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Brain Tumor Detection and Classification Using MRI Brain Images

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Abstract - *Detection and classification of brain tumors is an important task in the medical imaging and over time, there have procedural development and extensive research. The complexity of the brain as a diagnosable organ, the presence of noise, poor comparison and depth heterogeneity within images, efficient features extraction, and the right type necessitates the development of efficient techniques for the detection and classification of brain tumor. We employed number of computerized algorithms for categorization and detection, including the k-means clustering set of rules for pre-processing brain tumor magnetic resonance images (MRI). Detection is accomplished the usage of marker-controlled watershed transform and grey-level co-occurrence matrix (GCLM) is employed to extract features. To categorize, we employ the Support Vector Machine (SVM) and Artificial neural network (ANN). Implemented using various supervised mastering models, with the comparison between them proving more accurate results in less time, is being widely used*

Key Words: Brain Tumor; MRI; Gray-Level Co-Occurrence Matrix; ANN; SVM; Watershed Transform

1. INTRODUCTION

Tumor detection and classification is a method that has undergone continuous development and research throughout time, with its importance in cancer classification and therapy, and the identification of brain tumors presenting new challenges for organ complexity. Since tumors must be classified by several criteria such as size, density and location, this increases the potential for errors and the risk of poor accuracy. This complicates the task even more as it is likely to generate noise in the magnetic resonance image and lacks specific limitations such as low, dementia and limitations. Consequently, a cost-effective and efficient approach is required.

The formation of additional cells in the brain is known as a brain tumor. In order to grow, some cells divide and form additional tissue that is not needed. This is called a tumor. Tumor cells multiply and eat away at the brain tissue. There are two kinds of brain tumors: benign and malignant. Benign tumors develop slowly, but malignant tumors grow extremely rapidly and spread to the brain, where they can press on the brain in the skull, killing healthy brain cells. To identify the location, form, and amount of brain tumor tissue, an MRI scan of the brain is necessary. To assess the kind, location, and volume of brain tumor tissue, an MRI scan of the brain was required. MRI is a sophisticated technology for medical imaging that generates high-pixel images with very good quality of organs in the human body, and is used to select appropriate diagnoses at the right time for brain tumor disease patients is important to process[1].

The purpose of our effort was to build an automated process for the identification and classification of brain tumors that would be better to present methods. In contrast to the previously used K-means clustering method for principal segmentation, we used the latest version K-means clustering approach to substantially increase the pre-processing of the MRI image [2] [3]. K-means clustering and watershed segmentation are techniques that are widely used for cancer detection [4]. Furthermore, from a technical point of view, K-means clustering is less complex, and segmentation can be easily constructed by comparing desirable features to the brain architecture. Traditional k-means had problems with sensitivity to outliers and noise, as well as poor scaling over time; The updated version addressed these and many other concerns. Morphological techniques using marker and mask processes are used to improve images to reduce noise, blurring, and scan uniformity. Watershed segmentation with linked component labeling technology provides superior segmentation results, with perimeter, area, entropy, and singularity with value. All parameters characterizing tumor size and other features were extracted using the created method [5].

Pre-processing compensates for the lack of over-segmentation induced by the specified technology and considerably boosts the resilience of the procedure. We wish to refine and optimize the whole automated classification and detection process by extracting features with the aid of gray-scale co-occurrence metrics [6].

There are a variety of approaches and strategies for classifying brain tumors. We used two different techniques in our study: a support vector machine and an artificial neural network [7][8]. These methods have been shown to be more accurate and effective. SVM stands for Supervised Learning. It is a great tool for classifying and analyzing data. Even with large amounts of data, the SVM classifier learns quickly. SVM is used in the classification of two or more classes [9] [10]. Backpropagation network training involves supervised learning and is an excellent method for non-linear transformations such as sigmoid transfer functions [11][12][13].

In this paper, an algorithm to differentiate between benign and malignant tumors is presented. Watershed algorithms are used to segment brain tumors. For classification, GLCM features are retrieved from MRI of the tumor and support vector machines, and an artificial neural network is employed. The rest of the paper is arranged as follows. The methodology is described in Section II. The experiment is in Section III, while the conclusion is in Section IV.

