LABEL PROPAGATION WITH ROBUST INITIALIZATION FOR BRAIN TUMOR SEGMENTATION

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ABSTRACT

A fully automatic segmentation algorithm based on local and global consistency with robust label initialization is proposed for brain tumor segmentation in multi-parametric MR images. A tumor probability map is first computed using support vector machine (SVM) classification of voxel-wise features, and then aggregated with respect to the image intrinsic structures in a multi-scale manner. Salient candidate tumor regions are extracted from the multi-scale hierarchy by a novel strategy based on perceptually important points. Robust label initialization is finally generated taking into account the information from both SVM classification and salient candidate regions. Validation experiment results on multi-parametric MR images have demonstrated that improved tumor segmentation accuracy can be achieved compared with state-to-the-art methods.

Index Terms— support vector machine, multi-scale, perceptually important point, tumor segmentation

1. INTRODUCTION

Accurate segmentation of brain tumors in magnetic resonance (MR) images is important for diagnosis and therapy assessment in clinical practice. As the manual labeling is time-consuming and susceptible to intra- and inter-rater variability, considerable efforts have been made to the development of automatic approaches.

Many tumor segmentation methods have been proposed, such as statistical classification based methods [1], clustering based methods [2], and active model based methods [3]. Although the statistical classification methods with spatial constraints have achieved promising segmentation performance, these methods may suffer from the inconsistency between training and testing images due to image noise and inter-subject discrepancy. Clustering based and active model based methods typically need appropriate and reliable initialization to get good results, such as the number of clusters, the initial contour of tumor. To alleviate the impact of inter-subject image inconsistency and improve the discrimination power, interactive graph based methods have been widely used for segmentation, for instance, graph cuts [4] and random walks [5]. These methods extract statistical information for the target and background region from the seed points defined by users interactively, and then partition the image based on the model-based unary term and pair-wise smooth term according the predefined criterion. Therefore, locations and number of seed points are important for segmentation performance. It has been demonstrated that the segmentation results may vary much if the number of seed points is inadequate [5]. Typically, the target seed points selected interactively are located within the target region while the background ones are located near the target contour. However, such a procedure is time-consuming and its reliability is problematic for tumors with fuzzy boundaries.

To achieve fully automatic tumor segmentation, support vector machine (SVM) and normalized Guassian Bayesian classifiers have been adopted to pre-segment the tumor image for providing tumors' probability map to be further refined [6, 7]. However, these methods detect the tumor regions voxel by voxel, which may lead to many isolated voxels with high tumor probability. Post-process steps including thresholding and morphological operations are indispensible, and tuning the relevant parameters is nontrivial for different images. Moreover, the method in [7] just locates the largest 3D tumor region, which cannot handle images with more than one tumor region.

For effectively identifying tumor regions which cannot be easily distinguished from the normal tissue at the voxel level, a multi-scale framework for tumor detection has been proposed in [8]. However, image context information at different scales may have distinctive characteristics, which cannot be successfully captured by a single statistical model. Furthermore, the trained class model may also suffer from the inter-subject image inconsistency.

To overcome the limitations of existing tumor segmentation techniques, we propose a robust label initialization method for label propagation based tumor segmentation by integrating the SVM classification with a multi-scale image aggregation technique. The label propagation based tumor segmentation is a semi-supervised learning method and takes into account the tumor segmentation's local and global consistency [11], capable of alleviating the impact of inter-subject image inconsistency

that cannot be successfully handled by the SVM classification. The main components of the proposed method are 1) a multi-scale representation of tumor saliency maps by aggregating statistical classification probability information computed by supervised learning with respect to the image intrinsic structures; 2) a novel strategy based on perceptually important points (PIP) [9] for detecting the salient candidate tumor region; and 3) a label propagation method in view of the tumor segmentation's local and global consistence [11].

2. METHODS

The tumor segmentation is accomplished under the local and global consistency framework with robust label initialization generated by statistical classification and multi-scale saliency aggregation.

