Data-Driven Brain MRI Segmentation Supported on Edge Confidence and A Priori Tissue Information

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Abstract—Brain magnetic resonance imaging segmentation is accomplished in this work by applying nonparametric density estimation, using the mean shift algorithm in the joint spatial-range domain. The quality of the class boundaries is improved by including an edge confidence map, that represents the confidence of truly being in the presence of a border between adjacent regions; an adjacency graph is then constructed with the labeled regions, and analyzed and pruned to merge adjacent regions. In order to assign image regions to a cerebral tissue type, a spatial normalization between image data and standard probability maps is carried out, so that for each structure a maximum a posteriori probability criterion is applied. The method was applied to synthetic and real images, keeping all parameters constant throughout the process for each type of data. The combination of region segmentation and edge detection proved to be a robust technique, as adequate clusters were automatically identified, regardless of the noise level and bias. In a comparison with reference segmentations, average Tanimoto indexes of 0.90–0.99 were obtained for synthetic data and of 0.59–0.99 for real data, considering gray matter, white matter, and background.

Index Terms—Brain MRI, edge detection, image segmentation, mean shift, nonparametric estimation.

I. INTRODUCTION

Segmentation of the brain structures from magnetic resonance imaging (MRI) is applied in the study of many disorders, such as multiple sclerosis, schizophrenia, epilepsy, Parkinson’s disease, Alzheimer’s disease, cerebral atrophy, etc. MRI is particularly suitable for brain studies [1] because it is virtually noninvasive, and it presents a high spatial resolution and an excellent contrast of soft tissues [2]. Additionally, MRI segmentation is an important image processing step to identify anatomical areas of interest for diagnosis, treatment, surgical planning, image registration and functional mapping.

In MRI, the tissues are characterized by voxel intensities originated from spatially differentiated MR signals. The goal of the segmentation procedure in medical applications is to partition an image into significant anatomical regions, which are homogeneous according to a specific property; this is carried out by finding the discriminating tissue properties and by labeling the voxels considering these features.

MRI segmentation using pattern recognition techniques has been particularly successful for brain images [3]. Statistical pattern recognition approaches usually define a parametric model, which assumes a particular probability density function (pdf) of the selected features. Parametric methods are useful when the distribution of features for the different classes is well known, or can be adequately modeled. A parametric approach frequency used is the mixture model, where the mixture components are normally distributed [4]–[7]. Model parameters are commonly determined by maximum-likelihood (ML) [2], [8] or maximum a posteriori (MAP) estimates [9], using algorithms such as expectation-maximization. Nevertheless, in MRI the distribution of tissue classes is not necessarily a known statistical function, which results in a biased estimation, thus producing poor segmentations [4]. Also, one major tissue class is usually associated with a number of normal components within the mixture, thus requiring the estimation of a significant amount of parameters; this can cause stability and convergence problems. Furthermore, borders between classes in the pdf can be complex and not expressible with a parametric form [10].

Segmentation stability and convergence can be improved by using nonparametric clustering algorithms which do not rely on predefined distributions, being rather built directly from the actual data samples, without requiring knowledge or assumptions about their statistical properties [3], [4]. In such methods, the problem is to find clusters of voxels with homogeneous features, by finding the cluster centers and the class membership assignments of each cluster [6]. Most of the published clustering techniques are usually inadequate to analyze feature spaces directly from real data, because they rely upon a priori knowledge of the number of clusters present (e.g., k-means), or they implicitly assume a given cluster geometry, which makes them unable to handle the complexity of the real feature space. Since these techniques impose a rigid delineation over the feature space and require a reasonable guess for the number of clusters present, they can return erroneous results when the embedded assumptions are not satisfied. Therefore, arbitrarily structured feature spaces can only be analyzed by nonparametric methods [11]. As a robust alternative, a clustering technique which does not require prior knowledge of the number of clusters, and does not constrain their shape, is built upon the mean shift (MS). This is an iterative technique which estimates the modes of the multi-variate distribution underlying the feature space. The number of
clusters is obtained automatically by finding the centers of the densest regions in the space [12].

