

# Segmentation and Detection of Brain Tumor by using Machine Learning



Priyanka Arya, Satyasundara Mahapatra, Anil Kumar Malviya

**Abstract:** *The segmentation and detection of brain pathologies in medical images is an indispensable step. This helps the radiologist to diagnose a variety of brain deformity and helps in the set up for a suitable treatment. Magnetic Resonance Imaging (MRI) plays a significant character in the research area of neuroscience. The proposed work is a study and probing of different classification techniques used for automated detection and segmentation of brain tumor from MRI in the field of machine learning. This paper try to present the feature extraction from raw MRI and fed the same to four classifier named as, Support Vector Machine (SVM), Decision Tree (DT), k-Nearest Neighbors (KNN), and Artificial Neural Network (ANN). This mechanism was done in various stages for Computer Aided Detection System. In the preliminary stage the pre-processing and post-processing of MR image enhancement is done. This was done as the processed image is more likely suitable for the analysis. Then the k-means clustering is used to sectioning the MRI by applied mean gray level method. In the subsequent stage, statistical feature analysis were done, the features were computed using Haralick's equation for feature based on the Gray Level Co-occurrence Matrix. Feature chosen dependent on tumor region, location, periphery, and color from the sectioned image is then classified by applying the classification techniques. In the third stage SVM, DT, ANN, and KNN classifiers were used for diagnoses. The performances of the classifiers are tested and evaluated successfully.*

**Keywords:** *Artificial Neural Network, Decision Tree, k-Nearest Neighbors, Machine Learning, Magnetic Resonance Image, Support Vector Machine.*

## I. INTRODUCTION

Detection and Segmentation of tumor in the present scenario of medical science is a tedious and challenging job for doctors. Magnetic Resonance Imaging (MRI) along with computed thermograph is the most important resources that are used frequently by the radiologist for inspection of internal human body parts without any dissection. Whereas, the manual inspection methodology is highly time taking as

well as wastage precious work hours. It is very difficult to study the human brain, identifying its different part is a big task in its simplest state as its structure is very complex [1]-[5]. Again to study on infected brain (i.e. brain with tumor), compared with the original shape of the brain and identified the reality of tumor itself is a big task for the radiologist. With the advent of cutting edge technology the researchers are trying to analyze the different functions of brain and how the irregularity affects the human biomechanics. So that presence of tumor inside the brain is perfectly identified in less time. In general tumors are classified into two form named as benign and malignant [6]-[8],[19]. Whatever may be the form, but it is still a major complexity for medical science to dissect. Researchers are trying to implement machine learning techniques in order to reduce the tediousness of inspection work related in segmentation of brain tumor from MRI. Still there is no conclusive evidence to prove which classification technique is best suited for the former mentioned purpose. Also it is yet to be determined that if a single technique can be applied to all parts of the brain with same effectiveness or not.

Computed thermographs and magnetic resonance images are the go to method for medical fraternity for detection of tumor. These methods are quite reliable but they have their own limitations [9]-[10]. The images processed through these methods are various stages of gray varying from region to region of the brain. So when the abnormal tissue does not have very distinct feature it is quite difficult to detect the abnormality. Not only are the scans done in various layers but also if the size of abnormality is relatively small it again becomes very tedious task to detect the presence of tumor. In addition to this a single MRI can consist up to 20 image set that taken from different direction. According data provided by clinical oncology society of America, more than 17,500 people will die to brain tumor or nervous system cancer in America only [11]. The rest of the world data reaches to half a million people. This says that huge amount of information are needed to be analyzed for wellbeing of these human being. So on the way of getting proper prognosis still there is lack of exact boundary in the process of scanning brain image and store its information. The concepts of machine learning play a vital role and are the demand of the day. A numerous method of classification is already developed [1]-[5], [12]-[31]. The requirement is to be checked these methods on various parameters such as accuracy, sensitivity, processing speed, real time application ready or not, and many more things [15], [20], [21], [23], [24] with the help of huge amount of brain MRI dataset. Another requirement is finding an optimal or quick solution by using the available clustering and classification techniques in different size of image taken from different angle is a challenging task.

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This paper deals with the testing of different classification techniques used on huge amount of brain MRI dataset and evaluate their performance on Statistical Texture and Morphological features. The rest of the paper is organized as follows. Section 2 discussed on previous work made toward this path and presented with their respective findings.

The different materials and methods that are used in this paper is discussed in Section 3. The performance of different classification function in the form of discussion is presented in Section 4. Section 5 conclude the paper and provide the scope on future related work.