2. METHODOLOGY

2.1 Images Preprocessing

To eliminate noise and undesired distortion in the photos, before putting them into segmentation, we examine the images at the lowest point in this stage and filter them according to the appropriate criteria. We can either apply a mean filter to the image or use contrast enhancement to draw the boundaries of the image more clearly [14]. Our usual proposed method is offered. K-means clustering has been researched and used for primary segmentation, and because it subsequently reduces the potential for noise and increases the detection process to a significant degree [15]. Each picture is separated into K groups, which may be readily identified owing to their closeness to the architecture of the human brain. Clusters are formed by studying each image and employing all points to build a new mean. By specifying K clusters for all sample spaces, the entire data set is rearranged. Clusters occupy all the data points and cover the complete data space. The Euclidean distance of each data point is now computed from its mean. If the known distance is the shortest feasible distance or is already closest to its mean, we continue. This process continues until all the data points are in their nearest cluster and their transfer is less than the previously defined cut-off number. The use of k-means to pre-process the images greatly assists in overcoming the over-segmentation issue of the watershed approach.

$$T_i^{(u)} = \{ y_r : \| y_r - n_i^{(u)} \|^2 \le \| y_r - n_i^{(u)} \|^2 \ \forall_k, 1 \le k \le 1$$

$$n_i^{(u+1)} = \frac{1}{|T_i^{(u)}|} \sum_{y_k \in T_i^{(u)}}$$

2.1 Marker-Controlled Watershed Algorithm Detection

Approach

Before identifying tumors, we must now perform morphological enhancements on the first segmented image produced by pre-processing the images. Adding and removing pixels, as well as contrast changes known as dilation and erosion, are the most basic steps. By replacing the markers in the foreground image, we use several rounds of masking and marking to identify. The whole process is shown in Figure 1 from start to finish. Because the morphological formation is a structural form, as a reference for erosion, we construct a disc-shaped structure. The picture is converted to grey, then opened morphologically after a variable separation. If the difference is less than the threshold, the limit function converts a segmented image with a meaningful change to a pixel value of 0, and 255 if the difference is large. The next step is the duplication reduction process that occurs after this gray transition to a complete binary image. When the image is reconstructed using an image mask, the foreground and background objects appear to be different. The black streaks and stem marks disappear when the bottles are opened one by one. To find the relevant previous tags, the distribution is now calculated by re-sizing the image and computing the regional maxima. After that, we overlay this pre-image marker and clean the border and marking blocks, as well as any missing pixels, using repeated closures and erosions. We must first compute the Euclidean range transform of a gray or binary picture. We need to split it into watersheds. Furthermore, the Sobel function gave better results for edge recognition and discrimination than the Canny variant, thus Sobel was selected.

Tumor identification is a strategy that has gained a considerable lot of interest in the last several years, and the most optimal method is to use a marker-controlled conventional watershed transformation. Denoising techniques have evolved over time and can be employed in combination with conventional filters, offline filters, and nonlinear anisotropic separation. They are used in the Markov field approach [16], the wavelet-based approach [17], and the analytical correction process. Water separation is a 92.76 percent better-classified technique that gets its name from the natural process of collecting water in reservoirs and the introduction of gray images as geographic sites. When submerged in water, local minima are thought to resemble holes in which they raise the water level and bring it closer to the surface. Water is collected in vessels equal to the water flow of the earth's surface by the flow at the bottom of its slopes. A dam is the widest point or intersection of two bodies of water, and these dams or water lines divide the picture into several groups. This is a water separation procedure where the MRI is completed and the gray image images are filled with linear lines that distinguish between different dimensions as a boundary. Dehydration is a popular method because it can also dissociate noncancerous body tissues.

To separate the image, we first "mark" the objects in front as described above, and then use a canal and a water line (the point where two bodies of water meet) to split the image. Let's try (the boundary where two bodies of water meet) Let's see how it goes. Find and label the objects in the front, such as a plant in it, and count the marks on the

back, which are part of the dark area that should be separated. Boundaries at both the front and back markers are necessary to create water flow, so the transition process can begin now. In order to enlarge the tumor further and produce a clear distinction between tumor and brain, we perform watershed segmentation a second time. We can now view the tumor as the original black-and-white image because the threshold was 255 for the tumor and 0 for the rest. We were able to identify the markers and define the boundaries accurately by reconstruction by repeated opening and closing, ensuring that there was no disaggregation. Superimposition was employed [19] to enhance contrast and ensure that borders were not highlighted with clear tumors visible against a pitch-black background.

