FEM IS EMPLOYED TO SOLVE THE DIFFUSION MODEL

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ABSTRACT

Using this knowledge we have developed a method to locate the regions occupied by brain tumors. Initially our method extracts the brain by removing the unwanted non-brain regions like skull, scalp, fat and muscles. Then the brain is segmented into well known regions like GCOAAM and background using I2SOM algorithm. In T2 scans the tumor intensity characteristics are analyzed by BC method. So the images are analyzed for symmetric property along the central vertical line. The average true positive volume fraction and false positive volume fraction on all tumors is 91.4% and 4.0%, respectively. The experimental results showed the feasibility and efficacy of the proposed method.

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Introduction

Most of the current conventional diagnosis techniques are based on human experience in interpreting the MRI-scan for judgment; certainly this increases the possibility to false detection and identification of the brain tumor. On the other hand, applying digital image processing ensures the quick and precise detection of the tumor [7]. One of the most effective techniques to extract information from complex medical images that has wide application in medical field is the segmentation process [5, 8]. The main objective of the image segmentation is to partition an image into mutually exclusive and exhausted regions such that each region of interest is spatially contiguous and the pixels within the region are homogeneous with respect to a predefined criterion. Widely used homogeneity criteria include values of intensity, texture, color, range, surface normal and surface curvatures. Color based segmentation using K-means clustering for brain tumor detection has been proposed, in which better results were obtained using the developed algorithm than that in other edge detection algorithms [9]. A modified method was proposed that additionally takes into account the symmetry analysis and any significant prior information of the region of interest as well as the region area and edge information in the tumor location of pathological cases [10]. However, all of these research efforts pushed the limit of tumor detection accuracy, they have been based on edge detection and were employed to filter out less relevant information while preserving the basic structural properties of an image which significantly reduces the amount of data to be processed in the subsequent steps such as feature extraction, image segmentation, registration, and interpretation. This is why with the recent developments. On computational intelligence; the design of computerized medical diagnosis systems has received more and more attention. These reasons motivated us to propose two automated diagnosis systems; the first system is completely based on modified classical image processing algorithms, while the second system is based on probabilistic FEM based classifier to interpret medical images obtained from clinical tests.

I. PROBLEM OVERVIEW

In this paper we propose a fully automatic method to detect brain tumor. We make use of bilateral symmetry property of human brain to detect the abnormality and maxima transform to locate the tumor region. The structural arrangement of the whole brain is similar on the both side of hemisphere and is symmetrical about the vertical axis through the brain centre. In section III we discuss about different algorithms .In section IV we discuss general Structure and Analysis of Tumor Growth Model. In section V we discuss about Tumor Growth Model Parameters Training and Abnormality Detection.

II. IMAGE PROCESSING PROPOSED APPROACH AND SIMULATION RESULTS

A. FEM-Based Tumor Growth Prediction

Overview of the Proposed Approach

The proposed tumor growth prediction system consists of three main phases: training, prediction, and validation. The flowchart is shown in Fig. 1. Suppose the longitudinal study has $n + 1$ time points. For the purpose of validation, we use first n time-point images for training, predict the tumor status at the n+ 1th time point, and validate with the $n + 1$th images. In clinical practice, all $n + 1$ images are used to train the model parameters and predict the tumor status at a future time point. The training phase is composed of five steps. First, image registration and segmentation are conducted on the brain images. Second, tetrahedral meshes are constructed for the segmented brain and tumors, respectively. Third, the reaction–diffusion model is applied as the tumor growth model, and FEM is used to solve this PDE. Fourth, the parameters of the tumor growth model are optimized by HOPSPACK. Fifth, after computing the parameters based on the first n image, the model parameters for prediction at the

$n + 1$th time point are estimated by an exponential curve fitting based on the nonlinear least-squares method. In the prediction phase, the estimated growth parameters are applied to the tumor growth model to compute the predicted result for time point $n + 1$ using image at time point n. In the validation phase, the predicted result is validated by comparing with image $n + 1$

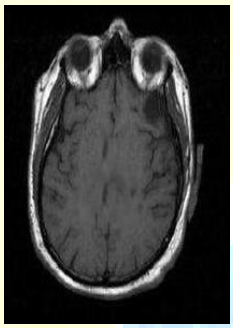
B. Image Acquisition

In our proposed approach we first considered that the MRI scan images of a given patient are either color, Gray-scale or intensity images herein are displayed with a default size of 220×220. If it is color image, a Gray-scale converted image is defined by using a large matrix whose entries are numerical values between 0 and 255, where 0 corresponds to black and 255 to white for instance. Then the brain tumor detection of a given patient consist of two main stages namely, image segmentation and edge detection.

C. Registration and Image Segmentation

The baseline study is used as the reference study, and all other studies are registered to it via a rigid transformation. Then, the brain is segmented by a graph-cut-oriented active appearance method (GC-OAAM) [10]. This method synergistically combines the active appearance, live-wire, and GC methods to take advantage of their complementary strengths. The details can be seen in [10].

