3D variational brain tumor segmentation on a clustered feature set

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ABSTRACT

Tumor segmentation from MRI data is a particularly challenging and time consuming task. Tumors have a large diversity in shape and appearance with intensities overlapping the normal brain tissues. In addition, an expanding tumor can also deflect and deform nearby tissue. Our work addresses these last two difficult problems. We exploit the various MRI modalities and their texture characteristics to construct a multi-dimensional feature set. Further, we extract clusters which provide a compact representation of the essential information in these features. The main idea in this paper is to incorporate these clustered features into the 3D variational segmentation framework. In contrast to the previous variational approaches, we propose a segmentation method that evolves the contour in a supervised fashion. The segmentation boundary is driven by the learned inside and outside region voxel probabilities in the cluster space. We incorporate prior knowledge about the normal brain tissue appearance, during the estimation of these region statistics. In particular, we use a Dirichlet prior that discourages the clusters in the ventricles to be in the tumor and hence better disambiguate the tumor from brain tissue. We show the performance of our method on real MRI scans. The experimental dataset, includes difficult instances with tumors that are inhomogeneous in appearance, small in size and in proximity to the major structures in the brain. Our method shows good results on these test cases.

Keywords: MRI segmentation, Variational methods, Clustering methods, Tumors

1. DESCRIPTION OF THE PURPOSE

Radiation oncologists, radiologists, and other medical experts spend a substantial portion of their time segmenting medical images. In particular, the task of labeling brain tumors and edema in MRI images is highly time consuming and there exists significant variation between the labels produced by different experts. Further, in most cases the 2D image slices are labeled independently without taking into account the global 3D brain structure leading to potentially inaccurate segmentations. Subsequently, a large amount of research has been focused on semi-automatic and fully automatic methods for detecting and/or segmenting brain tumors from MRI scans.

The process of segmenting tumors in MRI images as opposed to natural scenes is particularly challenging. The tumors vary greatly in size and position, have a variety of shape and appearance properties, have intensities overlapping with normal brain tissue, and often an expanding tumor can deflect and deform nearby structures in the brain giving an abnormal geometry also for healthy tissue. Therefore, in general it is difficult to segment a tumor by simple unsupervised thresholding.[1] Alternatively, different machine learning (ML) classification techniques have been investigated: SVMs (Support Vector Machines),[2] MRFs (Markov Random Fields),[3] and most recently CRFs (Conditional Random Fields).[4] Apart from the work on classification techniques, recently discrete segmentation approaches using graph cuts have been proposed for brain tumor segmentation.[5,6] On the other hand among the continuous approaches, the variational and level set methods have also been explored with considerable interest in the past few years .[7–10] The variational methods were originally formulated in an unsupervised[11,12] fashion, subsequently for the MRI segmentation task, the level sets are typically applied without initial training .[8,10] In the case of brain tumor segmentation, the lack of shape or intensity priors on the tumors, makes it challenging to proceed in an unsupervised manner. Some recent progress has been made to create semi-supervised[13] (based on user interaction) or supervised variational methods.[7] We propose a supervised variational method that incorporates additional appearance priors to better disambiguate the tumor from the surrounding deformed brain tissue. The formulation extends the Chan-Vese region-based segmentation model[14] in a similar way to texture-based approaches.[12] But instead of using an unsupervised approach we use existing manually labeled data to learn a statistical model and Dirichlet prior from a set of clustered features. The previously proposed clustering [15] and fuzzy clustering methods [16,17] for MRI tumor segmentation, attempt a direct tumor, non-tumor classification. In this paper we perform clustering

to parsimoniously describe the salient information in the extracted MRI features. The brain tissues and the tumor each, then are characterized by one or more of the clusters. We summarize the main contributions of this paper as follows*:

- We extract clusters from a high dimensional feature set and integrate these clusters into a 3D variational segmentation framework.
- By using a Dirichlet prior that disambiguates the tumor from the surrounding brain tissue, we address difficult segmentation cases, where a tumor grows next to the ventricles. Experimental results of these challenging cases show good performance of our method.

2. METHOD

In this section we present general formulation of the 3D variational segmentation problem and our proposed clustering procedure to handle multivariate data.

