Automatic Segmentation of MR Brain Tumor Images using Support Vector Machine in Combination with Graph Cut

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Keywords: MRI Segmentation, Brain Tumor Segmentation, Meningioma, Graph Cut, Support Vector Machine.

Abstract: This work focuses the attention on the automatic segmentation of meningioma from multispectral brain Magnetic Resonance imagery. The Authors address the segmentation task by proposing a fully automatic method hierarchically structured in two phases. The preliminary unsupervised phase is based on Graph Cut framework. In the second phase, preliminary segmentation results are refined using a supervised classification based on Support Vector Machine. The overall segmentation procedure is conceived fully automatic and tailored to non-volumetric data characterized by poor inter-slice spacing, in an attempt to facilitate the insertion in clinical practice. The results obtained in this preliminary study are encouraging and prove that the segmentation benefits from the allied use of Graph Cut and Support Vector Machine frameworks.

1 INTRODUCTION

Magnetic Resonance (MR) imaging has become an important tool for the clinical study of brain pathologies. The high resolution and contrast and good soft tissue differentiation allow physicians accurately locate specific pathologies. A precise segmentation of pathological and healthy tissues composing the MR image is important for understanding the pathology, for evaluating the evolutionary trend, for planning the best surgical approach or possible alternative solutions. Automated methods of segmentation represent a valuable solution by supporting human operators with varying degrees of automation, in tracing the boundaries of the different tissue regions and by automatically providing volumetric computation of the pathological MRI signal (Clark et al., 1995, Kaus et al., 2001; Withey and Koles, 2008; Balafar et al., 2010).

The last 20 years have seen a rapid growth in the use of semi-automatic or fully automatic segmentation methods in MR brain tumor studies. Several techniques have been proposed in studies distinguished by the type of brain tumor treated, by the tissue features extracted in different MRI modalities. The proposed techniques make use of individual images or multispectral patterns and are supervised or unsupervised (Gordillo et al. 2013, Bauer et al. 2013). Despite the sizable achievement obtained, novel approaches are continuously investigated to provide robust solutions and fulfil hard accuracy and reproducibility requirements. In the last few years Support Vector Machine (SVM) methods (Vapnik 1995; Schoelkopf and Smola 2002) have shown excellent performances in MRI segmentation studies aimed at identifying a variety of neurological conditions (Verma et al. 2008, Bauer et al., 2013). Recent studies propose the allied use of SVM and regularisation procedures to introduce spatial consistency in classification results (Bauer et al. 2011).

This work focuses the attention on the automatic segmentation of meningioma from multi-spectral brain MR imagery. Meningioma is one of the few benign tumors found in the brain region. Precise tumor detection contributes to formulate surgical indications in elderly patients harboring intracranial meningiomas and supports surgical planning for a complete surgical resection (Greenberg et al. 1999, Caroli et al. 2005).

The Authors address the segmentation task by proposing a fully automatic method hierarchically structured in two phases. The preliminary unsupervised phase is based on Graph Cut

Binaghi E., Omodei M., Pedoia V., Balbi S., Lattanzi D. and Monti E..
Automatic Segmentation of MR Brain Tumor Images using Support Vector Machine in Combination with Graph Cut.
DOI: 10.5220/0005068501520157
In *Proceedings of the International Conference on Neural Computation Theory and Applications* (NCTA-2014), pages 152-157
ISBN: 978-989-758-054-3

framework (Boykov and Funka-Lea 2006). In the second phase preliminary segmentation results are refined using a supervised classification based on Support Vector Machine (SVM) (Vapnik 1995). The supervised classification makes use of multichannel intensities of Post Gadolinium T1-weighted (T1c) and T2-weighted FLAIR image (T2f). Additional textural and contextual features are considered and systematically added during the experimentation in order to measure their effective contribution. The proposed hybrid strategy synergically combines the mutual advantages of the unsupervised and supervised techniques. The Graph Cut segmentation takes into account topological constraints and identify spatially consistent regions subsequently refined by the SVM which is able to capture complex multivariate relationships in the data.

The overall segmentation procedure is conceived fully automatic and tailored to non-volumetric data characterized by poor inter-slice spacing, in an attempt to facilitate the insertion in current clinical practice.

2 THEORETICAL BACKGROUND

This section briefly outlines the basic concepts of Graph Cut and SVM adopted in the proposed hybrid segmentation strategy.

2.1 Graph Cut

Within the graph theoretical approach, the segmentation problem is modeled in terms of partitioning a graph into several sub-graphs such that each of them represents a meaningful object of interest in the image (Wu and Leahy, 1993; Rother et al. 2004, Peng and Liu, 2010). Proceeding from these principles several methods were investigated.