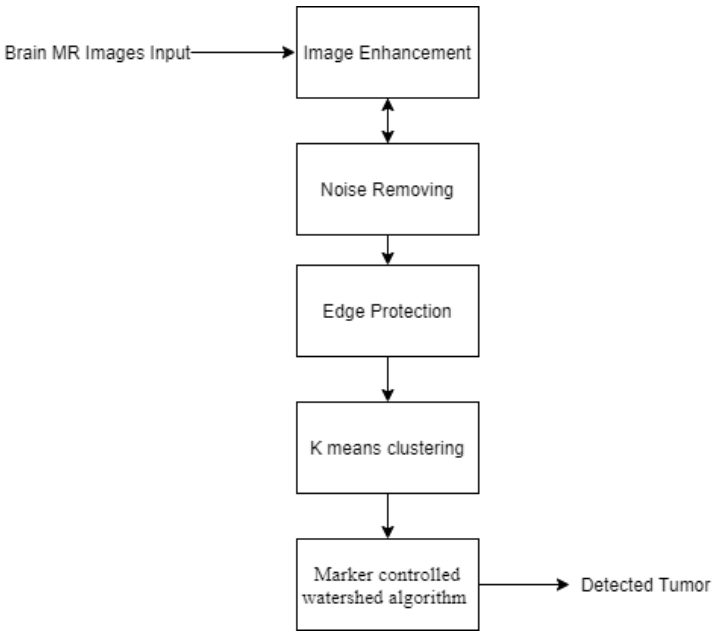


Fig:1 Depicts the whole process

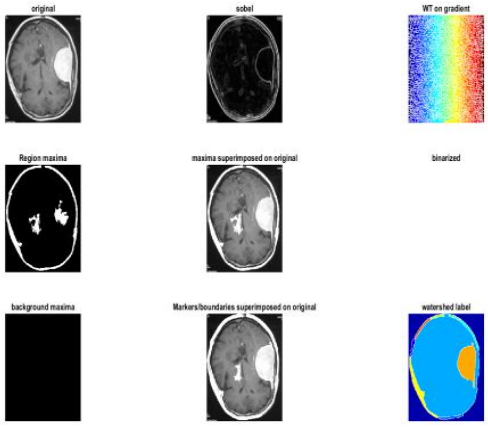


Fig:2 Depicts the infection

The border method and regional approach are the two major techniques of segmentation. Watershed segmentation combines these two methods to provide a robust tool to quickly locate edges and areas. Watershed transformation is a segmentation method based on morphological gradient[20].

2.2 Features Extraction

Features are the characteristics of images so that they can be retrieved to make a meaningful analysis using them. They attempt to describe images in a collection of specific features called features that serve as inputs to classification systems. Watershed features are not adequate and additional may be required for a particular categorization. Much effort has been done in reviewing and comparing alternative MRI image extraction techniques, and we have landed on GLCM [21] for our approach. Using this, the following characteristics are retrieved, which are subsequently utilized for classification Correlation, Symmetry, Mean Entropy, RMS, Variance, Contrast, Kurtosis, Skewness IDM, Area, MajorAxis, MinorAxis, Eccentricity, Solidity, Equi-diameter, circumference, Energy, SD, Energy, circularity, Smoothness, square, density [22][23].

These are just a few variables. Additional features may also be discovered. As the name indicates, the co-occurrence matrix is used to quantify and analyze the distance and relative adaption between two pixels of different intensities. This cohesive matrix will be used to determine their 'd' distance and size if we have pixel 'i' in the image sample at full resolution and another pixel 'j' at different intensities. We utilize the angles between the data for directed analysis. We have lowered the amplitude and increased the number of gray levels since it is particularly sensitive to the amplitude of the sample.

Contrast The intensity difference between a pixel and its neighboring pixels in an image is known as contrast.

$$Con = \sum_{i=1}^{k}\sum_{j=1}^{k}(i-j)^2 p_{ij}$$

Where $p_{ij=}\frac{g_{ij}}{n}$, the total number of pixel pairings is given by n.

Correlation of a pixel with its adjacent pixel in an image is expressed as

$$Corr = \sum_{i=1}^{k}\sum_{j=1}^{k}\frac{(i-m_r)(i-m_c)}{s_r s_c} p_{ij}$$

$$Corr = \sum_{i=1}^{k}\sum_{j=1}^{k}\frac{(i-m_r)(i-m_c)}{s_r s_c}p_{ij}$$

Where $m_r = \sum_{i=1}^{k} i\sum_{j=1}^{k} p_{ij}$ and $m_c = \sum_{i=1}^{k} j\sum_{j=1}^{k} p_{ij}$

And $\sigma_r^2 = \sum_{j=1}^{k}(i-m_r)^2\sum_{j=1}^{k} p_{ij}$

Energy factor is also computed provided by

$$E = \sum_{i=1}^{k}\sum_{j=1}^{k} p_{ij}^{\ 2}$$

Homogeneity a number that measures the closeness of the dispersion of items in the GLCM to the GLCM diagonal.

$$H = \sum_{m,n}\frac{p(m,n)}{1+|m-n|}$$

Compactness The smoother and rounder a tumor's surface is, the more benign it is, and the more complex the tumor surface is, the more malignant it is. C may be used to analyze this feature. and can be defined as:

$$C = \frac{A}{4\pi P^2}$$

P signifies the circumference of the lesion area, which is equal to the sum of the number of pixel points at the tumor's edge; A denotes the area of the wound region, which is equal to the total of all pixels at the wound's edge; and A denotes the area of the wound region, which is equal to the total of all pixels at the wound's edge[22].