2.1 3D region based active contour model

Given an image volume $I : \Omega \rightarrow \Re^+$ defined on a open and bounded domain $\Omega \subset \Re^3$ the binary segmentation task consists of finding a regular surface Γ that splits the domain Ω into two disjoint regions Ω_1, Ω_2. Following,[18] this region based binary segmentation problem is equivalent to minimizing the following energy:

$$E(\Omega_1, \Omega_2) = -\int_{\Omega_1} \log\, p_1(\mathbf{x})\, d\mathbf{x} - \int_{\Omega_2} \log\, p_2(\mathbf{x})\, d\mathbf{x} + \nu|\Gamma| \tag{1}$$

where p_1, p_2 are the probability density functions that model the two regions. Using the level set function $\phi : \Omega \rightarrow \Re$ to represent the surface as $\Gamma = \{x \in \Omega | \phi(\mathbf{x}) = 0\}$, we can minimize the above energy using the evolution equation in ϕ as:

$$\frac{\partial \phi}{\partial t} = \delta(\phi)\left(\log\, p_1 - \log\, p_2 + \nu\, \mathrm{div}\left(\frac{\nabla \phi}{|\nabla \phi|}\right)\right) \tag{2}$$

where, $H(\phi)$, $\delta(\phi)$ are regularized Heaviside and Dirac delta functions respectively.

2.2 Extension to multiple features

Let $\mathcal{I} = \{I_1, I_2, \ldots, I_m\}$ be the set of feature images, we can consider the feature set as multivariate data $\mathbf{I} : \Omega \rightarrow \Re^m$, where each pixel location corresponds to a m dimensional vector $\mathbf{I}(\mathbf{x}) = [I_1(\mathbf{x})\ I_2(\mathbf{x}) \ldots I_m(\mathbf{x})]$.[19] We propose a clustering approach to handle the multivariate image data. We use the K-means algorithm with an Euclidean distance measure in the space of the features to obtain K cluster centers $\mathbf{c}_k \in \Re^m$, $k = 1, 2, \ldots, K$.. We define a "cluster image", $\hat{I} : \Omega \rightarrow \{1, 2, \ldots, K\}$ corresponding to a given vector image $\mathbf{I}$ as

$$\hat{I}(\mathbf{x}) = \underset{k}{\mathrm{argmin}} \parallel \mathbf{I}(\mathbf{x}) - \mathbf{c}_k \parallel^2 \quad \forall \mathbf{x} \in \Omega$$

A set of feature images are thus replaced by a single "cluster image" in the active contour segmentation model. The evolution equation then the same as (2) , with the pixel probability densities now defined on the range of the "cluster image" (Figure 1).

2.3 Separating tumor and ventricles using a Dirichlet prior

Most variational segmentation techniques are used in an unsupervised setting where the region statistics are refined as the curve evolves.[11,12] This might be quite effective if the region statistics are distinct. But, as mentioned earlier, one of the main problems in brain tumor segmentation is that the appearance of tumor and surrounding tissue are not always clearly separated (not even in the feature space). As an example see Figure 1. We therefore have to use additional prior information to help the segmentation. The tumor doesn't have a particular shape prior. In addition, the surrounding tissues (like the ventricles) can be deformed and therefore don't preserve a shape prior. We chose to use a prior on the appearance that better disambiguate the two regions.

*This work is not being currency presented or submitted to any other conference or journal other than SPIE

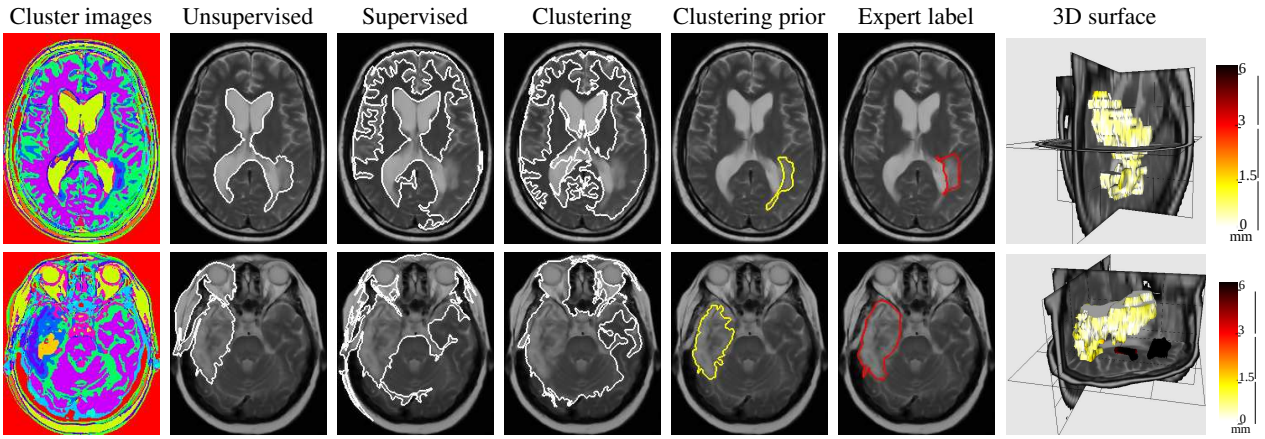


Figure 1: Comparative results of different segmentation methods (rows represent different patients). col 1 - colors represent clusters; 2 col *white* - unsup. feat. hist. automated label; 3 col *white* - sup. feat. hist. automated label; col 4 *white* - cluster hist. automated label; col 5 *yellow* - cluster hist. + prior automated label; col 6 *red*- manual label; col 7 - 3D surface with distance error (color coded)