The aim of a volumetric segmentation problem is to assign to each voxel v ∈ V a label representing the membership of the voxel to a specific region Li; in the case of binary segmentation aimed to subdivide the image into Object (Obj) and Background (Bkg), the goal is to find the optimal labeling L = (L_{Bkg};L_{Obj}). We assume that each voxel *v* has two cost values, R*v*(O_{Obj}) and R*v*(O_{Bkg}), related to Object and Background labeling respectively. Each pair of voxels (*v,w*) belonging to the set N of pairs of 3D neighboring voxels has a cost $B_{v;w}$. The cost $B_{v;w}$ is related to the type of labeling of the pair of voxels. The optimal labeling L = (L_{Bkg};L_{Obj}) is obtained by minimizing the following cost function:

$$E(L) = \lambda R(L) + B(L)$$

where

$$R(L) = \sum_{v \in V} R_v(O_v)$$

$$B(L) = \sum_{v,w \in N} B_{v,w} \delta_{L_i,L_j} \; ;$$

$$\delta_{L_i,L_j} = \begin{cases} 0 \text{ if } L_i = L_j \\ 1 \text{ if } L_i \neq L_j \end{cases}$$

R(L) and *B(L)* are called Regional and Boundary terms respectively. The application of Graph Cut requires the identification of object and background prototypes with which to initialize the overall segmentation process. Usually this task is accomplished through an interactive session in which users manually select seeds on the image.

Recently there have been some proposals exploiting solutions for automatically initializing Graph Cut-based segmentations of biomedical images (Santle et al., 2012).

The present study uses the max-flow/min-cut algorithm (Boykov and Kolmogorov 2004) as optimization framework and adopts an automated initialization procedure based on k-means clustering algorithm.

2.2 SVM

SVM is a classification algorithm based on kernel methods (Vapnik 1995; Schoelkopf and Smola 2002) able to map the original parameter vectors into a higher (possibly infinite) dimensional feature space through a kernel function. Classes which are non-linearly separable in the original space can be linearly separated in the higher dimensional feature space.

Let {(xi, yi)} a supervised training set of elements for a two-class classification problem, with xi ∈ X ⊆ Rn and yi ∈ {-1, 1}. Considering the case of linearly separable data, the solution to the classification problem consists in the construction of the decision function

$f_{w,b}(x) = \text{sgn}(g_{w,b}(x))$ with $g_{w,b}(x) = w^t x + b$ that can correctly classify an input pattern x that is not necessarily from the training set.

SVM classifier defines the hyperplane that causes the largest separation between the decision function values for the "borderline" examples from the two classes. Mathematically, this hyperplane can be found by minimizing the cost function:

$$J(W) = \frac{1}{2}\|W\|^2 \quad \text{subject to}$$

$$W^T X_i + b \geq +1 \text{ for } y_i = +1$$

or

$$W^T X_i + b \leq -1 \text{ for } y_i = -1$$

The extension to the nonlinear classification is based on the function $g' = W^T \varphi(X) + b$ in which the non liner operator $\varphi(.)$ is introduced.

In this case the SVM cost function to be minimized is

$$J(W,\xi) = \frac{1}{2}\|W\|^2 + C\sum_{i=1}^{l}\xi_i \quad \text{subject to}$$

$$y_i\left(w^t\phi(X_i)+b\right) \geq +1-\xi_i \text{ with } \xi_i \geq 0, i = 1,2,....l$$

Linearly non separable data are analyzed with kernel functions such as higher order polynomials and Gaussian Radial Basis Functions (RBF). Suykens (Suykens et al. 2002) proposed a new formulation of SVM by adding a least squares (LS) term in the original formulation of the cost function.

3 FULLY AUTOMATED MENINGIOMA SEGMENTATION

The salient aspect of the overall segmentation strategy is the use of a supervised learning procedure based on SVM model, able to learn from a set of labeled image elements the invariant common properties of the pathological and healthy classes. The trained classifier automatically assigns labels to elements never seen during the training phase.

The use of the two MR modalities, T1c and T2f, is motivated by the fact that each scan depicts different characteristics of the tissues. The combined use of the two images allows obtaining higher discriminant power than just by analyzing one of them.

The SVM classifier acts as a dichotomizer receiving in input a multidimensional pattern including intensities of T1c and T2f MR elements and contextual/textural features derived from the two scans respectively. The supervised classification procedure is built on the top of an unsupervised unidimensional Graph Cut-based segmentation of T1c and T2f MR images. The unsupervised stage facilitates the subsequent supervised task by identifying an intermediate hybrid class distributed in a limited area and subsequently subdivided by the SVM in meningioma and healthy tissue.