## II. RELATED WORK

Machine learning is one of the most prominent area of research in the field of emerging medical science. Menze et al. [12] point in his paper that during the last two decades research devoted to segmentation has grown manifold which is enough to show the importance of the work. Mathematical Methods such as nearest neighbor, neural networks and support vector mechanism are go to method in order to apply machine to recognize patterns and hence make the correct decisions for the recognition of tumors from MR images. Also it was found that human ratings varied in segmentation of various tumor sub region with dice coefficient varying from 0.74 to 0.85. Also it pointed no one single algorithm gave best results for different sub regions simultaneously. Benson C.C et al. [13] proposed method to enhance MR images based on morphological features and skull stripping specially for T1, T2 and FLAIR axial images. It claims to help in better diagnosis of tumor region in MRI's. J.Jaya et al. [14] proposed method for enhancing MRI by applying median filter, weighted median filter and adaptive filter. N. B Bahadure et al. [15] used Berkeley wavelet transform (BWT) based segmentation and support vector mechanism based classifier to improve accuracy for analysis of MRI and succeeded in achieving 96.51% accuracy, 97.72% sensitivity, and 94.2% specificity. P. Kumar et al. [16] used four stage method for segmentation and classification in which principal component analysis (PCA) was utilized to reduce dimensionality and afterward SVM classifier was applied for segmentation and managed to achieve accuracy level of 94%. Similar method was also applied by Y. Zhang et al. [17] as he used kernel SVM and for enhancement K-fold stratified cross validation was applied. GUOLI SONG et al. [18] also did similar work but in addition applied GLCM for hybrid feature extraction and was able to attain 98.36% accuracy. Marco Alfonse et al. [19] also used SVM in addition with fast fourier transform (FFT) for automatic classification of MRI in malignant and benign categories and achieved very high accuracy rate of 98.9%. Ayse Demiharan et al. [20] introduced segmentation method to classify MRI in tumor, white matter (WM), edema, cerebrospinal fluid (CSF) and gray matter (GM) by using learning vector quantization (LVQ) and stationary wavelet transform. Average Dice similarity were found to be in order of 0.91 for white matter, 0.96 for cerebrospinal fluid, 0.61 for tumor, 0.87 for gray matter and 0.77 for edema. Selvaraj Damodharan et al. [21] also classified MR images in same category as Ayse Demiharan et al. [20] but used a different methodology. They applied Neural Network concept for the classification and obtained dice range as 0.61 to 0.74 for CSF, 0.94 to 0.995 for WM, 0.90 to 0.992 for GM, 0.97 to 0.99 for tumor region. Ayal Raj Deepa et al. [22] also applied ANN to classify for

similar categorization and was able to attain accuracy of 93.47%. Mohammad Havaei et al. [23] proposed novel method for automatic tumor segmentation using Deep Neural Network (DNNs) for specialized detection of glioblastomas. It uses a final layer which implements a fully connected layer that allows 40 fold up speed. It leads to very fast segmentation which is an order of 25 second to 3 minutes for entire brain. Antonios Makropoulos et al. [24] proposed method for precise intensity based segmentation for developing child brains from early preterm period to term equivalent age, into 50 brain regions. Average dice index varied from 0.7 to 0.9 for different parameters. Bharath Hariharan et al. [25] proposed convolutional neural networks to classify category-independent region proposals (R-CNN) specially designed for Simultaneous Detection and Segmentation (SDS). Darko Zikic et al. [26] use multi-channel intensity information from a small patch around each point for labeling. CNN is applied in a sliding-window fashion in the 3D space, for each point inside the brain masks. Accuracy is in range of 83.7% with a deviation of 9.4 on either side. Mariam Saii et al. [27] used anisotropic diffusion filter at preprocessing and then SVM for segmentation and was able to achieve accuracy rate up to 95.5% depending upon dice coefficient. Daniele Ravi et al. [28] used novel dimensionality reduction method via T-distributed stochastic neighbor method and then semantic Texton Forest for categorization of tissue. Chao Ma et al. [29] used combination of random forest and active contour modeling for segmentation of tumor and was able to achieve accuracy of 0.9. V. Anitha et al. [30] used K mean algorithm with DWTBW to reduce computational time for segmentation. Bharanidharan N et al. [31] used GLCM with k-NN classifier to achieved 85% efficiency.

## III. MATERIALS AND METHODS

This section comprises of data, the source from where the dataset of brain MRI is taken, and the algorithm being used for performing brain MRI tissue segmentation and classification. Fig.1 demonstrates the stream outline of the proposed algorithm. The datasets of T1 weighted contrast enhancement magnetic resonance image was obtained from [32] and is publically available. The following sections of materials and methods are responsible for the proposed evaluation procedure of brain MRI.