2.1. Statistical classification by support vector machine

As a powerful discriminative classifier, SVM has been widely used for medical image analysis. In this paper, image intensities from multi-parametric MR images are used as features for SVM classification of tumor voxels. For each voxel i, the intensities of voxels within a predefined neighborhood centered at i are vectorized as the input for the classifier. A two-class SVM classifier for distinguishing tumor from normal tissues is built based on the training images for providing the hard classification result as well as classification probability of tumor for testing images, generating tumor-prob map and non-tumor-prob map [6]. The tumor-prob map shows the tumor saliency at the voxel level.

2.2. Multi-scale saliency aggregation

As no spatial context is taken into consideration in the aforementioned SVM classification procedure, many isolated salient regions occur in the tumor-prob map due to the intensity overlap between tumor and non-tumor regions, most of which are mis-classified due to intensity discrepancy across different images and imaging noise. Instead of adopting ad-hoc thresholding and morphological operations, these uncertain regions are removed by an aggregation procedure according to the multi-scale intrinsic image structures.

Multi-scale framework could provide robust and abundant information which facilitates the detection of target region. In this paper, an efficient method called segmentation by weighted aggregation (SWA) [10] is adopted. SWA operates by recursively coarsening the initial image and produces multi-level images until the whole image contains only one cluster by modeling the image voxels as graph nodes. The coarsening algorithm is summarized in Alg.1. This generated hierarchy contains segments at different scales which capture discrete image characteristics. At the bottom of the hierarchy, segments may represent specific tissue information, such as grey matter (GM), white matter (WM), cerebral spinal fluid (CSF), necrotic region, active tumor and edema. As the level increases, the segments represent the non-tumor region and tumor region instead. The original SWA algorithm does not provide a method for tumor detection. In [8] the aggregation procedure is integrated with a Bayesian model for the tumor segmentation. Such a Bayesian model suffers from the image variability between training and testing images. Furthermore, the hierarchies of different images generated by the SWA algorithm may vary very much so that the Bayesian model's performance may degrade when the segments at different scales capture discrete image characteristics.

Alg.1. The procedure of SWA algorithm.

Input: Graph $G^0(V^0, W^0)$ built based on the voxel level images, each voxel i corresponds to a node $v \in V^0$, each edge $w \in W^0$ reflects the pair-wise similarity between voxels within the 6-neighborhood. The similarity is defined as $w_{ij}^0 = exp(-\|I_i - I_j\|^2/\sigma^2)$, where I indicates the image intensity vector.

- **While $|V^t|$!= 1, construct G^{t+1} from G^t:**
  1) Seed selection: select a representative set of nodes V^{t+1} from V^t such that
  $$\sum_{v \in V^{t+1}} w_{uv} \geq \beta \sum_{o \in V^t} w_{uo}, \forall u \in V^{t+1}, 0 < \beta < 1$$
  2) Define the inter-scale interpolation matrix P^t:
  $$P_{vU}^t = \frac{w_{vU}}{\sum_{O \in V^{t+1}} w_{vO}}, v \in V^t, U \in V^{t+1}$$
  3) Calculate the aggregative properties for $U \in V^{t+1}$:
  $$I_U = \sum_{v \in V^t} \frac{P_{vU}^t I_v}{\sum_{o \in V^t} P_{oU}^t}$$
  4) Calculate W^{t+1}:
  $$w_{UV}^{t+1} = \sum_{(u \neq v) \in V^t} P_{uU}^t \, w_{uv}^t P_{vV}^t$$
  5) Modify W^{t+1} using aggregative propeties:
  $$w_{UV}^{t+1} = w_{UV}^{t+1} \times exp(-\|I_U - I_V\|^2/\sigma^2)$$
  6) t = t+1

  end while

Output: The hierarchy of multi-level graph.

Instead of building classification models on image segments of different levels, we apply the aggregation procedure to the voxel-wise tumor-prob map according to the multi-level hierarchy generated by the SWA algorithm based on multi-parametric images. This procedure is equivalent to an adaptive smooth procedure for adaptively removing isolated tumor regions and enhancing highly reliable tumor regions with a view to the intrinsic image intensity structures. The aggregations of image intensity and tumor probability are illustrated in Fig. 1.