Before the segmentation process, T1c and T2f MR images are co-registered for their combined use in the analysis and a logarithmic contrast enhancement is applied in order to enhance the similarity between the edema and brain tissues in the T2f image.

3.1 Graph Cut Based Segmentation

Graph Cut segmentation is separately applied to T1c and T2f images allowing the labeling of intermediate hybrid regions. The intersection of these initially identified regions is subsequently analyzed and classified by the SVM to identify meningioma areas. The initialization of the Graph Cut segmentation is automatically accomplished through the use of the k-means clustering algorithm. The segmentation of T1c image in three sub-volumes allows to identify a hybrid region including all the contrast enhanced tissues: meningioma, vessel and skull tissues.

From the segmentation of T2f image a partition of the original volume in three regions is also obtained corresponding to "air", "brain/edema/meningioma" and "skull" respectively. By intersecting the hybrid region originally identified in T1c with the "brain/edema/meningioma" region identified in T2f we obtain a refined region of interest to be presented in input to the SVM classifier for the identification of meningioma areas.

3.2 Supervised Multispectral Classification

The present study considers the following features: gray scale values from T1c and T2f scans (I_{t1c},I_{t2f}), first order texture features: mean (M) , variance (Var), skewness (S), kurtosis (K) and entropy (E) computed on T1c and T2f scans, intensities in neighborhoods of voxels of both scans (I1-I26) . All proposed features have been analyzed systematically in the experimental evaluation phase in order to determine the combination that is most appropriate for the classification task (see section 4). The features have been normalized to have zero mean and unit variance.

A binary hard categorization is performed by the SVM classifier that labels co-registered voxels belonging to the region identified in the unsupervised phase, as Meningioma (M) and Healthy tissue (H). The SVM classifier is configured as soft-margin LS model with Kernel RBF. During the training phase, the SVM learns an approximation for the true input–output relationship based on a given training set of examples constituted by N

input-output pairs $\{x_i, y_i\}, i = 1, \ldots, N$. The input pattern $x_i = [f_1^i, .. f_m^i]$ is an m-dimensional feature vector where m is the number of features considered in the current configuration, and $y_i \in \{M, H\}$ is a supervised label denoting the membership in the meningioma or healthy class.

After the segmentation, if the tumor area presents necrosis and dishomogeneity, small holes within the tumor mass classified as healthy tissues may appear . A morphological procedure is therefore used to refine the segmented masks making the tumor area segmented more solid and compact.

4 EXPERIMENTS

The segmentation method was experimented on multispectral datasets of 10 patients. Each dataset is composed of T1c and T2f scans. The T1c is acquired using a 3D sequence characterized by 1 mm isotropic voxels, the inter-slice spacing of 1 mm and the slice thickness of 1 mm; the T2f sequence includes an in-plane resolution between 0,75 and 0,81 mm and slice thickness of 5 mm. The spacing between slice is 6 mm for cases 1,3,6,7,8,10 and of 6.5 mm for cases 2,4,5,9. Performances were assessed by adopting a behavioral comparison strategy in which the masks obtained by the automated segmentation were compared with the masks obtained through a manual segmentation of the T1c images. Manual labeling was performed by a team of three experts with the support of a slice-by-slice manual annotator.

The strategy adopted for the definition of a suitable reference standard starting from combination of multiple manual segmentations, is Majory Voting (Heckemann et. al 2006).

4.1 Metrics

MRI segmentation was performed with the purpose of determining the volume of pathological tissues and their spatial distribution. The metrics adopted for the volume estimation error is the normalized absolute difference in size between reference and segmented data.

Spatial overlap between reference and automated maps is measured in terms of Jaccard (J), Precision and Recall indexes (Bouix et al. 2007).

Common agreement between experts and automated segmentation is quantified directly by the Williams' index. If this index is greater than one for a given rater, it can be concluded that current rater agrees with the other raters at least as well as they agree with each other (Williams 1972).

4.2 Results

A trial and error phase was conducted in which several configurations of the segmentation procedure were considered distinguished by different values of main parameters involved.

A first set of parameters was varied to tune the Graph Cut model and the LS-SVM classifier. The k-means algorithm has been used to initialize Graph Cut segmentation. The value of k parameter was set equal to three. The k value has been assessed taking into account the expected MR signal in both the MRI sequences considered. The value of the standard deviation (σ) for Gaussian RBF kernel was chosen as 0.5 in the SVM classifier.

