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3D multimodal MRI brain glioma tumor and edema segmentation: A graph cut distribution matching approach

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ABSTRACT

This study investigates a fast distribution-matching, data-driven algorithm for 3D multimodal MRI brain glioma tumor and edema segmentation in different modalities. We learn non-parametric model distributions which characterize the normal regions in the current data. Then, we state our segmentation problems as the optimization of several cost functions of the same form, each containing two terms: (i) a distribution matching prior, which evaluates a global similarity between distributions, and (ii) a smoothness prior to avoid the occurrence of small, isolated regions in the solution. Obtained following recent bound-relaxation results, the optima of the cost functions yield the complement of the tumor region or edema region in nearly real-time. Based on global rather than pixel wise information, the proposed algorithm does not require an external learning from a large, manually-segmented training set, as is the case of the existing methods. Therefore, the ensuing results are independent of the choice of a training set. Quantitative evaluations over the publicly available training and testing data set from the MICCAI multimodal brain tumor segmentation challenge (BraTS 2012) demonstrated that our algorithm yields a highly competitive performance for complete edema and tumor segmentation, among nine existing competing methods, with an interesting computing execution time (less than 0.5 s per image).

1. Introduction

Glioma tumor could be considered as a primary malignant brain tumor that could seriously threaten an important number of patients, with a survival prognosis not exceeding one year for high-grade glioma [1,2]. Such tumors are often accompanied with peritumoral edema, which corresponds to an extensive perifocal swelling [3]. Magnetic Resonance Imaging (MRI) is the main modality for evaluating the pathological regions. Segmenting precisely the tumor and edema regions in MRI is, therefore, an essential pre-processing task towards thorough and reproducible diagnosis of brain tumors. Manual segmentation could be so prohibitively time-consuming, and could never be reproducible during clinical routines. Therefore, automatic or semi-automatic segmentation algorithms would be highly recommended in order to surmount such disadvantages. Several past research studies investigated such problem [4–6] by segmenting both the tumor and the edema regions in one or multiple modalities (T1,T1C,T2 and Flair), and this remains yet a challenging task. Most of the existing algorithms are still not fast and not flexible enough, especially for realistic clinical scenarios and needs. One could notice some difficulties inherent to the brain tumor segmentation because, in general, brain tumors have shape and intensity characteristics that may vary dramatically from one subject to another, which impedes building reliable models from training data. For instance, the brain tumor region shape may be arbitrary, and does not necessarily fall within a category (or class) of shapes that could be learned from one finite set of training subjects as is the case of most medical image segmentation problems. Furthermore, in some cases, tumors might have intensity profiles that would be so similar to the other normal regions within the considered image. The past research studies addressed different variants for this segmentation

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problem and several of them used multi-modal MRI [6,7]; other works used only a single modality [8,11]. Among studies, one could notice that several of them focused only on the tumor as a target region [9,10,13], whereas others addressed both the tumor and the edema segmentation [11]. Most of the existing methods require a time-consuming external learning phase, which requires building a large, manually-segmented training set [6]. In [6], the authors used three MRI modalities (T1,T1C and T2) and texture characteristics to construct a multi-dimensional feature set. Then, they learned a statistical model for tumor and normal tissues, thereby obtaining a 3D supervised segmentation of the brain tumor. Several other studies addressed both edema and tumor in order to provide richer clinical information that could be somehow useful. For instance, the authors of [11] presented a Bayesian formulation for incorporating soft model assignments so as to delimit brain tumor and edema. The study in [9] presented an unsupervised change detection method based on gray level histograms for brain tumor and edema segmentation. Comparatively to our proposed approach, various other tumor/edema segmentation algorithms were presented at the MICCAI BraTS 2012 challenge. The authors of [5] used a standard forest classification based on spatially non-local features along with initial probability estimates for individual tissue classes. The initial tissue regions probabilities were therefore based on local intensity information alone, and one parametric GMM-based model was used for the estimation step. Another competitor in the challenge [4] integrated random forest classification with hierarchical conditional random field regularization within an energy minimization scheme. The authors of [19] presented a semi-automatic tumor-cut algorithm. The user would be consequently required to provide the maximum diameter of the edema region visible on FLAIR images, and subsequently, a level set method would be then used to segment the target regions. Although effective in some cases, such mentioned training-based algorithms could be faced to one evident difficulty in extracting the substantial variations within tumor shape and intensity. The ensuing results depended on the characteristics, the variability, and the mathematical description of the training set. For instance, an unseen tumor different from all those within the training set may not be found.