2.3 Classification

Artificial neural networks

Separation is one of the most powerful areas for research and applications for artificial neural networks (ANNs). There is a branch of Artificial Intelligence called ANN. The back distribution method was used to train the neural network[24]. A neural network is a mathematical model for processing information that is derived from human systems (such as a brain or nerve cell) and allows neutral networks to be taught and studied in the same way that the human brain is. During the training time, the weight will be adjusted and some formulas will be used for learning. Back extension network is one of the most popular neural networks. This mesh has been used in various applications. First, the classification of special things, which separates just one piece of knowledge from a known object. We will use the same strategy to locate a large number of neurons in the hidden layer of the same analysis given a restricted amount of repeats.

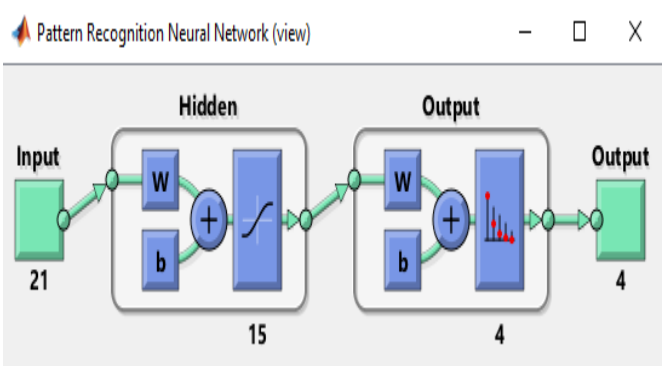
The excel sheet prepared during feature extraction is supplied as input to the neural network. Therefore, the input would be a 250*22 matrix where 250 are the number of samples and 22 are the number of features. Our target would be given as a 250*2 matrix where the representation will be combination of 0 and 1. For example Benign will be 1 0; Malignant will be 0 1.

The training strategy modifies the weight and bias values according to Levenberg-Marquardt optimization. It minimizes a mix of squared errors and weights and then picks the ideal combination to form a network that generalizes effectively. The process is dubbed Bayesian regularization.

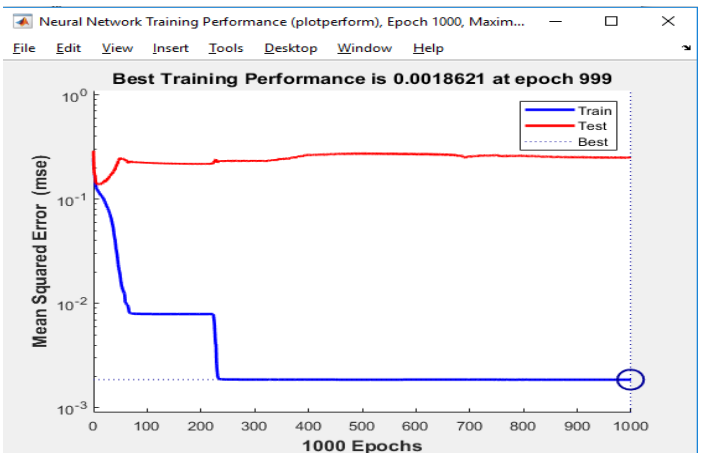
The training and testing data are broken in the ratio of 80:20

Validation stops are disabled by default (max fail = inf) so that training may continue until an appropriate mix of mistakes and weights is found."

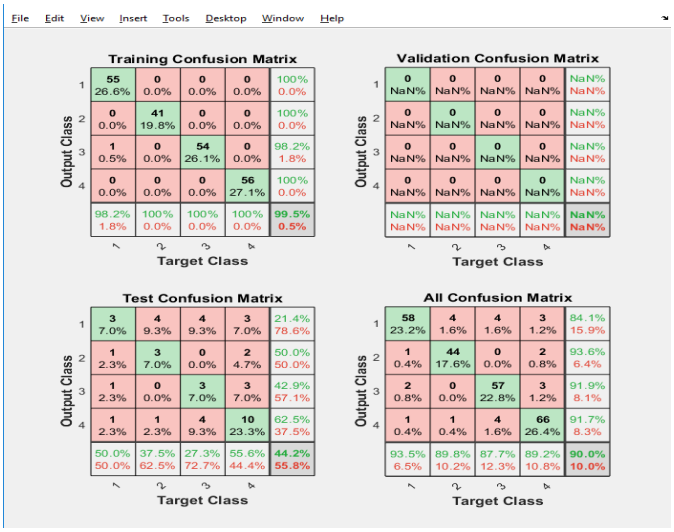
The network architecture is:



