Brain Tumour Identification Using NN Classification by Wavelet Transform Method in MRI Images

Ch. Siva Naga Malleswary[1], B. Siva Hari Prasad[2]
[1]PG Scholar, [2]Senior Assistant Professor
Department of Electronics and Communication Engineering, Lakireddy Bali Reddy College of Engineering, Mylavaram, Andhra Pradesh, India.

Abstract **-** This paper has focused on the brain tumor detection techniques. The brain tumor detection is a very important vision application in the medical field. This work has firstly presented a review on various well known techniques for automatic segmentation of heterogeneous image data that takes a step toward bridging the gap between bottom-up affinity-based segmentation methods and top-down generative model based approaches. The main objective of the work is to explore various techniques to detect brain tumor in an efficient way. It has been found that the most of existing methods has ignored the poor quality images like images with noise or poor brightness. Also the most of the existing work on tumor detection has neglected the use of object based segmentation. So to overcome the limitations of earlier work a new technique has been proposed in this research work. The technique has shown quite effective results than neural based tumor detection technique. The design and implementation of the proposed algorithm is done in MATLAB using image processing toolbox. The comparison has shown that the proposed technique has achieved up to 94 % accuracy which was 78 % in neural based technique. Also for high corrupted noisy images the proposed technique has shown quite effective results than the neural based tumor detection.

Keywords **-** *Magnetic Resonance Imaging, Glioma, Brain Tumor, Brain Tumor Segmentation, Deep Learning, Convolutional Neural Networks*