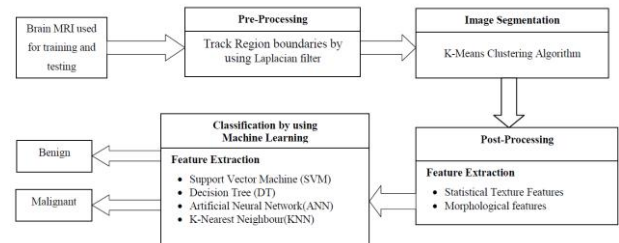


Fig. 1: Methodology of the proposed algorithm

### A. Pre-processing

The central goal of pre-processing is to improve MR image quality and make it further suited in the form for processing by machine system or by human. A process like reduction and removal of noise from the image, enhancement of appearance or image, tracking the region or boundaries are done.

- **Track Region Boundaries:** In this work Laplacian filter is used as sharpening filter which is one of the Spatial Sharpening Filters having second order derivative to enhance fine details of the MRI (including noise) much more than the first order derivative [33].
- Digital implementation of Laplacian (two dimensional) in equation 1 is acquired through including these two segments:

$$\nabla^2 f(x, y) = [f(x + 1, y) + f(x - 1, y) + f(x, y + 1) + f(x, y - 1)] - 4f(x, y) \quad (1)$$

This filter sharpened the image including the noise, which requires smoothing filter to reduce and remove this noise. So Averaging filter is used, which simply average the number of pixels contained in neighbor of the filter mask. In general, average filtering of an image  $f(x, y)$ , size  $M \times N$  having weighted average filter of size  $m \times n$  is given in the equation 2.

$$g(x, y) = \frac{\sum_{s=-a}^a \sum_{t=-b}^b w(s, t) f(x+s, y+t)}{\sum_{s=-a}^a \sum_{t=-b}^b w(s, t)} \quad (2)$$

Where,  $a=(m-1)/2$  and  $b=(n-1)/2$ . So as to produce a total filtered image  $g(x, y)$  this equation value of  $x$  and  $y$  is applied to  $x=0, 1, 2, \dots, M-1$  and  $y=0, 1, 2, \dots, N-1$ .

### B. Image Segmentation

Brain MRI segmentation is a perplexing issue in the discipline of medical imaging. There are different methods, for example, threshold based, neural network rooted, cluster-based, and edge-based [34]. There is various kind of clustering: Fuzzy C-means clustering method, subtractive clustering method, mountain clustering method, and K-means clustering method. In this work, k-means clustering is used for segmentation of images. Segmentation using k-means is the most proper for the present framework so as to accomplish a binarized picture with gray level. The input MRI of six numbers is given below in Fig.2.

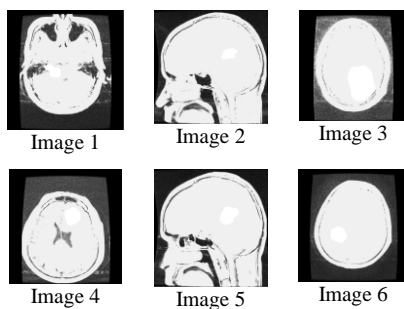


Fig.2: Input Brain MRI Image

K-Means Clustering is a mechanism where data is divided in  $k$  number group and identifies a given arrangement of data/information into  $k$  number of disjoint group or cluster. There are two phases of k-means, the principal stage assesses the  $k$  centroid and the subsequent step, takes each point to the gathering which has the immediate centroid from the corresponding information point. Distance is determined by the Euclidean distance. Recalculation of the new centroid of each bunch depends on the gathering of the centroid. Another Euclidean partition is determined among each inside and each datum point, and allocates the focuses in the bundle having a most extreme Euclidean separation. K-means is an iterative figuring which restricts the aggregate of the separation from every item to its bunch centroid over every one of the groups.

Now, let us have a picture having a resolution of  $(x \times y)$ ,

and the image to be bunch into  $k$  number of group. Let  $p(x, y)$  be a data pixel to be bundle and  $c_k$  is the gathering centers. K-means computation is as per the following:

1. At first, initialization the quantity cluster  $k$  and centre is carried.
2. For every pixel, ascertain the Euclidean span  $d$ , between the centre and each pixel by the equation:  
 $d = \|p(x, y) - c_k\| \quad (3)$
3. Now, assigning every pixel to the proximity centre dependent on distance  $d$ .
4. Recalculate new location of the centre using the equation :  
 $c_k = \frac{1}{k} \sum_{y \in c_k} \sum_{x \in c_k} p(x, y) \quad (4)$
5. Rehash the procedure until the procedure fulfils the tolerance limit or error value.
6. Lastly, reshape the group pixels into an image.

The corresponding segmented image of the input MRI are generated and presented in the Fig. 3 below.