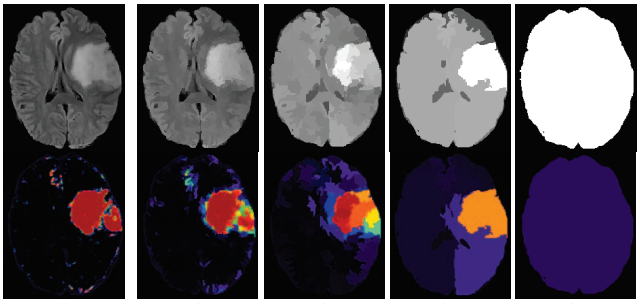
2.3. Candidate tumor region detection

The aggregation described above can be partitioned into two stages. At stage 1, non-tumor and tumor voxels merge into large regions respectively. At stage 2, large non-tumor and tumor regions merge into mixed regions at very coarse scales. As the hierarchy of different images contains different number of scales, a novel detection strategy is proposed to extract the salient candidate tumor region from the multi-scale hierarchy of tumor-prob map for different images. The tumor probability value of each voxel changes at different scales, a trace of tumor probability can be obtained for each voxel by traversing the hierarchy. Assuming that the probability values do not vary too much at stage 1 and change dramatically between stages 1 and 2 since tumor and normal tissue become mixed with each other at stage 2, we identify the boundary scale as the first perceptually important point [9] for each voxel, which could be calculated as:

$$max_s \left| Tp_0 + (Tp_e - Tp_0) \times \frac{s}{e} - Tp_s \right|, \quad (1)$$

where Tp_s is the tumor probability at scale s, Tp_0 and Tp_e are the tumor probabilities at the first and last scales, respectively. The identification of the first perceptually important point is schematically illustrated in Fig. 2.

Once all voxels' boundary scales between stages 1 and 2 are available, the boundary scale for the whole image is computed by majority voting of voxels' boundary scales. Then the candidate tumor regions are extracted from the tumor probability segments of the image's boundary scale as following: the mean and standard deviation of probability of each segment at this scale are calculated and the regions with probability far away more than one standard deviation from the mean value are selected as candidate regions. Our method can successfully handle images with multiple tumors.



scale 1 scale 4 scale 7 scale 10 scale16

Fig.1. Aggregation of FLAIR image and tumor-prob map of a randomly selected subject.

2.4. Segmentation with local and global consistency

Segmentation with local and global consistency (LGC) is a graph theory based segmentation approach. Given labeling information of a number of voxels, labels of unlabeled voxels can be predicted by exploiting the consistency between voxels based on the cluster assumption [11]. The segmentation can be solved by minimizing the following energy function:

$$Q(F) = F^T(I - S)F + \mu(F - L_{ini})^T(F - L_{ini}), \quad (2)$$

where I is an identity matrix and S is the normalized similarity matrix, F is the segmentation label vector and L_{ini} is the initial label vector. The first term of the function is a local consistency constraint, and the second term measures the consistency between the labeling result and the initial label information. The minimization of $Q(F)$ can be achieved using an iterative procedure:

$$F^{m+1} = (1 - \alpha)SF^m + \alpha L_{ini}. \quad (3)$$

It is worth noting that good label initialization and appropriate similarity definition between voxels is crucial for the segmentation [6]. The similarity between voxels i and j is computed according to image intensity similarity and spatial proximity as:

$$s_{ij} = exp(-\frac{\|I_i - I_j\|^2}{\sigma_I^2}) \times exp(-\frac{\|L_i - L_j\|^2}{\sigma_L^2}), \quad (4)$$

where I and L are intensity and location of the voxels i and j.

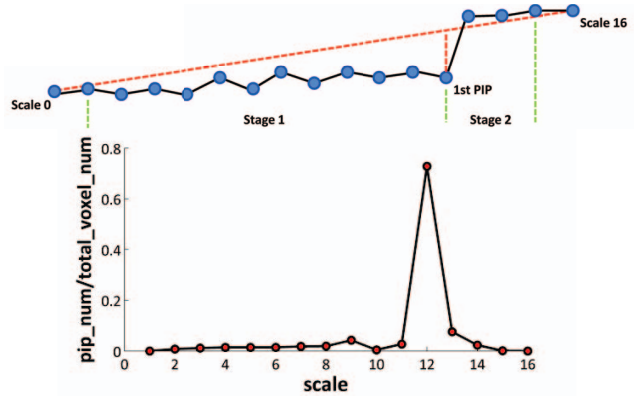


Fig.2. The illustration of the first PIP (top) detection and its incidence rate at all scales (bottom), where the highest rate indicates the boundary scale for the whole image.