I. INTRODUCTION

Gliomas are the brain tumors with the highest mortality rate and prevalence [1]. These neoplasms can be graded into Low Grade Gliomas (LGG) and High Grade Gliomas (HGG), with the former being less aggressive and infiltrative than the latter [1], [2]. Even under treatment, patients do not survive on average more than 14 months after diagnosis [3]. Current treatments include surgery, chemotherapy, radiotherapy, or a combination of them [4]. MRI is especially useful to assess gliomas in clinical practice, since it is possible to acquire MRI sequences providing complementary information [1]. The accurate segmentation of gliomas and its intra-tumoral structures is important not only for treatment planning, but also for follow-up evaluations. However, manual segmentation is time-consuming and subjected to inter- and intra-rater errors difficult to characterize. Thus, physicians usually use rough measures for evaluation [1]. For these reasons, accurate semiautomatic or automatic methods are required [1], [5]. However, it is a challenging task, since the shape, structure, and location of these abnormalities are highly variable. Additionally, the tumor mass effect change the arrangement of the surrounding normal tissues [5]. Also, MRI images may present some problems, such as intensity inhomogeneity [6], or different intensity ranges among the same sequences and acquisition scanners [7]. In brain tumor segmentation, we find several methods that explicitly develop a parametric or non-parametric probabilistic model for the underlying data. These models usually include a likelihood function corresponding to the observations and a prior model. Being abnormalities, tumors can be segmented as outliers of normal tissue, subjected to shape and connectivity constrains [8]. Other approaches rely on probabilistic atlases [9]–[11]. In the case of brain tumors, the atlas must be estimated at segmentation time, because of the variable shape and location of the neoplasms [9]–[11]. Tumor growth model scan be used as estimates of its mass effect, being useful to improve the atlases [10], [11]. The neighborhood of the voxels provides useful information for achieving smoother segmentations through Markov Random Fields (MRF) [9].Zhao at al. [5] also used a MRF to segment brain tumors after a first over segmentation of the image into super voxels, with a histogram-based estimation of the likelihood function. As observed by Menze et al. [5], generative models generalize well in unseen data, but it may be difficult to explicitly translate prior knowledge into an appropriate probabilistic model. Another class of methods learns a distribution directly from the data. Although a training stage can be a disadvantage, these methods can learn brain tumor patterns that do not follow a specific model. This kind of approaches commonly consider voxels as independent and identically distributed [12], although context information may be introduced through the features. Because of this, some isolated voxels or small clusters may be mistakenly classified with the wrong class, sometimes in physiological and anatomically unlikely locations. To overcome this problem, some authors include information of the neighborhood by embedding the probabilistic predictions of the classifier into a Conditional Random Field [12]–[15]. Classifiers such as Support Vector Machines [12], [13] and, more recently, Random Forests (RF) [14]–[21] were successfully applied in brain tumor segmentation. The RF became very used due to its natural capability in handling multi-class problems and large feature vectors. A variety of features were proposed in the literature: encoding context [15], [16], [21], first-order and fractals-based texture [14], [15], [18], [21], [22], gradients [14], [15], brain symmetry [14], [15], [19], and physical properties [19]. Using supervised classifiers, some authors developed other ways of applying them. Testimony et al.[19] developed a two-stage segmentation framework based on RFs, using the output of the first classifier to improve a second stage of segmentation. Geremia et al. [20] proposed a Spatially Adaptive RF for hierarchical segmentation, going from coarser to finer scales. Meier et al. [23] used a semi-supervised RF to train a subject-specific classifier for post-operative brain tumor segmentation. Other methods known as Deep Learning deal with representation learning by automatically learning an hierarchy of increasingly complex features directly from data [24]. So, the focus is on designing architectures instead of developing handcrafted features, which may require specialized knowledge [25]. CNNs have been used to win several object recognition [26], [27] and biological image segmentation [28] challenges. Since a CNN operates over patches using kernels, it has the advantages of taking context into account and being used with raw data. In the field of brain tumor segmentation, recent proposals also investigate the use of CNNs [29]–[35]. Zikic et al. [29] used a shallow CNN with two convolutional layers separated by max-pooling with stride 3, followed by one fully-connected (FC) layer and a softmax layer. Urban et al. [30] evaluated the use of 3D filters, although the majority of authors opted for 2D filters [31]–[35]. 3D filters can take advantage of the 3D nature of the images, but it increases the computational load. Some proposals evaluated two-pathway networks to allow one of the branches to receive bigger patches than the other, thus having a larger context view over the image [31], [32]. In addition to their two-pathway network, Havaei et al. [32] built a cascade of two networks and performed a two-stage training, by training with balanced classes and then refining it with proportions near the originals. Lyksborg et al. [33] use a binary CNN to identify the complete tumor. Then, a cellular automata smooths the segmentation, before a multiclass CNN discriminates the sub-regions of tumor. Rao et al. [34] extracted patches in each plane of each voxel and trained a CNN in each MRI sequence; the outputs of the last FC layer with softmax of each CNN are concatenated and used to train a RF classifier. Dvoˇr´ak and Menze [35] divided the brain tumor regions segmentation tasks into binary sub-tasks and proposed structured predictions using a CNN as learning method. Patches of labels are clustered into a dictionary of label patches, and the CNN must predict the membership of the input to each of the clusters. In this paper, inspired by the groundbreaking work of Simonyan andZisserman [36] on deep CNNs, we investigate the potential of using deep architectures with small convolutional kernels for segmentation of gliomas in MRI images. Simonyan and Zisserman proposed the use of small 3 _ 3 kernels to obtain deeper CNNs. With smaller kernels we can stack more

II. RELATED WORK

The project is processed on brain tumor MRI images for detection and Classification on different types of brain tumors [7-9]. We are going to use image processing techniques in this paper for detection of tumor from MRI images like histogram equalization , image adjustment, image segmentation are used for Detection of tumor. Fig. 1 explains flow of tumor detection and classification

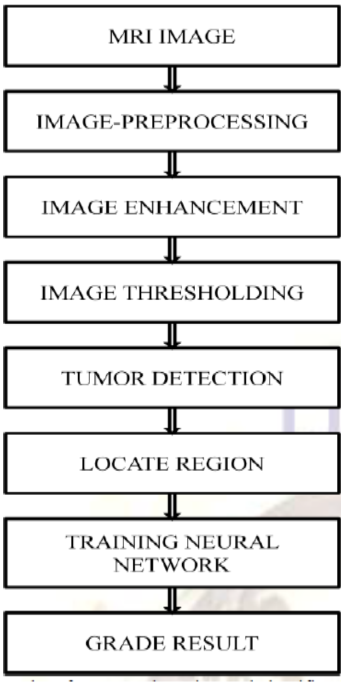


Fig.1: Flow for tumor detection and Classification

Block Diagram:

