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Automated 3D segmentation of brain tumor using visual saliency

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ABSTRACT

There is a growing availability of medical imaging data from large number of patients, involving visual information from images in different modalities along with an associated complexity of the features of interest. It has therefore become essential to develop automated delineations to assist doctors and/or radiologists to analyze and speedup medical image understanding, preferably avoiding any user intervention. We present here a novel approach for the reliable, automated, and accurate 3D segmentation of brain tumors from multi-sequence magnetic resonance images. The tumor volume, detected using visual saliency, is evaluated in three-dimensions for small as well as large ROIs and/or VOIs. The proposed segmentation method is applied on the publicly available standard BRATS data set, and is found to achieve very high accuracy with good reliability (or repeatability) and robustness of results. Its robustness, is also investigated by measuring the impact of tumor size on segmentation accuracy, on the basis of the weak linear correlation. The results demonstrate that the segmentation generated by the proposed algorithm can be used for accurate, stable contouring, for both high- and low-grade tumors, as compared to several related state-of-the-art methods involving semi-automatic and supervised learning.

1. Introduction

The large size of medical image data, the complexity of Features Of Interest (FOIs), and the necessity to process these on time, both accurately and efficiently, are making the job of doctors and radiologists increasingly difficult. Therefore, it has become essential to develop automated delineation of Regions Of Interest (ROIs) and Volumes Of Interests (VOIs) to assist and speedup medical image understanding. Over the last decade cancer has become the deadliest killer worldwide [29]. By the time physical manifestations become evident, often metastasis has set in. This results in failure of local tumor control and poor patient prognosis. Radio-imaging, like magnetic resonance imaging (MRI), computed tomography (CT), positron emission tomography (PET), etc., constitutes one of the best noninvasive approaches for detection, diagnosis, treatment and prognosis of cancer. Particularly, the integration of diverse multimodal information in a quantitative manner provides specific clinical solutions for accurately estimating patient outcome [15].

Among different cancers of the brain, Glioblastoma multiforme (GBM) remains the most common and lethal form of primary tumor in adults with poor prognosis. The treatment and diagnosis of GBM is mostly guided by histopathology and

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immunohistochemistry [18]. Repeated tumor biopsies in brain tumor is a very challenging problem. Therefore, noninvasive methods like imaging hold immense promise for assessing the state of the tumor. The high spatial resolution of MRI provides minute details of abnormalities, in terms of both shape and volume, in brain tumors. Due to its superior contrast in soft tissue structures, MRIs are routinely used for the diagnosis and characterization of tumors for the disease management. Particularly, MR imaging is very safe because it does not involve any exposure to radiation [29].

Medical experts manually segment different regions of interest (ROIs) for detection, diagnosis and planning of treatment. Automated medical image analysis, on the other hand, overcomes human bias and can handle large volumes of data. Variation in blood flow (perfusion) within a tumor causes variation in imaging features like necrosis and contrast. It was observed [45] that regions of tumor that are poorly perfused on contrast-enhanced *T*1*C*-weighted images may exhibit areas of low (or high) water content on *T*2-weighted images and low (or high) diffusion on diffusion-weighted *FLAIR* (Fluid-Attenuated Inversion Recovery) images. Thus high (or low) cell densities can coexist in poorly perfused volumes, with the creation of perfusion-diffusion mismatches. Regions having poor perfusion and high cell density are of particular clinical interest, because they contain cells which are likely to be resistant to therapy. This highlights the utility of superimposing multiple channels of MR imaging, like *FLAIR*, *T*2, and contrast enhanced *T*1*C* components, in identifying and extracting heterogeneous tumor region(s).

Humans can easily identify the salient (or relevant) parts of an image mainly due to the attention mechanism of the human visual system. “Visual saliency”, coined by Ullman and Sha’ashua [35] was extended by Itti et al. [20] towards the development of a computational architecture. Computational models of saliency take images as input and generate a topographical map of how salient or attention grabbing each area of the image can be to a human observer [7]. Such models seem to predict based on certain aspects of human eye movement [14].

Visual saliency can be defined as the outcome of comparing a region with its surrounding, with respect to unpredictability, contrast and rarity [1,25,26,38,43]. The comparison can be done in terms of low level feature similarity. In Ref.[40] authors proposed a novel distance metric learning method termed Semantic Preserving Distance Metric Learning (SP-DML). It encodes the low level feature similarity and semantic similarity in a new unified feature space, from which the similarity/dissimilarity between two image patches can be measured by applying the learned distance metric. In case of the image regions with low visual similarities but high semantic similarities, the traditional similarity measures may not perform well. To deal with this problem many well known approaches have been proposed in the literature based on Hypergraph Learning [39,41].

Saliency detection methods can be broadly classified into (i) biological [20,37], (ii) fully computational [32,42] and (iii) hybrid [4,17]. Algorithms employing the bottom-up strategy detect saliency by using low-level features, like color, intensity, orientation. Those using the top-down strategy include some learning from the training data involving the position or shape of a salient object [34]. It has been observed that often attention is immediately drawn to a salient item, in spite of the existence of many other items (or distracters), without any need to scan the entire image. A visually salient region is typically rare in an image, and contains highly discriminating information. This concept is, therefore, expected to have a major bearing towards the fast identification of an ROI or tumor from a medical image.

Computer Aided Detection (CADe) can be of help to doctors and radiologists in identifying abnormalities, which are comparatively rare, in a medical image. The objective of this research is to improve the present CADe systems by minimizing user interactions, thereby saving precious time of doctors while reducing possibility of human error. Application of visual saliency to medical images is being studied in literature. Jampani et al. [22] investigated the usefulness of three popular computational saliency models, extended from the natural scene framework, to detect abnormalities in chest X-ray and color retinal images. Visual saliency was also applied for automated lesions detection [9,31] from retinal images. Alpert and Kisilev [2] developed a medical saliency model for detecting lesions and microcalcifications in mammograms, MRIs of brain, and stenoses of angiographic images. However sufficient validation study, with respect to ground truth, is not provided. Erihov et al. [12] designed a shape asymmetry-based saliency model for detection of tumors from brain MRI and breast mammograms.

Motivation

Several brain tumor segmentation methods have been developed over the past decade, encompassing supervised as well as semi-supervised techniques [5,19]. While supervised learning involves a separate training phase with a large amount of training data, the semi-supervised methods require user interaction/supervision during segmentation [3]. Cordier et al. [8] developed a multi-channel patch-based segmentation method, which builds a patch database by extracting several patches from the training data for which label maps are available. During testing it searches for similar patches from the training database using some similarity measure. The labelling is performed using leave-one-out scheme. Festa et al. [13] designed a random decision forest, with 50 trees each of depth 25 voxels, for classification-based brain tumor segmentation. Meier et al. [27] used a maximum a posteriori probability (MAP) rule based classification forest for image segmentation. Zhao et al. [44] generated a set of supervoxels which were then labeled using Graph Cuts on a Markov Random Field.

It has been established [30] that semi-automatic segmentation is more robust than manual segmentation, with reference to inter-user variability, while providing comparable output accuracy. Therefore automated algorithms, which are more accurate and require negligible user interaction, are of major interest. Guo et al. [16] employed semi-automatic active contours for segmenting multimodal brain tumors, with the user being required to draw a region of interest (ROI) roughly surrounding the tumor. Grow-Cut [36] is a popular region growing algorithm for semi-supervised segmentation, where the user