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P. Shanthakumar^{a,*}, P. Ganeshkumar^b

^a Department of Computer Application, R.V.S. College of Engineering and Technology, Dindigul, Tamil Nadu 624005, India ^b Department of Information Technology, K.L.N. College of Engineering, Sivagangai, Tamil Nadu 630611, India

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ABSTRACT

Indefinite and uncontrollable growth of cells leads to tumors in the brain. The early diagnosis and proper treatment of brain tumors are essential to prevent permanent damage to the brain or even patient death. Accurate data regarding the position of the tumor and its size are essential for effective treatment. Hence, an entirely computerized automatic system to provide accurate tumor data is compulsory for physicians. Such developments are necessary to diagnose brain tumors during brain surgery. Brain magnetic resonance (MR) images are proposed for the detection and segmentation of the tumor region via a completely automatic and highly accurate method. The approach discussed in this paper employs an adaptive neuro fuzzy inference system (ANFIS) based on the automatic seed point selection range. The pixels intensity of the proposed algorithm is not dependent on the tumor type. The tumor's segmentation results are evaluated based on various criteria, including similarity index (SI), overlap fraction (OF), extra fraction (EF) and positive predictive value (PPV), which corresponded to values of 0.817%, 0.817%, 0.182%, and 0.817%, respectively, in this study. These results indicate that the approach proposed in this study performs better compared to many conventional processes. The significance of this work is the differentiation of brain abnormalities from the healthy brain tissue.

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1. Introduction

Brain tumors affect people of all ages. A tumor is a mass of tissue made up of accumulated abnormal cells. Most benign brain tumors are noncancerous and are not destructive, and they generally do not spread to nearby tissues, although in some cases benign tumors can be serious. Malignant brain tumors are cancers that originate in the brain and distinctively grow faster than benign tumors, forcefully expending into surrounding tissue. Magnetic resonance imaging (MRI) is widely used to better understand such tumors and to quantify their evolution. Manual segmentation of tumors in MR images by experts is time-consuming, subjective and susceptible to inter-expert variability. Therefore, automatic segmentation is needed as an alternative to manual segmentation. However, the tumor progression often varies regarding the tumor shape, location and volume among patients and even within the same patient. Therefore, automatic segmentation is highly complex, due in part to tumor variability of several factors, such as texture, intensity, shape and size.

* Corresponding author.

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E-mail address: santhan.mca@gmail.com (P. Shanthakumar).

Brain tissue and tumor segmentation in MR images have become a topic of great interest. The most widely used types of MRI scans are T1-weighted and T2-weighted scans. In T1 scans, fat and water molecules are differentiated to indicate damaged tissue areas. Darker areas (called hypointense lesions) indicate areas of tissue loss. The visibility of damage can be further enhanced by injecting the non-radioactive element gadolinium, which enhances inflammatory lesions. In T2 scans, areas with more water content become visible as hyperintense spots, which indicate regions of tissue loss. For accurate image segmentation, features must be accurately extracted. The brain is comprised of different tissues such as the white matter (WM), cerebrospinal fluid (CSF) and gray matter (GM). During the segmentation of the MR brain images, variability in certain aspects, such as tumor shape, location, size, intensity and textural properties, makes the segmentation process difficult. In tumor segmentation, the intensity feature plays a vital role in differentiating tumor from other soft brain tissues. However, intensity alone is not sufficient, and therefore other texture-based features, such as local binary patterns (LBPs), gray level-based features, the gray level co-occurrence matrix (GLCM), and wavelet characteristics, can be extracted.

Automatic tumor segmentation aids physician's in disease diagnoses by not requiring manual labeling. Glioblastoma multiforme (GBM) brain tumors are the most commonly occurring tumor found in brains across patients of all ages. The automatic segmentation of tumors becomes critical due to the variations in the texture, intensity, shape and size of such tumors.

Non-tumor brain structures, such as blood vessels, and soft tissues, are often misidentified as tumors, leading to many false positives (FPs). Most existing techniques for tumor segmentation are not fully automatic. Hence, the existing manual tumor segmentation methods are not fully accurate in detecting tumors.

In this study, an automated technique is proposed that employs textural features to describe the blocks of each MRI slice, along with other features. The process flow of the proposed technique is shown in Fig. 1, which utilizes a trained classifier to differentiate the blocks and to detect the blocks that contain tumor tissue. The classification of the blocks provides an initial coarse segmentation of the MRI image. The textural-based classifier is built using an adaptive neuro fuzzy inference system, one of the most widely accepted algorithms that have been utilized successfully in many imaging and medical applications.

There are several classifying techniques that are used for tumor detection and segmentation, although most existing systems are not fully automated. Such algorithms rely on a specific classifier algorithm that requires manual segmentation.

A computer aided classification technique is proposed, which combines conventional MRI and perfusion MRI for differential diagnosis. Their method consists of ROI definition, feature selection, classification and feature extraction. The feature extraction includes tumor shape and intensity features and rotation-invariant texture features. The features subset selection is carried out using support vector machines (SVMs). The binary SVM classification was applied on 102 brain tumors, and the obtained accuracy, sensitivity, and specificity were 87%, 89%, and 79%, respectively, for differentiation of metastases from gliomas and 87%, 83%, and 96%, respectively, for the discrimination of high grade from low grade neoplasm's [1]. A Bayesian formulation was used to incorporate soft model assignments into the calculation of conventionally model free affinities. The resulting model-aware affinities were united into a multilevel segmentation by the loaded aggregation algorithm, and the technique for detecting and segmenting the brain tumors was applied to multichannel magnetic resonance (MR) volumes. The simulation results showed improved performance over conventional systems [2]. An efficient brain tumor detection was proposed in [3], which consisted of three steps: enhancement, segmentation and classification. The enhancement process was applied to enhance the image quality before the segmentation phase. The authors used mathematical morphology to increase the contrast in the MRI images. Then, a wavelet transform was applied to the segmentation process to crumble the MRI image. Finally, a k-means algorithm was executed to extract the tumor region. The experimental results were analyzed. Pixel level variation was used to detect abnormalities in the brain region. The brain abnormalities were diagnosed using the pixel distribution surrounding the abnormal tissues in the brain image [4].

Hamamci et al. [5] presented cellular automata (CA)-based seeded tumor segmentation method for contrast-enhanced T1 weighted magnetic resonance (MR) images. The CA-based segmentation method was established according to graph-theoretic methods to show that the iterative CA framework solves the shortest path problem. A sensitivity parameter is introduce to adopted the heterogeneous tumor segmentation problem was also implemented. Then, a tumor probability



Fig. 1. Process flow of the proposed tumor detection system.

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