A DISTRIBUTION-MATCHING APPROACH TO MRI BRAIN TUMOR SEGMENTATION

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ABSTRACT

This study investigates a fast distribution-matching algorithm for brain tumor segmentation. From a very simple user input, we learn a non-parametric model distribution which contains all the statistical information about the normal regions in the current brain image. We state the problem as the optimization of a cost function containing (1) an intensity distribution matching prior which measures a *global* similarity between non-parametric distributions, and (2) a smoothness prior to avoid the occurrence of small, isolated regions in the solution. Obtained following recent bound-relaxation results, the optimum of the cost function yields the complement of the tumor region in nearly real-time. Based on global rather than pixelwise information, the proposed algorithm does not require a complex learning from a large training set, as is the case in existing methods. Therefore, the ensuing results are independent of the choice of a training set. Quantitative evaluations and comparisons with several existing methods over publicly available data demonstrate that the proposed algorithm can yield a competitive performance.

Index Terms— Image segmentation, brain tumors, MRI, distribution matching, bound relaxation, graph cuts

1. INTRODUCTION

Segmenting precisely brain tumor regions in Magnetic Resonance (MR) images is an essential pre-processing step towards thorough and reproducible diagnosis of brain tumors. Manual segmentation is prohibitively time-consuming, and is not reproducible. Therefore, automatic or semi-automatic algorithms are highly desirable. Although several studies addressed the problem [1, 2, 3, 4, 5, 6, 7, 8], existing algorithms are still not fast and flexible enough for clinical use, mainly because of the difficulties inherent to brain tumor segmentation. In general, brain tumors have shape and intensity profiles that can change significantly from one subject to another. The shapes of brain tumors can vary arbitrary, and do not necessarily follow a familiar (previously seen) pattern which can be learned from a finite set of training subjects, as is the case in many other medical image segmentation problems. Furthermore, in some cases, the tumor region might share the same intensity profile with other normal regions within the image.

Most of existing methods require an intensive learning from a large training set and a heavy computational load. The authors in [3] used manually segmented data to learn a statistical model for tumor and normal tissues, and embedded the ensuing prior information in a conditional model that discriminates between normal and abnormal brain regions. The study in [5] used a discriminatively trained conditional random field (CRF) and a level set formulation. The authors in [8] incorporated clustered features collected by various MRI modalities and texture characteristics into a variational segmentation framework. The method in [4] is based on pseudo-conditional random fields. Although effective in some cases, training-based algorithms may have difficulty in capturing the substantial variations in tumor shape and intensity. The ensuing results depend on the characteristics, variability, and mathematical description of the training set. For instance, an unseen tumor different from all those within the training set may not be found.

This study investigates a fast distribution-matching algorithm for brain tumor segmentation. From a very simple user input, we learn a non-parametric model distribution which contains all the statistical information about the image within the normal regions in the current brain image. We state the problem as the optimization of an energy function containing (1) an intensity distribution matching prior which measures a *global* similarity between non-parametric distributions, and (2) a smoothness prior to avoid the occurrence of small, isolated regions in the solution. The optimum yields the complement of the tumor region in nearly real-time. Based on global rather than pixelwise information, the proposed algorithm does not require a complex learning from a large training set, as is the case in existing methods. Therefore, the ensuing results are independent of the choice of a training set. Optimization of global, distribution-matching priors has recently attracted a significant interest in the computer vision community [9, 10, 11, 12, 13]. Several studies have shown that, in the context of color image segmentation [9, 10, 11], such global priors can yield outstanding performances unattainable with standard, pixel-wise constraints commonly used in image segmentation [14]. In this work, we consider the Bhattacharyya measure of similarity between distributions [9, 10]. Our formulation leads to a difficult optimization problem which cannot be directly amenable to fast optimizers that are often used in the context of image segmentation, e.g., graph cuts [15]. One can use standard gradient-descent procedures, e.g., actives curves [13, 12], but such procedures result in slow, computationally intensive algorithms. Alternatively, in this work, we use the recent bound-relaxation results in [9, 10], thereby obtaining a nearly real-time brain tumor segmentation algorithm. Quantitative evaluations and comparisons with several existing methods over publicly available data demonstrate that the proposed algorithm can yield a competitive performance.

