PARTIAL VOLUME ESTIMATION OF BRAIN CORTEX FROM MRI USING TOPOLOGY-CORRECTED SEGMENTATION

Andrea Rueda\textsuperscript{1,2}, Oscar Acosta\textsuperscript{1}, Pierrick Bourgeat\textsuperscript{1}, Jurgen Fripp\textsuperscript{1}, Erik Bonner\textsuperscript{1}, Nicholas Dowson\textsuperscript{1}, Michel Couprie\textsuperscript{3}, Eduardo Romero\textsuperscript{2} and Olivier Salvado\textsuperscript{1}

\textsuperscript{1} CSIRO Preventative Health National Research Flagship, ICTC, The Australian e-Health Research Centre - BioMedIA, Herston, Australia.
\textsuperscript{2} BioIngenium Research Group, Universidad Nacional de Colombia, Bogotá, Colombia
\textsuperscript{3} ESIEE Informatics Department, Université Paris-Est, Marne-la-Vallée, France

ABSTRACT

In magnetic resonance imaging (MRI), accuracy of brain structures quantification may be affected by the partial volume (PV) effect. PV is due to the limited spatial resolution of MRI compared to the size of anatomical structures. When considering the cortex, measurements can be even more difficult as it spans only a few voxels. In tight sulci areas, where the two banks of the cortex are in contact, voxels may be misclassified. The aim of this work is to propose a new PV classification-estimation method which integrates a mechanism for correcting sulci delineation using topology preserving operators after a maximum a posteriori classification. Additionally, we improved the estimation of mixed voxels fractional content by adaptively estimating pure tissue intensity means. Accuracy and precision were assessed using simulated and real MR data and comparison with other existing approaches demonstrated the benefits of our method. Significant improvements in GM classification were brought by the topology correction. The root mean squared error diminished by 6.3\% (\(p < 0.01\)) on simulated data. The reproducibility error decreased by 9.6\% (\(p < 0.001\)) and the similarity measure (Jaccard) increased by 3.4\% on real data. Furthermore, compared with manually-guided expert segmentations the similarity measure was improved by 12.0\% (\(p < 0.001\)).

Keywords: Brain tissue segmentation, partial volume classification, magnetic resonance imaging, topology correction, sulci detection.

1. INTRODUCTION

Accurate segmentation of brain tissues, namely gray matter (GM), white matter (WM), and cerebro-spinal fluid (CSF), from magnetic resonance imaging (MRI) can allow in-vivo quantification of structural modifications appearing during neurodegenerative diseases. When using MRI, accuracy may be hampered by artifacts such as intensity inhomogeneity, noise and partial volume (PV). The former is mostly due to the sensitivity of the receiver coils, but could also be due to non-homogeneous tissue MR properties throughout the brain. It can be characterized by a low frequency multiplicative bias field. The noise is Rician distributed and can strongly affect the classification. PV appears when the size of anatomical features being imaged is comparable to the image resolution. PV or signal averaging produces blurring at the interfaces between pure tissues. In brain, for instance, it can affect the detection of opposed banks of GM in deep sulci, affecting further processing such as the measure of cortical thickness.

PV estimation has received considerable attention in the past few years and different approaches have been proposed [1, 2, 3, 4, 5, 6]. Classification schemes may go through a high resolution labelling as in [4] or be performed in the original voxel spacing. Voxels can be modelled as a linear combination of the intensity distributions of the possible tissue types in that voxel [7]. The goal of the PV estimation methods is therefore to compute the fractional content of pure tissue. This requires both pure and mixed voxels to be previously classified. Shattuck et al. [2] implemented a maximum a posteriori (SMAP) classifier, which combined a tissue measurement model with a prior model of the local spatial interactions, to obtain six tissue types: three pure and three mixed. The fractional content for the mixed voxels was calculated based on global averages of pure tissue types. Building on [2], Tohka et al. [5] proposed an algorithm based on a trimmed minimum covariance determinant (TMCD). Chiverton et al. [6] proposed a local adaptive gradient-controlled spatial regularizer (GSR), probabilistically modeling the PV, using a Markov random field to model the class membership and a Markov chain Monte Carlo (MCMC) simulation to adapt the model to the observed data, but the intensity inhomogeneity field was not explicitly modelled. The labelling may be still challenging because the intensity inhomogeneities and noise may lead to misdetection of mixed voxels in tight sulci.