The performance plot is:



The confusion matrix is:



Support Vector Machine

SVM [25] is a technique of evaluating data and discovering patterns in computer science and statistics. It is a supervised learning approach that may be used for regression as well as classification. The aim of SVM is to construct hyperplane and group data. The actual data is converted to a high-dimensional feature space using kernel functions, and the decision hyperplane is generated. Magnetic resonance image analysis has previously made significant use of SVM [26]. Support vector machines provide excellent results in both large and small data sets. However, as the amount of the data set rises, the SVM gets more complex. At the same time, the kernel functions used.

3. EXPERIMENT

3.1 Experimental Process

We did the image enhancement using the MATLAB function imadjust. Removing noise from the image by applying the Normal Shrink Denoising algorithm. The binomial filter technique was then used to perform edge protection on the denoised output. There are different segmentation methods available in image processing such as edge-based, threshold-based and clustering-based. With a set number of repetitions and k values, we constructed a k-means clustering method. The output picture generated after using the k-means clustering method for tumor identification is subjected to the marker-controlled watershed technique.

Unlike depth reading, machine learning does not employ the initial picture in the classification process, instead extracting characteristics from the training set. The classifier then uses the collected features to train and classify the test set.

We develop MATLAB GUI for classification. The technique for the classification experiment is as follows: to begin with, over 250 magnetic resonance images classified as malignant or benign were divided into two groups: testing and training. Second, distinct characteristics were retrieved from each image depending on the manually created tumor shape, which we detected using the detection method in the previous section, and modified the ROI to 128x128 size to extract different features it was done. The normalization applies to all extracted features. The SVM classifier and the ANN are trained using the feature vectors and sample tags corresponding to all of the pictures generated from the training set. Finally, by reading the feature vectors of the test set samples, computing the related prediction tag results, and comparing it to the actual test sample tags, the trained classifier assesses the classification accuracy.

$$M = \{(Y_i, d_i)\}_{i=1}^{N}$$

Here, Y_i is the i^{th} sample's input vector, d_i is the i^{th} sample's intended output, and N is the sample size. The database included more than 250 samples, with 80% to train the model and 20% samples being used for testing.

3.2 Evaluation Criterion

When diagnosing a brain tumor for specific cancers, this region is referred to as an FN (false negative) if the system identifies the tumor as benign. If the algorithm classifies the tumor as malignant then the area is called TP (True Positive). When a benign tumor is mistaken as malignant by the diagnostic system, it is termed FP (false positive). When the algorithm diagnoses a tumor as benign, it is referred to as a TN (true negative) [5]. We calculate accuracy on this.

$$Accuracy = \frac{TP}{TP + FN} \times 100\%$$

The ROC curve of the subject's operational characteristics was developed to more thoroughly assess the system's performance. The ROC curve is constructed by adding these coordinate points, with TPR (true positive rate) as the coordinate (y-axis) and FPR (false positive rate) as the abscissa.

3.3 Experimental Results and Analysis

The accuracy of both ANN and SVM come close to each within the range of 95 to 99 percentage. As a result, this detection and classification technique based on several features may be deemed acceptable for use in the detection and classification of brain tumors.

Table -1: Accuracy

Method	Accuracy
Support vector Machine (SVM)	95.86%
Artificial Neural Network (ANN)	97.15%

Table -2:SVM Algorithm classification effect

Evaluation Parameter	SVM Classifier
False negative	01
False positive	00
True negative	10
True positive	49
Sensitivity (%)	98%
Specificity (%)	100%
Accuracy (%)	95.86%

4. CONCLUSION

This article proposes a technique to detect and classify malignant and benign brain tumors based on various characteristics. The tumor part was sectioned using a marker-controlled watershed algorithm. The tumor portion of the brain MRI is used to extract GLCM features, which are then input into a feed support vector machine and ANN for classification. With the provided database, the two tumor types benign and malignant were effectively classified using the suggested method with a classification accuracy of over 95%. The suggested method can be used to classify additional tumor types such as medulloblastoma, lymphoma, and astrocytoma, and the accuracy of the system can be increased if a large database of these tumor types is provided. The purpose of this technology is to give doctors more diagnostic information.

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