2. PROPOSED METHOD

The proposed method does not require a heavy training. It uses only the image information and a simple user input. Fig.1 illustrates the algorithm. The user input amounts to three points (i.e., three clicks), two to divide the brain into two symmetric parts and one to identify the normal part, i.e., the part that does not contain the target tumor (refer to left-hand side image in Fig.1). We estimate a non-parametric model distribution of intensity, $\mathbf{M}$, from the image data within the normal part. Learned interactively from simple user inputs, $\mathbf{M}$ is a prior which contains all the statistical information about

the image within the normal regions in the considered brain image (refer to left-hand side image in Fig.1). The main step of the algorithm consists of finding within the abnormal part a region R whose intensity distribution most closely matches model $\mathbf{M}$ (refer to right-hand side image in Fig.1). Such region yields the complement of the tumor in the abnormal part and, therefore, the tumor which is our target.

We state the problem as the optimization of an energy function containing (1) an intensity distribution matching prior which measures a *global* similarity between non-parametric distributions, and (2) a smoothness prior to avoid the occurrence of small, isolated regions in the solution.

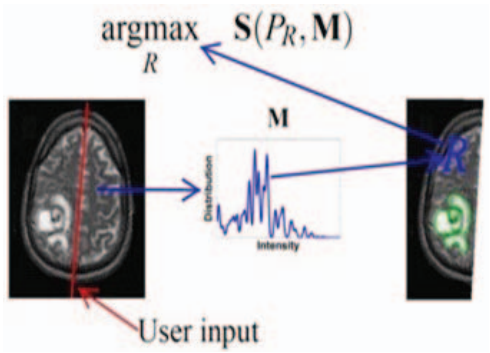
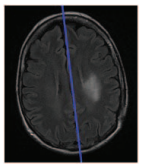
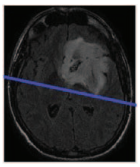


Fig. 1. A typical example which illustrates the main steps of the proposed approach.

The human brain can be divided into two parts often referred to as the left and right cerebral hemispheres. In general, brain tumors are located within one of these two parts, in which case the user has to define the vertical symmetry to learn model $\mathbf{M}$ (refer to the illustration in Fig. 2 a). For some subjects, the tumor can be shared by the two hemispheres, in which case the user has to define a horizontal symmetry to learn $\mathbf{M}$ (refer to the illustration in Fig. 2 b).



(a) vertical symmetry



(b) horizontal symmetry

Fig. 2. Illustration of two different types of user inputs: (a) vertical symmetry when the brain tumor is located within one of the two hemispheres; (b) horizontal symmetry when the tumor is shared by the two hemispheres.

2.1. Formulation

let $I_p = I(p) : \Omega \subset \mathcal{D} \subset \mathbb{R}^n (n \in \{2,3\}) \rightarrow \mathcal{Z} \subset \mathbb{R}$ be an image function defined from a fixed domain Ω to a set of intensity values $\mathcal{Z}$. Ω is a subset of the image domain defined by the user as the part containing the target tumor. Fig. 2 depicts two typical examples in which the user input, depicted by the blue line, divides the whole image domain into two parts. In Fig. 2 (a), Ω corresponds to the right-hand part of the image. In Fig. 2 (b), Ω corresponds to the upper part of the image. $\mathcal{D}$ is the whole image domain. Let $\bar{\Omega} = \mathcal{D} \setminus \Omega$ denotes the complement of Ω in $\mathcal{D}$. Recall that the user input amounts to three points (i.e., three clicks), two to define the blue line and divide the brain into two symmetric parts and one to identify the normal part ($\bar{\Omega}$), i.e., the part that does not contain the target tumor. Let $\mathbf{M}$ be the kernel density estimate of the distribution of image data within $\bar{\Omega}$, computed as follows:

$$\forall z \in Z \quad \mathbf{M}(z) = \frac{\sum_{p \in \bar{\Omega}} K_z(I_p)}{A(\bar{\Omega})} \tag{1}$$

where $A(R)$ represent the number of pixels in the region $R \subset \mathcal{D}$ and $\mathcal{K}_z(\cdot)$ is a kernel function, typically Gaussian:

$$\mathcal{K}_z(y) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{\|z-y\|^2}{2\sigma^2}\right). \tag{2}$$

Note that $\mathcal{K}_z(\cdot)$ can be chosen to be the Dirac function, which yields the normalized histogram. $\mathbf{M}$ is a prior model which contains all the statistical information about the image within the normal regions in the considered brain image.

The main step of the algorithm consists of finding within Ω (i.e., the abnormal part) a region R whose intensity distribution most closely matches model $\mathbf{M}$ (refer to right-hand side image in Fig. 2 for a typical example). Such region yields the complement of the tumor in Ω and, therefore, the tumor which is our target.