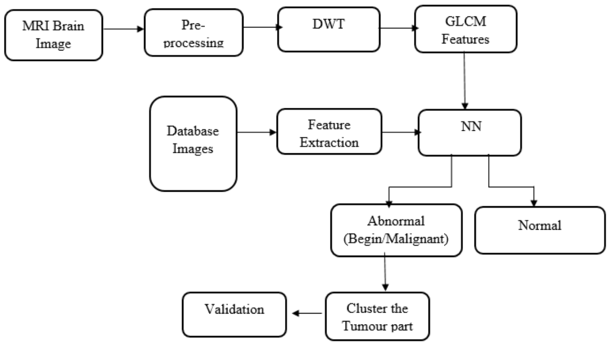


Fig.2: proposed method

The first step in my project is to extract tumor from MRI image. We are going to use various functions one by one for the detection of tumor from MRI image .Generally the MRI images are very dark in nature it is difficult to extract tumor from MRI image The fundamental enhancement is needed. First function is pre-processing of MRI image. In this pre-processing converting color MRI image into gray color MRI image. In gray scale image it is easy to identify properties of an image. The pixel values vary 0 to 255 range in gray scale image .Next step is image enhancement, by using this technique we are increase contrast of an whole image .Histogram equalization technique is used for image enhancements, and image adjustment is also another image enhancement technique it adjust intensity values of an image. These techniques increase the contrast of an whole image. Generally the intensity value of brain tumor cell higher than normal brain cell .Tumor is looking brighter in the MRI image. There is contrast difference between whole brain and tumor but human eye can't find the difference. Thresholding is the simple method of image segmentation. Segmentation sub divides an image into sub parts .In this paper our main aim is to separate tumor from the background. Segmentation sub divides an image into sub parts this process is continuous until the edges of the tumor gets detected .The threshold value is calculated from Eqn. (1) considered from [12]. In this paper segmentation is done by the single parameter i.e. intensity thresholding. The intensity value of tumor is higher than normal brain. So, this technique is best suited for the project to detect the tumor from back ground. The threshold value is compared with the each and every pixel of MRI image. If the threshold value is greater than pixel value of an image then remove that pixel from an image. If the threshold value is lower than pixel value of an image then that will remain as it is (i.e. not removed from the image). In this we are removing pixel by pixel in the MRI image with the threshold value. After thresholding we get binary image since the MRI image has only two values binary '0'(0),binary value'1'(255).The pixel values of an image greater than threshold value those pixel values set to binary value'1'(255),remaining set as binary '0'(0).The output image is tumor with dark background. While the segmentation there are gaps at the edges dilation operator is used for filling those gap and make continues at the edges.

III. TUMOR CLASSIFICATION

A suitable artificial neural network classifier is designed in this paper to identify the different grades of brain tumors. Artificial neural networks are composed of simple elements operated in parallel. These elements are inspired from biological nervous system. Each element in a network called neuron [4-5]. The sum of multiplication of weights and inputs plus bias at the node is positive then only output elements fires. Fire means it discharges energy to next element. Otherwise it doesn't fire. The artificial neural network is an adaptive system [10-11]. Adaptive means system parameters are changed during the operation. The system parameter is nothing but weights. Two layer feed forward neural network is taken in this paper .The two layer feed forward neural network consists of one input layer and one output layer and one hidden layer and one output. In the hidden layer 10 nodes are taken .In the two layer feed forward network two log sigmoid transfer function are used. The two layer feed forward network with two log sigmoid functions are more widely used in classification, pattern recognition .It gives better results in these classification. The neural network system is designed in two phases.