Different configurations of the classification procedure were also evaluated varying the number of training examples and the features considered. The configuration that showed the most balanced behavior after the trial and error phase is based on the following vector of features

$$x_i = [x_{t1c}, x_{t2f}] \text{ with}$$
$$x_{t1c} = [I^i{}_{t1c}, M^i{}_{t1c}, Var^i{}_{t1c}, S^i{}_{t1c}, K^i{}_{t1c}, E^i{}_{t1c}]$$
$$x_{t2f} = [I^i{}_{t2f}, M^i{}_{t2f}, Var^i{}_{t2f}, S^i{}_{t2f}, K^i{}_{t2f}, E^i{}_{t2f}]$$

and used a training set of 10.000 labeled samples randomly chosen within the ground truth masks.

Table 1: Mean values of Jaccard, Precision, Recall and Volume Error obtained by performing the leave-one-out cross-validation (Interpatient) and by training and testing the classifier on the same dataset (Intrapatient).

		Jaccard Index	Precision	Recall	Volume Error (%)
Interpatient	Mean	0.867	0.814	0.942	16.087
	Std	0.072	0.095	0.081	11.145
Intrapatient	Mean	0.959	0.967	0.991	4.750
	Std	0.031	0.031	0.004	3.152

As shown in Table 1, for the intrapatient analysis, the mean Jaccard coefficient over all 10 patients is 0.959, Precision and Recall have a value equal to 0,967 and 0,991 respectively; the Volume Estimation Error is equal to 4,750. The interpatient analysis has provided a Jaccard cofficient equal to 0,867, Precision and Recall equal to 0,814 and 0,942 respectively and a Volume Estimation Error equal to 16,087.

In Table 2 the results obtained using the Williams' index are listed. Numerical values clearly

Table 2: Williams' Indexes obtained by considering the manual segmentations (E1-E3) and the automatic segmentation (A) of the 10 cases under study.

W. I.	1	2	3	4	5	6	7	8	9	10
E1	1.0	1.0	1.0	1.0	1.0	0.9	0.9	1.0	0.9	1.0
E2	0.9	0.9	1.0	0.9	0.9	1.0	1.0	1.1	0.9	0.9
E3	0.9	1.0	0.9	1.0	0.9	1.0	1.0	0.7	1.0	1.0
A	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.1	1.0	1.0

indicate that the automatic segmentation method has a good behavior with respect to the inter-expert variability and often it shows a better behavior than other raters.

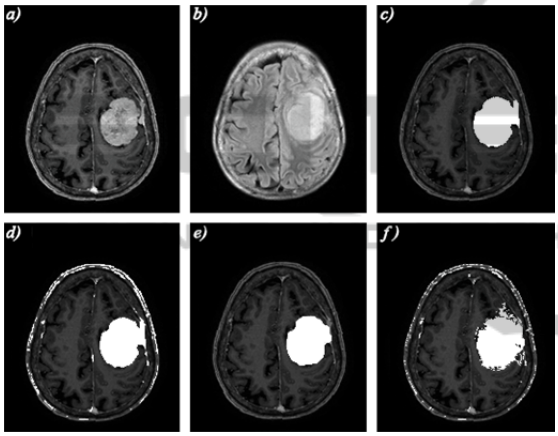

Figure 1: Results of one axial slice obtained by the interpatient analysis. a) Original T1c image, b) Original T2f image, c) Overlap between original T1c image and the ground truth mask, d) Overlap between original T1c image and the intermediate mask obtained by Graph Cut segmentation, e-f) Overlap between original T1c image and the final segmentation mask obtained by interpatient analysis, considering and without considering Graph Cut stage respectively.

Figure 1 shows an axial slice of one patient and the results obtained considering and without considering Graph Cut stage in the overall strategy. Results are clearly worse when not using the Graph Cut preliminarily. For the dataset shown in Figure 1, we obtained a Jaccard coefficient equal to 0.21109 and Volume Error equal to 363.4476 when no Graph Cut is applied. With the complete procedure, Jaccard is equal to 0.856 and Volume Error is equal to 7.119. The mean computation time for the training task is 60 seconds and for the segmentation task performed by the trained classifier is 159 seconds (without Graph Cut, 732 s.) on a single CPU running at 2.26 Ghz.

5 CONCLUSIONS

Our objective in this study was to develop a fully automatic hybrid image segmentation strategy for meningioma segmentation in Magnetic Resonance brain images. The supervised segmentation framework is built on the top of the Graph Cut algorithm initialized automatically. The strategy was tested on a preliminary collected data set. The results prove that the allied use of Support Vector Machine and Graph Cut produces accurate segmentation of tumors present in scenarios of varied complexity. Accuracy results obtained are encouraging. Future plans contemplate the acquisition of new data with which to perform a more significant interpatient analysis and to develop of a comparative evaluation with other methods.

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