We state the problem as the minimization of a discrete cost function with respect to a binary labeling $L_p = L_p : \Omega \rightarrow \{0,1\}$, which defines a variable partition of Ω: $R = \{p \in P / L_p = 1\}$ corresponding to the normal (non-tumor) region, and its complement in Ω, $\bar{R} = \{p \in P / L_p = 0\} = \Omega \setminus R$, which corresponds to the tumor region.

The optimal labeling is obtained by minimizing a global cost function containing a distribution-matching constraint based on the Bhattacharyya measure and a smoothness constraint. To introduce the cost function, let us first introduce the following notations for any binary labeling $L_p = L_p : \Omega \rightarrow \{0,1\}$:

- R is the variable region given by: $R = \{p \in P / L_p = 1\} \subset \Omega$.
- P_R is the kernel density estimate (KDE) of the distribution of image data within region $R = \{p \in P / L_p = 1\}$:

$$\forall z \in Z \quad P_R(z) = \frac{\sum_{P \in R} K_z(I_p)}{A(R)} \tag{3}$$

- $B(f,g)$ is the Bhattacharyya coefficient witch measure the amount of the overlap between two distributions f and g:

$$B(f,g) = \sum_{z \in Z} \sqrt{f(z)g(z)} \tag{4}$$

The algorithm consists of finding an optimal labeling L^{opt} that minimizes the following cost function:

$$L^{opt} = \min_L F(L), \tag{5}$$

with

$$F(L) = \mathbf{S}(P_R, \mathbf{M}) + \lambda \mathbf{R}(L) \text{ s.t } R = \{p \in P / L_p = 1\} \tag{6}$$

$\mathbf{S}$ is a distribution-matching constraint given by minus the Bhattacharyya coefficient:

$$\mathbf{S}(P_R, \mathbf{M}) = -B(P_R, \mathbf{M}) = -\sum_{z \in Z} \sqrt{P_R(z) M(z)}, \tag{7}$$

$\mathbf{R}(L)$ is a regularization prior to minimize the length of the partition boundary [16]:

$$\mathbf{R}(L) = \sum_{\{p,q\} \in N} S_{p,q} \delta_{L_p \neq L_q} \quad (8)$$

with

$$\delta_{x \neq y} = \begin{cases} 1 & \text{if } x \neq y \\ 0 & \text{if } x = y, \end{cases} \quad \text{and } S_{p,q} = \frac{1}{\|p - q\|} \quad (9)$$

N is some neighborhood system containing all pairs $\{p, q\}$ neighboring elements in Ω. The regularization prior avoids the occurrence of small, isolated regions in the solution. λ is a positive constant that balances the relative contribution of the distribution-matching and regularization terms. L^{opt} will give an optimal boundary-smooth region, $R^{opt} = \{p \in P / L_p^{opt} = 1\}$, whose intensity distribution most closely matches M. This optimal region is expected to correspond to the non-tumor region in Ω. Therefore, the tumor region is finally deduced from L^{opt} as follows:

$$R^{tumor} = \Omega \setminus R^{opt} = \{p \in P / L_p^{opt} = 0\} \quad (10)$$

2.2. Optimization

The global term $\mathbf{S}(P_R, \mathbf{M})$ in (6) leads to a difficult optimization problem. It has an analytical form which cannot be directly amenable to fast optimizers that are often used in the context of image segmentation, e.g., graph cuts [15]. Such global terms were commonly optimized via standard gradient-descent procedures, e.g., actives curves [13, 12], which result in computationally intensive algorithms. Alternatively, we use the recent *bound-optimization* algorithm in [9]. Rather than maximizing directly the initial cost function (i.e the Bhattacharyya coefficient in our case), one can solve a sequence of easier sub-problems, each corresponding to a bound of the cost function. The authors in [9] show that such iterative bound-optimization process also optimizes the initial cost function. Furthermore, each sub-problem is amenable to fast graph-cut optimization using the Boykov-Kolmogorov algorithm [15], and the bound-optimization process converges within few iterations (typically less than 5) [9]. Further details on bound optimization can be found in [9]. Also, the Boykov-Kolmogorov algorithm [15] is well established in the computer vision literature and, therefore, we omit its details here.

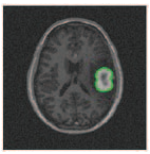
3. EXPERIMENTAL EVALUATIONS AND COMPARISONS

3.1. Evaluations and comparisons using the semi-synthetic image dataset in [1]

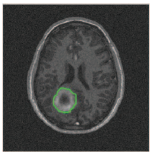
In this first set of experiments, we used the semi-synthetic image dataset recently proposed in [1]. This dataset comes with ground-truth segmentations, which allow quantitative and comparative appraisal of the proposed method. Fig. 3 depicts typical examples of the segmentation results of the proposed algorithm on two images from the dataset in [1]. The segmentations are depicted by the green curves superimposed on each of the images.