The objective of image segmentation is to cluster pixels into prominent image region. In this paper, segmentation of Gray level images is used to provide information such as anatomical structure and identifying the Region of Interest i.e. locate tumor, lesion and other abnormalities. The proposed approach is based on the information of anatomical structure of the healthy parts and compares it with the infected parts. It starts by allocating the anatomical structure of the healthy parts in a reference image of a normal candidate brain scan image as shown in Fig. 1 then it allocates the abnormal parts in the unhealthy patient brain. scan image by comparing it with the reference image information as shown in Fig. 2.



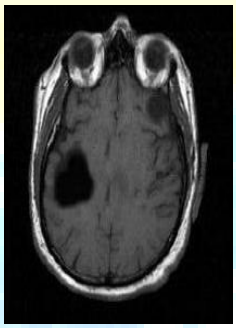


Figure 2: Normal Brain **Figure 3: Abnormal Brain**

Registration and Smoothing:

There are different types of noise encountered by different techniques, depending on the noise nature and characteristics, namely Gaussian noise and
impulse noise. In this paper we assumed that the main image noise is additive and random; that is spurious and random signal, n(i, j), added to the true pixel value I(i, j):

$$II(i,j) = I(i,j)+n(i,j) \quad (1)$$

In this algorithm the enhancement in spatial domain is based on direct manipulation of pixels in a small neighbourhood of pixels, it generally takes the form;

$$g(x,y) = T[f(x,y)] \quad (2)$$

in which f(x, y) is the input image, g(x, y) is the processed image, and T is an operator on f, defined over some neighborhood of (x, y). Then we applied the next enhancement in frequency domain which is based

on the concept of the convolution theorem and spatial filters. In this paper, the proposed noise enhancement algorithm is based on using spatial filters and includes the following:

- Smoothing filters that are used to reduce or remove Gaussian noise from the MRI image.
- Sharpening filters that are used for High lighting edges in an image, and are based on the use of first and second order derivatives.

D. Meshing

A tetrahedral mesh is built for the segmented tissues. The full meshing procedure is composed of the following three steps.

1. A surface mesh is first generated for the segmented tissues (brain and tumors) by the marching cube algorithm [11].i.e Brain portion extraction

2. This surface mesh is then decimated by the ISO2Mesh method [12]. i.e Tumor segmentation.

3. The volumetric mesh is finally generated from the surface mesh also by the ISO2Mesh method [12]. i.e Abnormality detection

As an illustration, the results for two sample slices obtained at different stages are shown in Fig. 3

Fig. 4: Flowchart of Proposed Method

Numerous Brain Extraction Algorithms (BEA) are available in literature. Our T2-BEA [11] makes use of anisotropic diffusion process [12], optimal thresholding and morphological processes [13] to separate the brain from non-brain portions. The diffusion process is used to highlight the brain from T2 head scan. Then an intensity threshold is computed using which a rough binary brain portion is generated. The morphological operations, erosion and dilation, and connected component analysis are then performed on the rough brain portion to produce the brain mask. Finally the brain mask is used to extract the brain from T2 scans

GENERAL STRUCTURE AND ANALYSIS OF TUMOR GROWTH MODEL

The reaction–diffusion model is adopted to model the growth and spreading of tumor cells in the Brain

$$\frac{\partial c}{\partial t} = -div\ -D\nabla c\ + S\ c,t\ - \mathrm{T}\ c,t \quad (3)$$

where c represents the tumor cell density, D is the diffusion coefficient of tumor cells, S(c, t) represents the source factor function that describes the proliferation of tumor cells, and T(c,t) is used to model the efficacy of the tumor treatment. Since our purpose is to predict the tumor growth before treatment, the treatment term T(c, t) is omitted. The source factor S(c, t) can be modeled using Gompertz law [3], which is defined as follows:

$$S\ c,t\ = \rho c \ln\left(\frac{C_{\max}}{C}\right) \quad (4)$$

where ρ is the proliferation rate of tumor cells, Cmax is the maximum tumor cell carrying capacity of the brain tissue Similar with [3], Cmax is set to 3.5 × 104 cells mm−3.

Combining (3) and (4) and omitting T(c, t), we can get

$$\frac{\partial c}{\partial t} = -div\ -D\nabla c\ + \rho c \ln\left(\frac{C_{\max}}{C}\right) \quad (5)$$

Based on [8] and [14], in this letter, It is important to note that in the diffusivity matrix diffusion in the radial direction is faster than other directions. Here, the diffusivity in the radial direction is set as λ(λ > 1) times than of those in other directions. The FEM is used to solve the PDE in the aforementioned reaction–diffusion model. Based on the Galerkin method [15], the continuous problem can be converted to a discrete problem in a sub vectorial space of finite dimension. In principle, it is the equivalent of applying the method of variation to a function space, by converting the equation to a weak formulation [15]. The details of implementation of the reaction–diffusion model by FEM can be found in [15]

CONCLUSION

In this paper we have developed an automatic image based method to detect tumors in 3D MRI head scans. Inter Hemisphere fissure (IHF) and symmetrical nature of the brain are used in the tumor detection. Experimental results on 10 data sets show that the proposed method performed well. In few cases, it performs better than the existing methods.

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