root of the mean squared difference between the estimated tissue volume and the true volume, computed over the corresponding tissue support. The tissue support is defined as the union of all voxels with a non-zero value for that tissue. It can be seen that our algorithm has the best

performance. Table 2 shows the estimated tissue volume for GM, WM, and CSF, computed over the corresponding tissue support. It can be seen that our algorithm has the best overall performance: in both the WM and CSF volume estimations, it is the closest to the true value, whereas in the GM volume estimation, it is the second closest to the true value. The EM-MRF algorithm is good at estimating the PV for GM. However, its performance is significantly poorer for WM and CSF, where an underestimation of more than 20% has been observed for CSF. Interestingly, our algorithm and the FCM algorithm give the best PV estimation for CSF, even though the CSF is usually the hardest to segment accurately for most existing algorithms.

Table 1. RMSE in PV estimation, computed over the correct tissue type

	GM	WM	CSF
Our Alg.	0.1299	0.1160	0.1323
FCM	0.2265	0.2269	0.1668
No MRF	0.2064	0.2138	0.3034
With MRF	0.2511	0.2216	0.3043

Table 2. Estimated tissue volume ( $\times 10^5$ ), computed over the correct tissue type. Percentage value in bracket indicates the level of over or under segmentation

	GM (8.99)	WM (6.639)	CSF (3.71)
Our Alg.	8.55 (-4.8%)	6.83 (2.9%)	3.70 (-0.2%)
FCM	8.48(-5.7%)	6.37 (-4.0%)	3.77 (1.8%)
No MRF	9.44 (5.1%)	5.83 (-12.1%)	2.72 (-26.6%)
With MRF	8.65 (-3.7%)	5.79 (-12.8%)	2.59 (-30.0%)

#### 4. Conclusions

Due to the limited resolution of the imaging device, it is possible that multiple tissues are present in one voxel, giving rise to the PVA artifact. Accurate partial volume estimation is an important problem in MRI tissue volume estimation. We proposed here a simple post-processing of the fuzzy tissue membership maps returned by the adaptive spatial FCM segmentation algorithm for PV estimation and show that good results could be obtained in spite of the simplicity of the approach.

#### Acknowledgements

This work is supported by the IEEE Systems, Man and Cybernetics Society, Hong Kong Chapter.

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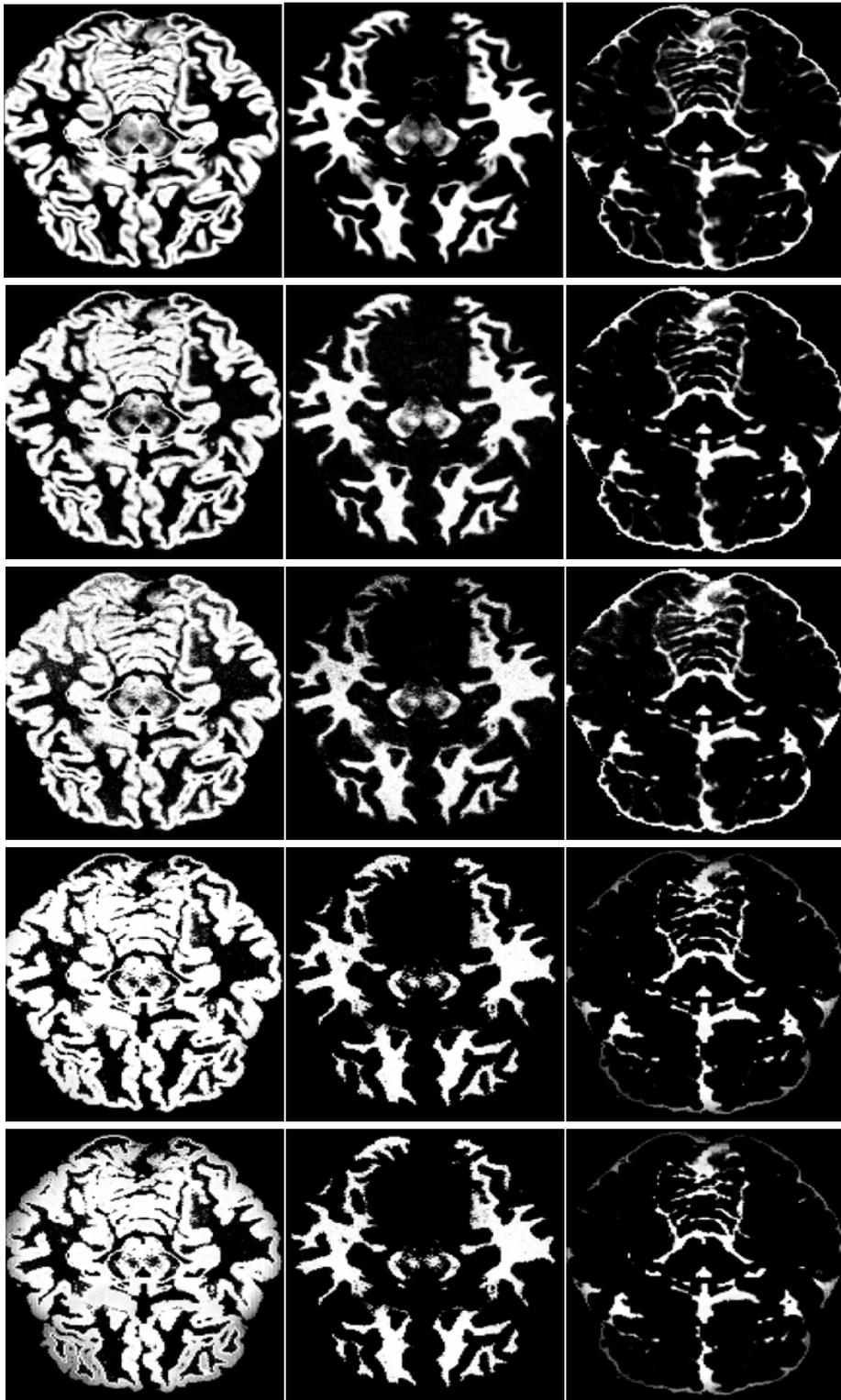


Figure 1: Soft segmentation as an estimation of PV for GM, WM, and CSF. The top row is the true PV for GM, WM, and CSF. The second to fifth rows are the PV estimation from our algorithm, FCM algorithm, EM-MRF without MRF regularization, and EM-MRF with MRF regularization, respectively.