In order to get reliable and compact label initialization, the SVM classification result and salient candidate tumor region are integrated. Particularly, Voxels within $SVM_t \cap Cand_t$ are used as initial labels for tumor, and voxels within $(SVM_t \cup Cand_t) \backslash (SVM_t \cap Cand_t)$ are used as unlabeled voxels, and the remaining voxels are labeled as non-tumor voxels, where SVM_t is the tumor voxels identified by the SVM classification and $Cand_t$ is the candidate tumor region detected by the method described in section 2.3.

3. EXPERIMENT RESULTS

The proposed algorithm is validated on a dataset of 7 subjects with gliomas of different sizes, shapes and

locations. Each subject has the T1-w, T2-w, FLAIR MR images, and the manual delineation results are used as ground truth for validation. All the images are pre-processed using a standard pipeline, including co-registration, skull-stripping, bias field correction, intensity histogram matching. A two-fold cross-validation is used to evaluate the proposed method. For the SVM classification, each voxel's $3 \times 3 \times 3$ neighborhood's intensity information of multi-parametric images constitutes a feature vector. Segmentation results generated by the method proposed in [6], SWA, LGC initialized by SWA result, and the proposed method are shown in Fig. 3, where only FLAIR image is illustrated. The initial label for the tumor region in Fig. 3 (b) is uneven which leads to the undersegmentation at the lower-right part in (f), while the result in (d) used for initialization leads to the oversegmentation at that part and undersegmentation at the upper-left part in (h). The visual inspection indicates that the proposed method can provide more reliable and compact initialization and subsequently improve the tumor segmentation performance as shown in (c) and (g).

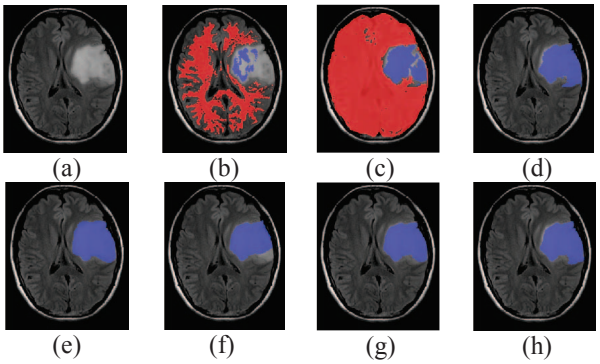


Fig.3. Segmentation results generated by different methods. (a) FLAIR image, (b) initial label computed by [6], (c) initial label computed by the proposed method, (d) segmentation by SWA, (e) manual segmentation, (f) segmentation result by [6], (g) segmentation by proposed method, (h) segmentation by LGC initialized with the SWA segmentation.

Table. 1. Jaccard similarity for different methods

	Method in [6]	SWA	LGC & SWA	Proposed method
Mean	0.76	0.781	0.780	0.805
Std	0.07	0.047	0.048	0.055

Quantitative evaluation of the segmentation performance is performed by computing Jaccard similarity between manual and automatic segmentation results, as defined by $\frac{Auto \cap Manual}{Auto \cup Manual}$. The Jaccard similarity measures for different methods are summarized in Table 1. The paired t-test is performed between the results generated by the proposed method and the other three methods respectively, yielding p-value 0.003, 0.025 and 0.023, which indicates that the improvement achieved by the proposed method is statistically significant.

4. CONCLUSION

A novel strategy has been proposed to identify tumor regions by integrating statistical classification information and hierarchy of intrinsic image structures. The identified tumor regions are spatially compact and reliable with respect to the image content, providing adequate and robust guidance for the subsequent segmentation. In conjunction with a semi-supervised learning method under local and global consistency framework, the proposed method can achieve promising tumor segmentation as demonstrated by experiments based on multi-parametric MR images.

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