We propose a robust method for classification of partial volume voxels using topology correction of brain tissue segmentations and fractional content estimation based on pure tissue local averaging. Firstly, an initial MAP classification of pure tissues WM, GM and CSF and mixed voxels WM/GM and GM/CSF is performed. Secondly, topology-constraints are introduced in the classification assuming that the GM is a continuous layer following the WM. A homotopic dilation of the WM over GM add robustness to the delamination of mixed voxels GM/CSF in deep sulci. Finally, the estimation of fractional content for mixed voxels is adaptively performed based on a local averaging of the neighbouring pure tissue voxels. The spatially dependent averaging helps to overcome the problem of intensity inhomogeneity. To our knowledge, none of the existing methods have addressed the problem of tissue classification using topology-correction operators, which improved the reproducibility by producing anatomically consistent classifications.

In the next section we first describe our methods, followed by experiments using simulated and real data. We also compare the results with other previously proposed methods. We show that tissue classification and tissue fractional content can be substantially improved.
2. METHODS

2.1. Pure tissue segmentation and MAP partial volume labelling

A first segmentation of pure brain tissues into GM, WM and CSF is performed based on an implementation of the Expectation-Maximisation segmentation method [8] followed in a second step by a MAP classification of mixed voxels as in [2]. This classification relies on both intensity and spatial information to label the voxels as belonging to the set \( \Gamma = \{ \text{WM, GM, CSF, WM/GM, GM/CSF} \} \). Here, the Colin atlas and associated tissue priors are first affinely registered [9], followed by a diffeomorphic Demons non-rigid registration [10]. Overall, the partial volume labelling builds upon the method proposed by [2], but assumes that each voxel contains at most two tissues [1], and PV classification is restricted to the region formed by a dilated GM (radius 2). The labelling is performed using a Potts model. As in [2, 5, 11], we use the ICM algorithm [12] to search for the optimal labelled image.

2.2. A topology preserving segmentation

After the MAP labelling, some of the sulci may be misdetected as the intensity of buried PV GM/CSF voxels is close to that of the GM. In that case, a voxel initially classified as GM must be reclassified as a mixture GM/CSF. In order to refine the PV classification and identify those buried GM/CSF voxels, we used a homotopic dilation of the consolidated WM = \{ WM, WM/GM \} constrained by the GM, resulting in a better delineation of deep sulci. A set of topology preserving operators, introduced by Couplie et al.[13], were sequentially applied to initially produce a corrected WM segmentation, homotopic to a filled sphere. Then, the resulting segmentation is homotopically dilated over the GM, without the deletion of original WM/GM convolutions and consequently preserving the folds. Fig. 1 shows 2D and 3D views before and after topology correction. The misdetected sulci were adequately corrected in the resulting GM.

![Fig. 1. (a) Initial and (b) topologically corrected WM-GM segmentations; marching cubes reconstruction of GM (c) before and (b) after the topology correction procedure.](image)