Another frequently used approach in segmentation consists on the integration of high-level knowledge. A digital atlas provides a priori information about the spatial distribution of probabilities that a voxel belongs to a given brain structure; this strengthens the process of defining complex organs [13], and can be used to find the most probable class membership. The use of a priori information atlases must be preceded by a registration step and this is carried out through a process of spatial normalization that minimizes a cost function between the atlas and the image. Several atlases have been proposed for brain segmentation [8], [14], [15].

This work proposes a nonparametric estimation strategy, based on the MS algorithm, that uses the local modes of the underlying joint space-range density function to define the cluster centers [16]–[18]. This algorithm has proven to be robust under the presence of different levels and types of noise and doesn’t assume a probability density function form. The quality of the class boundaries is improved by including an edge confidence map that represents the confidence of truly being in the presence of a border between adjacent regions. The confidence measure is also used to merge regions with weak edges, through the iterative application of transitive closure operations in a region adjacency graph (RAG). The fusion step is completed with a pruning process to eliminate very small regions. To automate class labeling, a MAP decision is taken, based on a digital brain atlas against which a spatial normalization is carried out. The robustness of the MS estimation and its edge-preserving filtering property, together with the edge and region analysis incorporated in the proposed method, make it amenable to process MR images with varying degrees of field inhomogeneity and additive noise.

The paper is organized as follows: MS algorithm and edge confidence map concepts are detailed in Section II. Region fusion is undertaken in Section III, and the incorporation of a priori information in Section IV. Section V presents a brief summary of the entire procedure. Results for synthetic and real data are presented in Section VI, and finally, the proposed algorithm is discussed to draw some conclusions in Section VII. It is important to point out that some preliminary results of this research have been published elsewhere [19], [20].

II. MEAN SHIFT AND EDGE CONFIDENCE MAP FILTERING

A. Nonparametric Estimation

Fukunaga [16] proposed a nonparametric method of kernel estimation to cluster observations set in different classes, by assigning each observation to the pdf of its nearest mode along its gradient direction; this is called the MS algorithm. Subsequently, in 1995, Cheng [17] generalized the MS as a mode seeking process of any real function. Comaniciu and Meer [18] first applied MS for color image segmentation; they proposed an algorithm, that is initialized with a data sample to find the cluster centers, to validate them, and finally, to delineate the clusters using the nearest neighbor method. Several works were published afterwards related to MS [11], [12], [19]–[22].

B. Mean Shift Algorithm

Let \( \{X_i\}_{i=1}^{n} \) be an arbitrary set of \( n \) observations in the \( d \)-dimensional Euclidean space \( \mathbb{R}^d \), drawn from an unknown probability density function \( f \). According to the a priori knowledge of \( f \) an estimate \( \hat{f} \) of the probability density function can be constructed based on a nonparametric strategy.

The feature spaces in an image are often characterized by very irregular data clusters whose number and shape are not available. This strongly suggests that a nonparametric approach, which provides reliable detection of the local maxima of the underlying density, should be employed for the analysis. The kernel density estimation is a simple and reliable estimation method, and for those kernels satisfying mild conditions the estimate is asymptotically unbiased, consistent in a mean square sense and uniformly consistent in probability.

The multivariate kernel density estimator with kernel \( K \) and window radius \( h \) (also called smoothing parameter or bandwidth), computed at the \( d \)-dimensional point \( \mathbf{x} \) is defined as [23]

\[
\hat{f}(\mathbf{x}) = \frac{1}{n h^d} \sum_{i=1}^{n} K \left( \frac{1}{h} (\mathbf{x} - X_i) \right).
\]

The quality of the estimate is expressed as the mean integrated squared error (MISE), and the optimal kernel yielding minimum MISE is the multivariate Epanechnikov kernel [23], given by

\[
K_{E}(\mathbf{x}) = \begin{cases} 
\frac{1}{2c_d} (d+2)(1 - \mathbf{x}^T \mathbf{x}), & \text{if } \mathbf{x}^T \mathbf{x} < 1 \\
0, & \text{otherwise}
\end{cases}
\]

where \( c_d \) is the volume of a unit \( d \)-dimensional sphere. By employing a differentiable kernel an estimate of the density gradient can be defined as the gradient of the kernel density estimate (1)

\[
\nabla \hat{f}(\mathbf{x}) \equiv \nabla \hat{f}(\mathbf{x}) = \frac{1}{n h^d} \sum_{i=1}^{n} \nabla K \left( \frac{1}{h} (\mathbf{x} - X_i) \right).
\]

