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Quick detection of brain tumors and edemas: A bounding box method using symmetry

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ABSTRACT

A significant medical informatics task is indexing patient databases according to size, location, and other characteristics of brain tumors and edemas, possibly based on magnetic resonance (MR) imagery. This requires segmenting tumors and edemas within images from different MR modalities. To date, *automated* brain tumor or edema segmentation from MR modalities remains a challenging, computationally intensive task. In this paper, we propose a novel automated, fast, and approximate segmentation technique. The input is a patient study consisting of a set of MR slices, and its output is a subset of the slices that include axis-parallel boxes that circumscribe the tumors. Our approach is based on an unsupervised change detection method that searches for the most dissimilar region (axis-parallel bounding boxes) between the left and the right halves of a brain in an axial view MR slice. This change detection process uses a novel score function based on Bhattacharya coefficient computed with gray level intensity histograms. We prove that this score function admits a very fast (linear in image height and width) search to locate the bounding box. The average dice coefficients for localizing brain tumors and edemas, over ten patient studies, are 0.57 and 0.52, respectively, which significantly exceeds the scores for two other competitive region-based bounding box techniques.

1. Introduction

Presently, many clinical centers maintain large archival databases of MR images of brain tumors for various purposes, as this information may help physicians and radiologists to diagnose and treat novel patients—e.g., by determining the effectiveness of various treatments on previous patients with similar tumor or edema volumes [25–27]. As these archived MR image databases may contain a large number of studies, it is important to index their contents effectively. The current practice of indexing and retrieving these images is typically based on only patient names, identifiers, keywords and manual annotations. Unfortunately, this does not allow users to retrieve similar or clinically meaningful images. If these tumors were segmented, the databases could be indexed based on various aspects of the tumor, such as its size, location and type. Properly indexed databases can help researchers as they seek to determine the growth patterns and other properties exhibited by brain tumors. This indexing would also allow radiologists to use tumor size and location to retrieve historical cases relevant to the current patient and so help formulate treatment plans.

Toward the aforementioned medical informatics task, MR slices are usually interpreted visually and subjectively by radiologists, who segment tumors by hand or by semiautomatic tools [25]. Both manual and semiautomatic segmentations are often tedious and time consuming. It would therefore be useful to have a completely automated and fast (preferably real time or near real time) segmentation tool. Moreover, for the purpose of indexing the images in the database, it is often sufficient to have an *approximate* segmentation for the tumor and/or edema regions. Here, we can trade-off accuracy for speed and convenience.

Many tumor segmentation methods found in literature are not fully automatic as they need user interaction to place a seed inside the tumor or edema region [8,17]. Region growing [19] based tumor detection techniques suffer high time complexity. Statistical pattern recognition based methods [13,21–23] fall short, partly because large deformations occur in the intracranial tissues due to the growth of the tumor and edema. These methods detect abnormal regions using a registered brain atlas as a model for healthy brains. However, these techniques need to significantly modify the brain atlas to accommodate the tumors, which typically lead to poor results. Most of the fuzzy models [5,18,19] work well only for hyper intensity (fully enhanced) tumors and exhibit poor performance on detecting non-enhanced tumors. This is because these fuzzy models typically use thresholding techniques or morphological operations (erosion or dilation) as pre- or post-processing

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leading to the border enhancing or non-enhancing tumors having very few bright pixels. Many researchers are now using Markov random fields (MRFs) [2,3], which involve estimating the parameters for a parametric model that has one set of parameters to express the probability that each specific voxel is a tumor, and another set to express the distribution over the labels for a pair of adjacent voxels.

We present an automatic, fast, and approximate segmentation technique that avoids these problems by locating a "bounding box"—i.e., an axis-parallel rectangle, around the tumor or edema on an MR slice. We can then use this bounding box to answer subsequent queries that ask about tumor position and size (albeit with a response that is approximately correct).

The input to our algorithm, fast bounding box (FBB), is a set of MR slices belonging to a single patient study. The output is a subset of slices that contain tumors or edemas, which are each labeled with an axis-parallel bounding box that circumscribes the tumor and edema region. We will see that different imaging modalities are good at identifying these regions: T1C for tumor and T2 for edema. On each input MR slice (axial view), FBB first locates the left–right axis of symmetry of the brain. A tumor or edema, which is considered an abnormality in the brain, typically perturbs this symmetry. Thus, the algorithm searches for an axis-parallel rectangle on the left side that is very dissimilar from its reflection about the axis of symmetry on the right side—i.e., the intensity histograms of two rectangles are most dissimilar, but the intensity histograms of the outside of the rectangles are relatively similar. We assume that one of the two rectangles will circumscribe the tumor/edema appearing in one hemisphere of the brain. Once these bounding boxes are found on all input slices, an unsupervised mean-shift clustering (MSC) [7] uses the locations (centroids) of these bounding boxes to find the largest cluster of consecutive MR slices; FBB then outputs this volume, encoded as a set of slices with their bounding box regions.