2.3. Partial volume relabelling and fractional content

Once the topologically corrected GM segmentation is obtained, the partial volume labelling is updated. We assume that each voxel contains at most two tissues and the new labelling corresponds to the mixed voxels WM/GM and GM/CSF. For each mixed voxel, its fractional content \( F_{j/k} \) between tissue \( j \) and \( k \) is computed using the observed intensity \( I_i \) and the robust local averages of the two pure tissue types \( \mu_j(x) \) and \( \mu_k(x) \), such that:

\[
F_{j/k}(x) = U \left( \frac{\mu_j(x) - I_i}{\mu_j(x) - \mu_k(x)} \right)
\]

where \( U(\cdot) \) is a limiter restricting the range of the fractional content to \([0, 1]\). Unlike [2], we compute a robust local average rather than a global mean in order to overcome issues related to the intensity inhomogeneity and variations of pure tissue signal across the image. For each pure tissue voxel, the local average is obtained using the interquartile mean (IQM) within a 5mm radius sphere, thus rejecting local outliers, over a denoised version of the original MR image. The noise is removed by applying the optimized non-local means method [14]. The average is restricted to the pure tissue voxels which are selected by eroding pure tissue segmentations, therefore reducing the influence of any mixed voxel. Finally, the computed averages are propagated back towards the location of the mixed voxels \( x \) resulting in values of \( \mu_j(x) \) and \( \mu_k(x) \) that represent the average of the closest pure tissue voxels, weighting accordingly the signal when computing the fractional content. The GM fractional content map is defined as \((1 - F_{\text{GM/WM}}) \cup (1 - F_{\text{GM/CSF}})\).

3. EXPERIMENTS AND RESULTS

3.1. Simulated MR data

To evaluate our method, named hereafter as Topologically-corrected Partial Volume (TPV), we firstly used the publicly available sets of simulated T1W MR 3D images \((181 \times 217 \times 181, 1\text{mm}^3\) voxels\) from BrainWeb [15], with noise levels ranging from 0% to 9%. One example of the resulting GM fractional content map on the synthetic brain volume, 3% noise level and 20% bias field, is shown in Fig. 2. It must be noted that compared to a classical MAP approach as in [2], the sulci were better delineated by the topological constraints. Indeed, the root mean squared (RMS) error significantly diminished by 6.3% \((p < 0.01)\). Overall, a good agreement was shown between the computed PV maps and the ground truth, available as fuzzy tissue membership volumes. RMS errors are shown in Table 1. As expected, the computed error was robust to the bias field, which additionally validates the local averaging approach rather than the global one. After the initial MAP segmentation, the topology correction and PV fractional content estimation takes less than 8 minutes in a standard Intel Core 2 Duo (3.00GHz, 2 GB RAM) running Linux.

![Fig. 2. Example of PV estimation of a simulated BrainWeb volume (3% noise, 20% bias field). (a) Original image, (b) MAP PV estimation, (c) Topologically-corrected PV, (d) ground truth.](image)
As pointed out by Chiverton et al. [6], the variability between image properties of the brain regions affects the performance of PV classifiers. To illustrate this effect, we used the automated anatomical labeling (AAL) template [16] to calculate the RMS error within each region as in [6]. Averaged results for different levels of noise are shown in Fig. 3. As a very low variability with respect to the bias field was observed, the depicted value corresponds to the average over all the bias field levels (0%, 20% and 40%). The smallest errors appeared in the amygdala (42xx), the insula (30xx), the supplementary motor area (24xx) and the olfactory (25xx); while lower agreement was found in the basal ganglia (70xx), the middle occipital (52xx) and the parietal superior (61xx).

We also compared our TPV method with the results presented by Chiverton et al. [6] (GSR) and Shattuck et al. [2] (SMAP). The results are depicted in Fig. 4. Evidence suggested that the local average intensity strategy makes the classification more robust to bias field variations, and in average it performed better than the others for low levels of noise (1% to 7%) and low bias field (20%).