Conditions on the kernel \( K(\mathbf{x}) \) and the window radius \( h \) to guarantee asymptotic unbiasedness, mean-square consistency, and uniform consistency of the estimate (3) are derived in [16]. For the Epanechnikov kernel (2) the density gradient estimate (3) becomes

\[
\nabla f_{E}(\mathbf{x}) = \frac{1}{n (h c_d)} \frac{d+2}{h^2} \sum_{X_i \in S_h(\mathbf{x})} (X_i - \mathbf{x})
\]

where \( S_h(\mathbf{x}) \) is a hypersphere of radius \( h \) having the volume \( h^d c_d \), centered on \( \mathbf{x} \) and containing \( n_x \) data points. The last term in (4)

\[
M_h(\mathbf{x}) \equiv \frac{n_x}{n (h c_d)} \sum_{X_i \in S_h(\mathbf{x})} (X_i - \mathbf{x}) = \frac{n_x}{n} \sum_{X_i \in S_h(\mathbf{x})} X_i - \mathbf{x}
\]

is known as the sample MS [18], [19], [21].

The quantity \( n_x / (h^d c_d) \) is the kernel density estimate \( \hat{f}(\mathbf{x}) \) computed within \( S_h(\mathbf{x}) \) and, thus, (4) can be written as

\[
\nabla f_{E}(\mathbf{x}) = \hat{f}(\mathbf{x}) \frac{d+2}{h^2} M_h(\mathbf{x})
\]

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which yields

$$M_h(x) = \frac{h^2}{d+2} \frac{\hat{\nabla} f(x)}{f(x)}.$$  \hfill (7)

This property can be used in an optimization procedure to climb over the estimated pdf surface, $f(x)$, to search for the local maxima, i.e., the modes of the distribution [19]. The MS vector is proportional to the normalized pdf gradient estimate $[11]$, $[17]$, points in the pdf gradient direction, and since it is aligned with the local gradient estimate in $x$, it can define a path leading $x$ to a stationary point (mode) of the estimated pdf, as it can be appreciated in Fig. 1.

The procedure computes $M_h(x)$ for each data point, shifts the kernel centers by these quantities, and iterates until the magnitudes of the shifts are less than a given threshold or a certain number of iterations is attained.

C. Edge Confidence Map

The most frequently used edge detection methods are based on gradient orientation. These methods rely in the coherence of edges close to the gradient direction, and their main drawback is the lack of a way to extract a reliable edge direction; this problem can be solved by using an edge confidence measure, as proposed in [24]. Gradient estimation is carried out using a differentiation mask, $W$, defined in an $(m \times m)$ window, and defining a gradient subspace in $R^{m \times m}$. As it can be observed in Fig. 2, each mask vector ($W_1$ and $W_2$) defines a subspace dimension, and the data $(d)$ is an arbitrary vector in $R^{m \times m}$ in the orthogonal complement of subspace.

Gradient estimation is equivalent to projecting the data into the gradient subspace, the projection is the vector $Pd$, and its orientation $\theta$ is the angle between the data projection and one of the mask vectors. The parameter $\theta$ can be used to define an ideal edge template, $t$, with the same estimated gradient orientation. A measure of confidence for the presence of an edge in the analyzed data can be defined as: $\eta = \frac{t^T d}{t^T t}$, which corresponds in the image domain, to the correlation coefficient between the normalized template and the data (Fig. 2). This edge confidence measure has the advantage of being independent of the gradient magnitude.

Since the gradient vector always points toward the direction of maximum increment, the estimated edge orientation is given by

$$\hat{\theta}_e = \hat{\theta} - \frac{\pi}{2} = -\tan^{-1} \left( \frac{\text{trace}[W^T D]}{\text{trace}[W D]} \right)$$ \hfill (8)

where $\hat{\theta}$ is the estimated gradient orientation, and $D$ is the data matrix, centered in each image voxel and of the same size that $W$. Edge orientation is used to define the template $t$ of an ideal edge model with orientation $\hat{\theta}_e$, and, thus, the confidence measure of each voxel, can be calculated by correlating the data matrix $D$ with its corresponding template.