For quantitative evaluations and comparisons, we used the Dice metric (DM). DM is commonly used in the literature to evaluate the similarity between ground-truth and automatic segmentations [2, 6]. DM is given by $DM = \frac{2V_{ag}}{V_a + V_g}$ Where V_a,V_g, and V_{ag} are the areas/volumes of the automatically segmented region, the corresponding ground-truth region and the intersection between them, respectively. DM is always in $[0, 1]$, with 1 indicating a perfect match between the two segmentations. The higher DM, the better the performance of the algorithm.

Table 1 reports DM for (1) the proposed algorithm; (2) manual segmentations by an expert (reported in [1]); and (3) the algorithm in [1]. The proposed algorithm yielded the highest DM mean. Furthermore, the proposed algorithm yielded segmentation in nearly real-time with a non-optimized Matlab/C++ code. It requires less than 0.5 seconds to process an image.



(a) Tum01



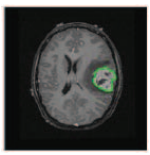
(b) Tum02

Fig. 3. Two typical examples of the segmentation results of the proposed algorithm on semi-synthetic image from the public dataset in [1]. The obtained segmentations are depicted by the green curves superimposed on each of the images. (a): an example showing a tumor fully enclosed within the right hemisphere, in which case the user input defined a vertical symmetry (Tum01). (b): an example showing a tumor shared by the two hemispheres, in which case the user input defined a horizontal symmetry (Tum02).

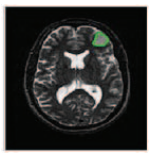
Tumor	Proposed algorithm	Expert	Algorithm in [1]
Tum01	0.936	0.917	0.965
Tum02	0.940	0.928	0.956
Tum03	0.921	0.886	0.929
Tum04	0.957	0.906	0.933
Tum05	0.936	0.820	0.876
DM mean	**0.938**	0.891	0.931

Table 1. Performance evaluations and comparisons over the semi-synthetic image dataset in [1]. We computed the Dice metric (DM) between three segmentation results and the ground truth provided in [1]. Second column: DM for the proposed algorithm; third column: DM for manual segmentation by an expert (reported in [1]); last column: DM for the algorithm in [1] (reported in [1]). The higher DM, the better the performance.

3.2. Real images



(a) Image 1



(b) Image 2

Fig. 4. Two typical examples of the results of the proposed algorithm on the real data used in [1, 2, 6]. The obtained segmentations are depicted by the green curves superimposed on each of the images.

In this second set of experiments, we run the proposed algorithms on the real tumor images used in [1, 2, 6]. For quantitative

evaluations/comparisons, we follow the same process in [1, 2, 6]. We assume that, for each image, the ground truth is the corresponding manual, human-expert segmentation provided in [1, 2, 6]. Table 2 reports the DM for the proposed algorithm and the methods in [1, 2, 6]. The results demonstrate that the proposed algorithm can yield a competitive performance. Fig. 4 depicts two typical examples of the results of the proposed algorithm on the real data used in [1, 2, 6]. The obtained segmentations are depicted by the green curves superimposed on each of the images.

Tumor	Proposed method	[1]	[2]	[6]
Image 1	0.944	0.71	0.80	0.932
Image 2	0.83	-	0.792	-
Image 3	0.751	0.49	0.70	0.847

Table 2. DM evaluations and comparisons over the real images used in [1, 2, 6]. For each image, the ground truth is the corresponding manual, human-expert segmentation provided in [1, 2, 6].

Fig. 5 examples of segmentation results which demonstrate the performance of the proposed algorithm on clinical T2-weighted MRI images showing different types of tumors. The obtained segmentations are depicted by the green curves superimposed on each of the images.



Fig. 5. Examples of segmentation results obtained with the proposed algorithm on clinical T2-weighted MRI images showing different types of tumors. The obtained segmentations are depicted by the green curves superimposed on each of the images.

4. CONCLUSION

We proposed a fast distribution-matching algorithm for brain tumor segmentation. Starting from a very simple user input, the tumor region is sought following the bound-relaxation optimization of a cost function containing an intensity distribution matching prior and a smoothness constraint. Quantitative evaluations and comparisons with several existing methods over publicly available data demonstrated that the proposed algorithm can yield a competitive performance, while relaxing the need for complex training.

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