In this work, we propose a novel distribution-matching, data-driven algorithm for 3D multimodal MRI brain glioma tumor and edema segmentation. We estimate a non-parametric model distribution that characterizes the normal regions in the current data. Then, we state our segmentation problems as the optimization of several cost functions of the same form, each involving two terms [15] (i) a distribution matching prior, which evaluates a global similarity between distributions, and (ii) a smoothness prior to avoid the occurrence of small, isolated regions in the solution. Obtained via recent bound-relaxation results, the optima of the cost functions yield the complement of the tumor region or edema region in nearly real-time. Based on global rather than pixel wise information, the proposed algorithm does not require an external learning from a large, manually-segmented training set, as is the case of the existing methods. Therefore, the ensuing results are independent of the choice of a training set. Quantitative evaluations over the publicly available training and testing data set from the MICCAI Multimodal Brain Tumor Segmentation 2012 challenge (BraTS 2012) demonstrate that the proposed algorithm yields a competitive performance. Over the real data of the mentioned challenge, our algorithm was well ranked for complete edema and tumor segmentation among the nine competing methods [14]. Our work builds on the Bhattacharyya-similarity bound derived by our co-author in a preliminary conference paper [26]. The following lists the main contributions of this study and the differences between our work and [26]:

(1) The main contribution of [26] is theoretical and focuses on the optimization aspects of the work. Specifically, it details the derivation of a bound of the Bhattacharyya measure, which allows using graph cuts. However, the proof-of-concept experiments in [26] were limited to color photographs and were based on an unrealistic assumption where the model distribution is learned from the ground truth. There are no medical imaging applications in [26]. In this work, we extend the application of the Bhattacharyya bound to the real problem of 3D Multimodal MRI Brain Glioma Tumor and Edema Segmentation.
(2) We report completely novel results, including quantitative evaluations/comparisons on the publicly available training and testing data set from the MICCAI multimodal brain tumor segmentation challenge (BraTS 2012). The results demonstrate that the proposed algorithm can yield a highly competitive performance among nine other competing algorithms.
(3) In this submission, we added new algorithmic components, which were designed specifically for multi-modal edema segmentation. The work in [26] cannot be applied directly to our problem; it did not consider any medical imaging application.
(4) To the best of our knowledge, our work is the first to investigate the idea of distribution matching in the context of brain tumor segmentation. Furthermore, it is the first to design a distribution matching algorithm in an interactive way, where the prior model is learned interactively from the current image data. Unlike the existing brain tumor segmentation methods, our work removes the need for and dependence on extensive learning from a large, manually segmented training set. In practice, this is an important advantage over the existing brain tumor segmentation algorithms.

The remainder of this paper is arranged as follows. Section 2 introduces the Multimodal Brain Tumor Segmentation Benchmark (BraTS2012 data). Section 3 describes the segmentation methodology. Section 4 reports the experimental results and contains a discussion. Finally, the conclusion's section draws several perspectives of this work.

2. Materials: multimodal brain tumor segmentation benchmark (BraTS2012 data)

The results reported in this research were based on approved evaluations using the Multimodal Brain Tumor Segmentation Benchmark (BraTS 2012 data) [14]. This section describes in details the data sets, notations and evaluation metrics that we used in this work. The Multimodal Brain Tumor Segmentation data set was introduced in the MICCAI 2012 Challenge by B. Menze, A. Jakab, S. Bauer, M. Reyes, M. Prastawa and K. Van Leemput [14]. This large and publicly available training and testing dataset was very useful and allowed us to compare efficiently our algorithm to others participating in the challenge. In the remainder of the paper, we will refer to this dataset as BraTS2012. We followed the standard evaluation protocol used for all algorithms via an online system provided by the Virtual Skeleton Database [17].

2.1. BraTS2012 data principle

BraTS2012 aims mainly at validating various segmentation approaches by evaluating and comparing 3D MRI brain tumor and edema segmentation algorithms. Segmenting brain tumors from multi-modal imaging data is one of the most challenging tasks in medical image analysis due to their unpredictable appearance and shape. Although many different segmentation approaches have been proposed in the literature during the past few years, it would be so hard to compare the existing methods because the validation datasets that could be used could differ widely in terms of input