Instead of the gradient magnitude, its normalized values $\rho$ are used, that is, the percentiles of their cumulative distribution of the gradient magnitude, as criterion for the presence of an edge. Finally, the confidence map ($\varphi$) is computed for each voxel as a linear combination of the cumulative distribution function and the measure of edge confidence

$$\varphi = \beta \rho + (1 - \beta) \eta$$ \hfill (9)

where $\beta$ is a constant between 0 and 1 which controls the blending of gradient magnitude $\rho$ and the local pattern $\eta$ information.

D. Coupling Mean Shift Filtering and Edge Confidence

An improved MS estimate can be obtained by weighting each voxel within the region by a function of its edge confidence ($\varphi$), so that voxels that lie close to an edge (edge confidence $\approx 1$) are less influential in the determination of the new cluster center. The modified MS that includes weighted edge confidence is, from (5)

$$M_h(x) = \frac{1}{\sum \left(1 - \varphi_i \right)} \sum_{x_i \in \tilde{S}_h(x)} \left(1 - \varphi_i \right) X_i - x.$$ \hfill (10)

This weighted MS procedure is applied for the data points specified both in the spatial and intensity domains, which constitute a joint spatial-range domain [21]. An Euclidean metric
is used to control the quality of the segmentation, which is dependent on the radii $h_s$ and $h_t$, corresponding to the resolution parameters of the kernel estimate in the spatial and intensity (range) domains. After the MS procedure is applied to each data, those points that are sufficiently close in the joint domain are fused to obtain the homogeneous regions in the image. The number of clusters present in the image is automatically determined by the number of significant modes detected. A filtered image can be drawn from the output of the MS procedure, by replacing each voxel with the gray level of the mode it is associated to.

III. FUSION OF REGIONS

Once the filtered image is obtained, the tissue regions must be delineated in the feature space, by clustering all those regions that are near within the spatial and range domains, that is, all those voxels that have converged to the same point are fused and labeled. The region delineation can be refined by incorporating a RAG that is then simplified with a union-find algorithm [25], as described next.

A. Region Adjacency Analysis

The most straightforward representation for graphs is the so-called adjacency matrix representation, in which boolean values are established to indicate if there exists an edge between regions. To construct the adjacency matrix, each labeled region of the filtered image is considered a vertex and a value of 1 is assigned to the adjacent labels, to identify neighboring regions and 0 otherwise.

The number of regions determined by the weighted MS procedure may turn to be arbitrarily large, which produces an over-segmentation of the image. In order to fuse together homogeneous adjacent regions that have been split apart by the MS procedure, a transitive closure operation [26] on the RAG can be performed. This operation links regions that have associated modes that are located within a distance of $h_b/2$ apart, and satisfy a weak boundary strength condition. Such a boundary strength measure can be derived directly from the edge confidence (9) by adding the confidence values for the voxels along the boundary separating the regions. Whenever the measure is below a given threshold ($\xi$), the regions are finally fused.

A reduction procedure is then carried out on the RAG by applying a union-find algorithm, in order to find the labels connected in the graph. The operations of transitive closure and union-find are applied iteratively until the number of regions between iterations, remains unchanged.

B. Pruning

When the fused image is obtained, a pruning process is applied to remove all the regions whose area is less than a minimum size ($\mu$). In order to make this removal, the RAG is traversed, unifying regions whose area is less than $\mu$ with a region that is either adjacent and the distance of its mode is a minimum to that of the region being pruned; or it is the only adjacent region having an area greater than the threshold. The pruning process is repeated iteratively, until the number of regions remains unchanged, or a given number of iterations is reached.

IV. INCORPORATION OF A PRIORI INFORMATION

The procedures mentioned up to now, produce homogeneous intensity regions, reducing as much as possible the number of regions that constitute the brain image volume. However, the number of regions can still be high, considering that in this work we are interested only on the identification of: gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF). In order to obtain the desired number of regions, the use of a priori knowledge, taken from probability maps, is proposed. Those maps represent the a priori probability of a voxel being either GM, WM, or CSF, after an image has been normalized to the map space [27], [28]. Since only GM, WM, and CSF maps are available, a fourth probability map for background and noncerebral tissue was calculated. Fig. 3 shows a coronal slice of the normalized probabilistic maps.