### 3.2. Real MR Data
#### 3.2.1. OASIS

Precision was assessed by applying the method to MR images of 20 young healthy subjects from the OASIS database [17], who underwent scans at baseline and subsequent sessions after a short delay (less than 90 days). The scans were T1W Magnetization Prepared RAPid Gradient Echo (MP-RAGE) in sagittal orientation with isotropic 1mm³ resolution (256 × 256 × 128 pixels). We compared the results with the MAP classifier as in [2]. Significant improvements in GM PV estimation were brought by the topology correction. The reproducibility error decreased by 9.6% (p < 0.001), measured as the RMS between the PV maps obtained on the rigidly registered baseline and repeat scans. Likewise, when comparing the crisp segmentations obtained by thresholding by 0.5 the baseline and repeat GM PV maps, the Jaccard similarity measure increased by 3.2%. To compute crisp segmentations, each mixed voxel was assigned to the tissue class with the highest fractional content and the obtained segmentation were subsequently compared.

#### 3.2.2. IBSR

Our method was also compared with both TMCD [5] and MMC [3] on 20 real MR images (1 × 1 × 3mm³) from the Internet Brain Segmentation Repository (IBSR). Since the ground truth is available as manual segmentations performed by clinical experts, we compared the segmentations obtained from the crisped PV maps. Fig. 5 shows an example of the ground truth provided by IBSR and a hard segmentation calculated after applying our method. Fig. 6(b) depicts the results of the comparison for the GM in the 20 normal subjects. As in [6], results of manual expert segmentation and pure tissue classification presented by Ibrahim et al. [18] (HMM) were included just for reference on IBSR data. Significant improvements in GM classification were demonstrated using the topology correction. The similarity measure (Jaccard) was improved by 12.0% (p < 0.001) with respect to the MAP classifier.

Poor similarity results were obtained in 5 cases, which exhibited strong shading artifacts that impeded a reliable GM and WM classification. Similar findings were presented in [3], who excluded them from the analysis. We also observed that the anisotropy in the images biased the computation of the local averages. Table 2 summarizes the mean (and standard deviation) similarity values for each repeat GM PV maps, the Jaccard similarity measure increased by 3.2%. To compute crisp segmentations, each mixed voxel was assigned to the tissue class with the highest fractional content and the obtained segmentation were subsequently compared.
method, excluding the volumes with too severe intensity inhomogeneity. In average, our TPV method performed better for WM and GM compared to the others, excepting averaged GM segmentation against [5]. It must be noted that when the PV maps were used to generate the crisp segmentations, the mixed GM/CSF voxels in deep sulci with fractional content above 0.5 might be wrongly reclassified as GM. Therefore, the contribution of topology correction in the segmentation cannot accurately be validated with this experiment. Nonetheless, we report this results for completeness.

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<th>MMC</th>
<th>TMCD</th>
<th>TPV</th>
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<tbody>
<tr>
<td>WM</td>
<td>0.648 (± 0.198)</td>
<td>0.696 (± 0.050)</td>
<td>0.701 (± 0.042)</td>
</tr>
<tr>
<td>GM</td>
<td>0.753 (± 0.120)</td>
<td>0.697 (± 0.064)</td>
<td>0.708 (± 0.045)</td>
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Table 2. Mean (± standard deviation) of Jaccard similarity index for each method.

The main contribution lies in two points: firstly, the restriction introduced by the WM to correct for the topology, assuming that the GM is a continuous layer following the WM, improved the classification of mixed voxels in opposed banks of buried sulci; secondly, the fractional content of mixed voxels is computed based on the local averages of pure tissue voxels, overcoming the issues related with intensity inhomogeneity and tissue MR properties across the image. Accuracy and precision were demonstrated and comparisons with other methods showed a good performance on simulated and real MR data. The regional variability in the results suggests the development of adaptive methods that exploits the particular properties per regions in order to improve the PV classification results.

5. REFERENCES


4. CONCLUSION

We have described a simple and fast technique to improve PV estimation of brain tissues from T1W MRI. It corrects for the topology errors in the segmentation and uses local averages to estimate fractional content. We show that fractional tissue content estimation can be improved, resulting in superior brain tissue segmentations.

Fig. 6. Jaccard similarity results for WM (a) and GM (b).