1) Learning/Training
2) Recognize/Testing

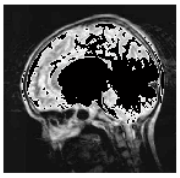
There are four steps in training process
1) Assemble the training data
2) Create the two layer feed forward network
3) Training the network
4) Simulate the network

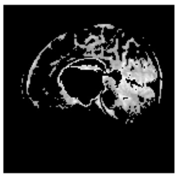
The known samples are applied to the two layer feed forward neural network is trained with back propagation algorithm .Training/Learning means changing the weights of the network. Change the weights until it gives the proper output. After training the neural network the network parameters are fixed. In this paper we trained the neural network with 36 MRI brain tumor samples. Total four classifications are in the brain tumors .Each of 9 samples for four different classes. Total 36 input MRI brain tumor samples are trained to neural network through back propagation learning/training. Train the neural network until it gives proper output. In the second stage i.e. in recognize/testing the unknown samples are applied to the trained network. The trained network compares the unknown sample with the all trained input samples and classifies the unknown sample based on trained input samples. In this paper totally four brain tumor grades exist. Take different known MRI samples for different grades and apply to trained neural network and check whether it is working properly or not. The proposed method gives correct output for the known samples and then it is tested for the unknown samples. The proposed method has given better performance in this paper.

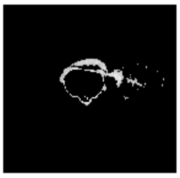
IV. CLUSTERING METHODS

The K-means algorithm is an iterative technique that is used to partition an image into *K* clusters. The basic algorithm is: Pick *K* cluster centres, either randomly or based on some heuristic. Assign each pixel in the image to the cluster that minimizes the distance between the pixel and the cluster centre. Re-compute the cluster centres by averaging all of the pixels in the cluster. Repeat steps 2 and 3 until convergence is attained (e.g. no pixels change clusters)In this case, distance is the squared or absolute difference between a pixel and a cluster centre. The difference is typically based on pixel colour, intensity, texture, and location, or a weighted combination of these factors. *K* can be selected manually, randomly, or by a heuristic. This algorithm is guaranteed to converge, but it may not return the optimal solution. The quality of the solution depends on the initial set of clusters and the value of *K*. In statistics and machine learning, the k-means algorithm is a clustering algorithm to partition n objects into k clusters, where $k < n$. It is similar to the expectation-maximization algorithm for mixtures of Gaussians in that they both attempt to find the centres of natural clusters in the data. The model requires that the object attributes correspond to elements of a vector space. The objective it tries to achieve is to minimize total intra-cluster variance, or, the squared error function. The k-means clustering was invented in 1956. The most common form of the algorithm uses an iterative refinement heuristic known as Lloyd's algorithm. Lloyd's algorithm starts by partitioning the input points into k initial sets, either at random or using some heuristic data. It then calculates the mean point, or centroid, of each set. It constructs a new partition by associating each point with the closest centroid.

Design Steps: K-Means algorithm is an unsupervised clustering algorithm that classifies the input data points into multiple classes based on their inherent distance from each other.







- **Step l:** Increment value= ([max – min]/number of clusters)
- **Step 2:** Initialize the centroids with k random intensities.
- **Step 3:** Find the difference between the four centroids and each pixel intensity of image.
- **Step 4:** Find the minimum difference from that four difference values.
- **Step 5:** Cluster the pixels based on minimum distance of their intensities from the centroid intensities.
- **Step 6:** Repeat the steps from step 3 to step 5 for all pixel intensities of input image.

Then the centroids are recalculated for the new clusters, and algorithm repeated by alternate application of these two steps until convergence, which is obtained when the points no longer switch clusters (or alternatively centroids are no longer changed). The quality of the final solution depends largely on the initial set of clusters, and may, in practice, be much poorer than the global optimum. Since the algorithm is extremely fast, a common method is to run the algorithm several times and return the best clustering found. A drawback of the k-means algorithm is that the number of clusters k is an input parameter. An inappropriate choice of k may yield poor results. The algorithm also assumes that the variance is an appropriate measure of cluster scatter.

V. CONCLUSION

In this paper the brain tumor detection and classification is successfully implemented by a novel algorithm for Brain Tumor Classification is presented. This new method is a combination of Discrete Wavelet Transform and Probabilistic Neural Network along with the implementation of GLCM. By using these algorithms an efficient Brain Tumor Classification method was constructed with maximum recognition rate Simulation results using Brain Tumor database demonstrated the ability of the proposed method for optimal feature extraction and efficient Brain Tumor classification. The ability of our proposed Brain Tumor Classification method is demonstrated on the basis of obtained results on Brain Tumor image database. On other Brain Tumor image databases the other combinations are there for training and test samples.

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