A. Image Registration

Prior to segmentation, a registration step between data and probabilistic maps must be applied. Image registration is carried out by first using an affine spatial transformation that takes images of different subjects into roughly the same coordinate system, followed by a nonlinear spatial normalization to correct gross differences in head shapes. The spatial transformation that maps each voxel to its equivalent location in the probability map, is determined by using template images placed in the same stereotactic space (Talairach and Tournoux), than the probability images. Template and probabilistic maps were taken from the digital atlas distributed with the statistical parametric
mapping (SPM) [28] and the registration procedure was carried out using the same software.

B. Region Classification

The choice of properties or, equivalently, the definition of a class, is the fundamental matter in the classification problem. Once the probability images have been transformed to the data space, the classification of cerebral MRI requires essentially to calculate the probabilities for each found region, and to assign them to the class with greater probability, according to a classification rule.

1) Bayesian Classifier: Bayes rule allows to compute the a posteriori probability, \( P(w_i|x) \), from the a priori probability \( P(w_i) \) and the class-conditional density \( p(x|w_i) \). Let \( R_{ni} = \{x_1, \ldots, x_n\} \) be the image regions obtained from the RAG analysis, to be classified into \( M \) classes, \( w_1, \ldots, w_M \). Each region is represented by a feature vector \( \mathbf{x} \), so that the \( M \) conditional probabilities are \( P(w_i|x), i = 1, 2, \ldots, M \). Assuming that the a priori probabilities \( P(w_i) \) and the class-conditional probability density functions \( p(x|w_i) \) are known, then the probability density of finding a region that is in class \( w_i \) has feature vector \( \mathbf{x} \) can be written as: \( P(w_i|x) = P(w_i|x)p(x) = p(x|w_i)P(w_i) \); rearranging terms, the Bayes formula [29] is

\[
P(w_i|x) = \frac{p(x|w_i)P(w_i)}{\sum_{j=1}^{M} p(x|w_j)P(w_j)}. \tag{11}
\]

The a priori probability represents the information of the prior knowledge contained in the probabilistic atlas. The likelihood of \( w_i \) with respect to \( \mathbf{x} \), \( p(x|w_i) \), quantifies the probability contributed by the observed data \( (R_{ni}) \), and indicates the class \( w_i \) for which \( p(x|w_i) \) is large enough to be the true class. In a classification task, the Bayes decision rule for a region \( R_{ni} \), represented by the feature vector \( \mathbf{x} \), amounts to assigning \( \mathbf{x} \) to class \( w_i \) if

\[
P(w_i|x) > P(w_j|x) \quad \forall \ j \neq i. \tag{12}
\]

For each homogeneous region found in the step of RAG analysis, the a posteriori probability is computed, and the regions are classified according to the Bayes decision rule, to obtain a probability map associated to each of the four desired classes in the brain image (background, CSF, GM, and WM). Next, a seed region is extracted, by searching the largest region with maximum probability in each map, to obtain four initial seeds, characterized by the intensity mode found by the MS algorithm. The classification of the other regions needs a distance measure that establishes how far the region’s intensity \( IR \) is from the seed’s intensity \( IS \). For each region \( R_n \), its distance to class \( w_i \) is

\[
d(R_n : w_i) = |IR_n - IS_i| \tag{13}
\]

and can be turned into a probability as follows:

\[
P(R_n : w_i) = 1 - \frac{d(R_n : w_i)}{\sum_{j=1}^{K} d(R_n : w_j)} \tag{14}
\]

where \( P(R_n : w_i) \) is the probability of the region \( R_n \) belonging to class \( w_i \), and \( R_n \) is assigned to the class with maximum probability \( P(R_n : w_m) = \max_{i} P(R_n : w_i) \).