Many other researchers have studied this idea of employing the innate left–right symmetry of human brain for various applications [11,12]. Studies demonstrate that detection of the tumor or edema exploiting the symmetry speeds up the tumor detection process and makes the detection task robust [15,33]. Accurately finding the axis of symmetry is a challenging and time consuming task [11]; fortunately the geometrical axis of symmetry of the skull is sufficient for our FBB method to localize brain tumor or edema accurately, and finding the geometrical axis of symmetry is easier than finding the actual axis of symmetry of the skull.

The novelty of the FBB segmentation technique lies in a proposed score function that locates the bounding boxes. The score function is based on Bhattacharya coefficient [7] of gray scale intensity histograms. We prove that under reasonable assumptions, this score function admits a very fast linear time search technique to locate the bounding boxes. In fact, while the complexity of finding bounding box using exhaustive search can be $O(h^2w^2)$, where h and w represent the height and the width of an MR image slice, our FBB search algorithm requires only $O(h+w)$ time. Some of the advantages of FBB include: (a) it does not need image registration, (b) it is an unsupervised technique, i.e., neither a training set of labeled images, nor an *a priori* parameter distribution is required, (c) it does not need intensity standardization in MR slices and (d) it can be implemented in real time. In addition, our FBB system can also be used as a seed for a more accurate boundary finder; for further details please see Section 3.4.

Section 2.1 describes the details of the FBB technique. FBB works for 2D slices; Section 2.2 presents a clustering scheme to merge these slices together into a single 3D volume, by first identifying slices that contain tumors/edemas, and then merging together a consistent set of labels for those slices. Section 3 presents extensive experimental studies.

Some of this material has appeared in the short conference papers [25–27]. This submission significantly extends those publications by providing mathematical derivations and additional empirical validations.

2. Fast bounding box algorithm

FBB operates in two sequential steps. First, the input set of 2D MR slices are processed individually, to find axis-parallel rectangles (i.e., potential bounding boxes) in. Next, these bounding boxes are clustered to identify the ones that actually surround the tumor/edema. These two steps are described in the following subsections.

2.1. Locating bounding boxes on 2D MR slices

In this section we elaborate the basic principle behind FBB: a change detection principle, where a region of change (D) is detected on a test image (I), when compared with a reference image (R). In FBB, after finding the axis of symmetry on an axial MR slice, the left (or the right) half serves as the test image I, and the right (or the left) half supplies as the reference image R. The region of change D here is restricted to be an axis-parallel rectangle, which essentially aims to circumscribe the abnormality. Our method is different from most of the change detection methods proposed to date (see [24] for example) in that we view this change as a region-based global change that differs from most techniques, which view the change as a local pixel-to-pixel changes—here tumor or edema is considered as the 'change' region in the test image and all other intracranial tissues except tumor or edema are considered as the 'no change' region. We utilize a novel score function that can identify the region of change D with two very quick searches–one along the vertical direction of the image and the other along the horizontal direction.

Fig. 1 illustrates the notations. I and R in Fig. 1(a) represent the test and the reference images, respectively, having same height h and same width w. The rectangular region $D = [l_x, u_x] \times [l_y, u_y]$ represents the region of change/region of interest containing (tumor or edema that we are looking for) between images I and R. FBB algorithm finds the rectangle D, i.e., the four unknown parameters l_x, u_x, l_y and u_y in two linear passes of the image. It first finds the best l_y and u_y values in a vertical sweep and then finds l_x and u_x in a

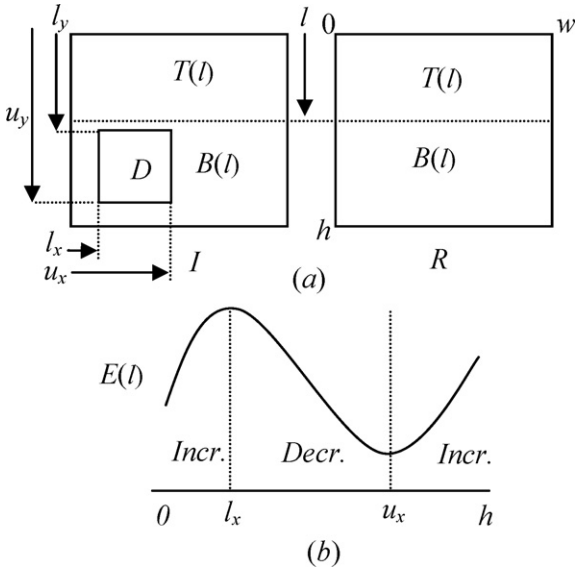

Fig. 1. (a) Finding anomaly D from test image I using reference image R. (b) Energy function plot.