We used manually labeled data for getting an initial statistics for tumor/brain regions in the clustered feature space. Most segmentation errors are caused by the vicinity of tumor and ventricles when part of the ventricles are incorrectly segmented as tumor (see Figure 1 (top row)). We designed a prior that penalizes the clusters predominant in the ventricles from having a high probability in the tumor. Hence, we assumed a Dirichlet prior for (p_1, p_2) skewed in such a fashion that those prominent clusters in ventricles have a very low prior probability and the rest of the clusters have uniform probability. We used images with manually segmented tumors and ventricles to identify the overlapping clusters.

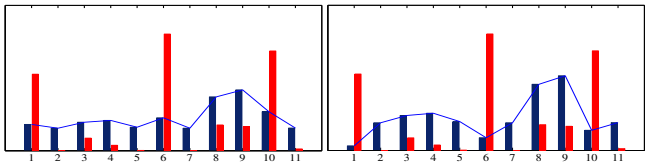
Given $\mathcal{D} = \{\hat{I}^{(1)}, \hat{I}^{(2)}, \ldots, \hat{I}^{(N)}\}$ a set of training cluster images. We denote θ_k the probability of cluster k and regard $\boldsymbol{\theta} = \{\theta_1, \theta_2, \ldots, \theta_K\}$ as parameters of a Bayesian system. Assuming a Dirichlet prior over the parameters i.e. $p(\boldsymbol{\theta}) \sim \mathrm{Dir}(\alpha_1, \alpha_2, \ldots, \alpha_K)$, where $\{\alpha_1, \alpha_2, \ldots \alpha_K\}$ are the hyper parameters, the posterior probability of a cluster is

$$p_i(\hat{I}(\mathbf{x}) = k|\mathcal{D}) = \mathbf{E}_{p(\boldsymbol{\theta}|\mathcal{D})}[\theta_k] = \frac{\alpha_k + M_k}{\sum\limits_k \alpha_k + \sum\limits_k M_k} \tag{3}$$

where M_k's are the counts of the clusters in the training data. Now we can observe that by choosing a relatively low value for α_k, we can suppress the posterior probability of the cluster k. (see Figure 2). The posteriors p_1, p_2 give the tumor/brain probabilities in (2) .

3. RESULTS

Our data set consists of 21 MRI volumes of patients having either a grade 2 astrocytoma, an anaplastic astrocytoma or a glioblastoma multiforme. The tumor (actually edema = tumor+swelling) area was manually segmented in each image by an expert radiologist. We divided the data in two sets, training on 15 patients and testing on the other 6 patients. We compare 4 segmentation methods: (1) traditional unsupervised segmentation with Parzen histogram on the feature set images; (2) supervised segmentation on the feature images where Parzen histograms were computed based on the training data; (3) supervised segmentation on the clustered image; (4) our proposed segmentation method that uses appearance priors to disambiguate the tumor from the ventricles. We tested difficult cases with small tumors, tumors growing very close to the normal anatomical elements in the brain (like ventricles, eyes) and non-homogenous tumors. In Figure 1 we show two of the test cases, using 2D slices that are representative of the performance of the four segmentation methods. The last column displays color coded 3D surface, showing the distance error between the segmentation label generated by our proposed method and the the manual label. In Figure 2 we present the Jaccard scores (overlap between labels and automatic segmentation) mean and standard deviation for all 21 MRI volumes. We see that the proposed method (last column) is the most stable (lowest std) and has the best Jaccard score.



(1) no penalty (2) clusters 1, 6, 10 penalized

	unsup. feat. hist.	sup. feat. hist.	cluster hist.	cluster hist.+ prior.
mean	37	40	21	**60**
std	32	23	20	**11**

Figure 2: (Left) Illustration of how ventricle clusters are penalized in the tumor hist.(blue), ventricle hist(red) (Right) Comparison of Jaccard scores

4. NEW OR BREAKTHROUGH WORK TO BE PRESENTED

We proposed the clustering based active contour model, that can incorporate multiple features. This lead to a novel supervised segmentation methodology, that uses appearance priors to better disambiguate tumor from the normal tissue.

5. CONCLUSIONS

We have presented a variational method for brain tumor segmentation. Existing region-based variational segmentation methods based on texture features are not suited for tumor segmentation as they are not discriminative enough when the appearance of tumor and normal tissue overlap. Using priors on the brain/tumor appearance calculated on a set of clustered features extracted from the MRI images, we are able to disambiguate the tumor from the surrounding tissue.

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