V. METHODOLOGY OVERVIEW

The segmentation methodology proposed can be summarized as follows:

1) computation of the edge confidence map from the data to be segmented (Section II-C);
2) filtering by weighted MS procedure (Section II-B);
3) region adjacency analysis, applying transitive closure operations and pruning (Sections III-A and B);
4) spatial normalization between image data and a priori probability maps (Section IV-A);
5) region classification computing the a posteriori probabilities for each region and selecting the corresponding seeds (Section IV-B).

VI. RESULTS

In order to test the proposed segmentation technique, the algorithm was implemented in 4D, in the joint spatial (x, y, z) and range (intensity) domain. Synthetic and real images were used, taken from the Internet Brain Segmentation Repository (IBSR) [30] and the BrainWeb: Simulated Brain Database (SBD) [31]. One type of synthetic data corresponds to five volumes simulating the brain, with a very simple three-dimensional (3-D) model, and the other to a simulated MRI volume for normal brain. The real data consist of 20 normal brain MR data sets and their corresponding manual segmentations, provided by the Center for Morphometric Analysis at Massachusetts General Hospital and available at IBSR.

A. Synthetic Data

As a first example, we utilize the synthetic sphere phantom model from the IBSR. The basic model is built from 52 slices of 256 × 256 pixels containing two concentric spheres, where the inner sphere represents WM and the outer sphere GM. GM pixels are drawn from a normal distribution N(107, 8), while WM pixels are drawn from distribution N(147, 5). Available test volumes are derived from this basic model by further contamination with varying intensity bias fields, producing from zero to full class overlap. In Fig. 4, the results of the different segmentation process steps for a single slice can be appreciated. In order to test the robustness of the proposed algorithm and its generalization capability, five synthetic volumes were processed under different noise conditions and without any variation of the parameters, which are shown in Table I.

Fig. 4 shows an example slice, where the intensities of the two contained classes are strongly overlapped due to bias artifacts; the intermediate results through all the segmentation process can also be observed. The first step is to compute the edge confidence map [Fig. 4(b)] starting from the original image [Fig. 4(a)]; in this step, the involved parameters are: the gradient window size, \( m_n \), the edge threshold, \( \delta \), and the blending factor, \( \beta \). The second step consists on filtering the original image, where the spatial radius, \( h_s \), and the intensity radius,
must be considered. The filtered image [Fig. 4(c)] contains many homogeneous regions (1165 in this example) which are labeled with an arbitrary color scale in Fig. 4(d); this result is then fed through the third step for region adjacency analysis, which reduces the number of regions through transitive closure operations. The threshold of boundary strength (ξ) and the intensity radius (hₐ) must be considered in this step, to merge and reduce the number of regions through transitive closure. The threshold of boundary strength is estimated to select seeds, and Fig. 5(f) shows the result obtained after transitive closure and Fig. 5(g) is the result obtained after pruning (step 3); Fig. 5(h) presents the mean-shift filtered image, labeled with the corresponding estimated intensities; Fig. 5(i) shows the final classification (step 5). Fig. 6 shows the results obtained for two slices. The first column shows the original images; the second, the segmented results applying the methodology and the third, the reference images. The similarity indexes (mean ± std) between the phantom brain segmented by the proposed methodology and the ground truth were as follows: 0.996 ± 0.005 for background, 0.871 ± 0.031 for CSF, 0.9 ± 0.012 for the standard metric in MRI segmentation analysis, and for performance comparison purposes they still have to be used.

The Tanimoto coefficient (TC), between the segmented image (X) and expert segmentation (Y), is the ratio of the number of elements they have in common classified as class k, to the number of all elements classified as class k. It is then defined as [29]

$$TC_{XY}(k) = \frac{n_{X \cap Y}(k)}{n_X(k) + n_Y(k) - n_{X \cap Y}(k)} = \frac{n_{X \cap Y}(k)}{n_Y(k)}$$

(15)

Fig. 5 shows all the intermediate results corresponding to each step of the methodology (see Section V). Fig. 5(a) is the original image; Fig. 5(b) presents the corresponding confidence map (step 1); Fig. 5(c) contains the mean-shift filtered image (step 2); Fig. 5(d) is the same filtered image, labeled to apply region adjacency analysis, Fig. 5(e) is the image obtained after transitive closure and Fig. 5(f) is the result obtained after pruning (step 3); Fig. 5(g) shows the segmented image, labeled with the corresponding estimated intensities; Fig. 5(h) presents the a posteriori probabilities for each region of image 5f, estimated to select seeds, and Fig. 5(i) shows the final classification (step 5).
Fig. 6. Two examples of synthetic brain segmentations: column (a) original images, column (b) segmented images, and column (c) reference images.

Fig. 7. Tanimoto indexes along the axial scans (slices) of a selected case. Comparison is made between a segmented synthetic brain (phantom) and the reference truth. Synthetic scans have been processed with the proposed methodology.

GM, and 0.924 ± 0.038 for WM. Fig. 7 shows the variation of the Tanimoto indexes throughout the phantom stack.

B. Real Data

The same procedure was applied to real data, by processing the 20 data sets and their manual segmentation collected from the IBSR. The expert manual segmentation is considered the reference set to be used to compare our procedure with other methods also available at the IBSR. Comparison is achieved through the computation of Tanimoto indexes between the experimental results and the reference. The parameter values used to process these volumes are shown in Table I, and were kept constant for all slices of all subjects; note that these are also the parameters used in the synthetic brain example. Two segmentations of coronal slices are shown in Fig. 8; the first column presents the original data, followed by the segmentation obtained with the proposed methodology in the second column, that can be compared with the manual segmentation carried out by the expert shown in the third column. Fig. 9 shows a 3-D view of a whole stack segmentation obtained with the approach (column b), for GM (row I), WM (row II), and CSF (row III), which can be compared with the corresponding reference in column (a).

Table II shows a comparison of the average TC, obtained by segmenting the 20 available volumes, with several approaches reported in the IBSR; the last row presents the quantification of our results obtained for the same volumes. It can be observed
TABLE II

<table>
<thead>
<tr>
<th>Method</th>
<th>Background</th>
<th>CSF</th>
<th>Gray</th>
<th>White</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adaptive MAP</td>
<td>0.999</td>
<td>0.069</td>
<td>0.564</td>
<td>0.567</td>
</tr>
<tr>
<td>Biased MAP</td>
<td>0.999</td>
<td>0.071</td>
<td>0.558</td>
<td>0.562</td>
</tr>
<tr>
<td>Fuzzy c-means</td>
<td>0.999</td>
<td>0.048</td>
<td>0.473</td>
<td>0.567</td>
</tr>
<tr>
<td>MAP (maximum a posteriori probability)</td>
<td>0.999</td>
<td>0.071</td>
<td>0.550</td>
<td>0.554</td>
</tr>
<tr>
<td>Maximum-Likelihood</td>
<td>0.999</td>
<td>0.062</td>
<td>0.535</td>
<td>0.551</td>
</tr>
<tr>
<td>Tree-structure k-means</td>
<td>0.999</td>
<td>0.049</td>
<td>0.477</td>
<td>0.571</td>
</tr>
<tr>
<td>Mean shift – edge conf. / MAP</td>
<td>0.996</td>
<td>0.210</td>
<td>0.594</td>
<td>0.628</td>
</tr>
</tbody>
</table>

that the proposed approach has a superior performance for the three segmented structures of interest.

The performance of the proposed algorithm for each stack can be observed and compared in Fig. 10, which shows the individual Tanimoto indexes for each volume obtained with other reported procedures, for both GM and WM. Stack ordering follows the degree of segmentation difficulty as assigned by human experts (IBSR), with stack one being the hardest to process and stack 20 the easiest.

The algorithm has been implemented on a PC desktop machine (Pentium III Xeon 1 GHz), using Matlab; on this platform, the segmentation of a 256 × 256 image takes about one minute in a slice implementation and 13 minutes for the volumetric implementation.

VII. DISCUSSION

Most of the brain segmentation techniques discussed in the field require conformance to diverse assumptions, such as a specific probability density distribution [7], [15], [32]–[34], piecewise linear gray level homogeneity [35], or a given number of tissue classes present in the image [1], [7], [15], [34]. Further, there are usually requirements for initialization procedures [32]–[35], or image preprocessing for bias correction [1], [2], [8], [33], [35], all performed previous to actual image segmentation. On the other hand, feature space analysis for image segmentation as proposed in this paper is exclusively guided by the data when the MS algorithm is applied, avoiding the aforementioned shortcomings (statistical assumptions, initialization or preprocessing). MS segmentation has found its applications in object recognition and tracking, and in color image segmentation and compression. To the best of our knowledge, the approach proposed in this paper is the first application of such a powerful technique to brain image segmentation.

The edge confidence map weighted MS algorithm has shown a good performance in the search and localization of the modes of an unknown pdf, allowing the delineation of homogenous regions of a cerebral MRI. Furthermore, the proposed classification strategy allows the identification of tissue type that each region corresponds to. Combination of edge confidence maps and homogenous regions segmentation, showed a good performance in presence of noise and intensity inhomogeneity, preserving the borders between regions, and proving to be robust in the separation of image classes. In the proposed strategy, the identification of neuroanatomical structures depends on the number of probabilistic maps available.

![Fig. 10. Tanimoto coefficients for (a) GM and (b) WM for each of the 20 case studies, as processed by six reported methods and the proposed procedure (adapted from [30]). The brain scans have been roughly ordered by their difficulty to be segmented: scan 1 is the most difficult and scan 20 the least.](image)

Even though the procedure does not require an initialization stage, the parameters might have to be tuned prior to segmentation. We carried out this process by estimating the set of parameters that best segmented a synthetic brain test image, considering the Tanimoto index as the evaluation criterion. These values were also successfully used for real images, thus indicating that a default parameter set can be determined.

Spatial resolution has a major effect in execution time: the greater the spatial radius, the larger the processing time. On the other hand, segmentation quality depends considerably on the intensity resolution: a small $h_\delta$ produces many regions, thus over-segmenting the image, while a higher intensity radius can produce sub-segmented images (few regions). Only image features with large spatial support are represented in the filtered image when $h_\delta$ increases, and only structures with very different intensity values remain independent when $h_\delta$ is large.
A value of edge threshold near zero or one produces, respectively, over or sub-segmentation; whereas a small blending factor (relevance of confidence larger than that of gradient magnitude) preserves weak edges and deals with bias effects. The boundary strength threshold is calculated from the confidence map, and influences the region fusion step, over-segmenting when its value is near zero, and highlighting the edges when it tends to one, producing sub-segmentation.

In summary, the parameters that have a higher influence in the algorithm performance are the kernel radii \( h_x, h_y \) and the blending factor \( \beta \). At this moment, the approach proposed here is not intended to be run in a fully automatic mode and, thus, an initial calibration step might be necessary for parameter tuning. In future work, an adaptive radii scheme can be proposed.

Figs. 8 and 9 provide a qualitative comparison between the segmentations obtained with the proposed method and the reference stack, in two-dimensional and 3-D view, respectively. The similarities between segmented structures can be clearly appreciated for GM and WM. In the case of the CSF reconstructions, it is seen that our algorithm is capable of detecting both intra- and extra-ventricular CSF, which the reference stacks do not include. While in a first impression this condition appears as segmentation noise, it is indeed a more complete description of the corresponding class. As for quantitative results, the performance of our method is clearly appreciated for brain simulations, where Tanimoto indexes of 0.87 and more were obtained for all structures. In real data our results show a better performance compared to the methods reported in [30] (see Table II), while other authors [15], [33] have obtained higher indexes for the same image cases. However, the lack of sensitivity of the performance measure for describing local changes makes it hard to argue about the overall superiority of one method with respect to the other. In this perspective, the method comparisons are more relevant in the domain of model assumptions, required preprocessing, or computational load.

To conclude, the main contributions of the method proposed in this paper are: 1) the application is totally driven by the data contained in the image, using a fixed parameter set that is not individually tuned to each case; 2) the MS estimation is robust even in the presence of severe bias inhomogeneity, without the need of a prior or simultaneous bias estimation and correction procedure; and 3) the use of an edge confidence map adequately preserves tissue boundaries, even for weak edges due to partial volume effects. Beyond initial parameter selection, the approach is fully automatic being, therefore, an alternative tool for radiologists, saving time and providing information that depends only on the image data.

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