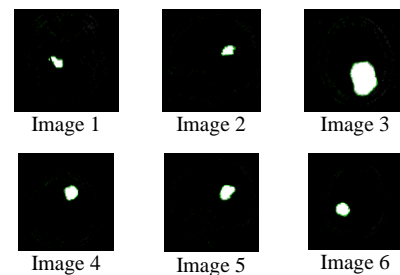


Fig.3: Generated segmented images of corresponding input Brain MRI images provided in Fig. 2

Although the k-means clustering has a huge advantage of being simple to implement, it has the accompanying downsides. The idea of the last bundling depends upon the optional assurance of introductory centroid. So if the basic centroid is haphazardly picked, the outcome varies for various introductory focuses. So as to get the ideal segmentation, the initial center should be carefully chosen. Another is the computation complexity which depends on the quantity of data elements, quantity of iterations and number of clusters.

### C. Post-processing

This stage deals with the two feature extraction methods implemented on the generated segmented image. They are Statistical Texture Feature extraction and Morphological Feature extraction.

- **Statistical Texture Feature extraction:** Statistical feature extraction is the framework where various attributes of image segments are measured. It is the technique of gathering a large amount of information about an image like contrast, color, shape, and texture. It also represents a crude image in its decreased structure to encourage basic leadership like example arrangement. Surface examination truth be told, is a significant parameter for an AI framework and for human visual discernment as it is used to improve the precision of the discovering system. Because of the perplexing structure of tissue like GM (gray matter), CSF, and WM (white matter) present in MRI of Brain, relevant feature extraction is inevitable.

In here, Gray Level Co-occurrence Matrix (GLCM) is applied for feature extraction that breaks down the provided image into texture attributes (Haralick's features) [35].

- Haralick et al. [36] introduced a standout amongst the most generally utilized picture analyzer uses GLCM also, texture feature. This framework seeks after two phases for feature extraction from the restorative image. In introductory advance, the GLCM is registered, and in the other advance, the surface highlights dependent on the GLCM are determined. Textural disclosures and assessment could refine the examination, different periods of the tumor (masterminding), and treatment feedback assessment. The measurements highlight equation for a part of the supportive attributes is recorded underneath.

$$M = \left(\frac{1}{m \times n}\right) \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} f(x, y) \quad (5)$$

$$E = - \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} f(x, y) \log_2 f(x, y) \quad (6)$$

$$K_{urt}(X) = \left(\frac{1}{m \times n}\right) \frac{\sum(f(x, y) - M)^4}{SD^4} \quad (7)$$

$$SD(\sigma) = \sqrt{\left(\left(\frac{1}{m \times n}\right) \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} (f(x, y) - M)^2\right)} \quad (8)$$

$$S_k(X) = \left(\frac{1}{m \times n}\right) \frac{\sum(f(x, y) - M)^3}{SD^3} \quad (9)$$

$$E_n = \sqrt{\left(\sum_{x=0}^{m-1} \sum_{y=0}^{n-1} f^2(x, y)\right)} \quad (10)$$

$$IDM = \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} \frac{1}{1+(x-y)^2} f(x, y) \quad (11)$$

$$C_{orr} = \frac{\sum_{x=0}^{m-1} \sum_{y=0}^{n-1} (x, y) f(x, y) - M_x M_y}{\sigma_x \sigma_y} \quad (12)$$

$$Var = \frac{\sum_x \sum_y (f(x, y) - Mean)^2}{n} \quad (13)$$

$$C_{homogeneity} = \sum_x \sum_y \frac{x(x, y)}{1+|x+y|} \quad (14)$$

$$C_{on} = \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} (x - y)^2 f(x, y) \quad (15)$$

Where, Equation 5 represent for Mean (M) where the normal power estimation of a picture, determined by including all the pixel estimations of an image and a short span of time, later the acquired amounts is isolated by the overall number of pixels in an image. Equation 6 used to calculate the Entropy (E), where the extent of information content and randomness of the intensity distribution. On the off chance that the sections of the framework have a similar greatness the entropy will be high. Equation 7 is used to calculate the feature Kurtosis ( $S_k$ ), where Kurtosis is the probability spread of an arbitrary variable. For an arbitrary variable X, the kurtosis is defined as  $K_{urt}(X)$ . Equation 8 is used to calculate the Standard Deviation (SD) features where the moment describing the probability spread of a studied population which serves as a level of in-homogeneity. A higher value shows a higher contrast of edges and better intensity level. Equation 9 evaluates the Skewness ( $S_k$ ) features, which is nothing but an asymmetry measure in the histogram. The skewness of an arbitrary variable (X) is signified by  $S_k(X)$ . Equation 10 used to calculate the Energy ( $E_n$ ), which measures the thickness of texture. It measures the similarity between the images and is said to be a moment of an angular second, and is characterized by the features of Haralicks GLCM. Equations 11 calculate the Inverse Difference Moment (IDM) or Local Homogeneity, where in the image, IDM rates the extent of local homogeneity. Inhomogeneous images have low IDM values while homogeneous images have high IDM values. The values may have a range or may

be single in order to distinguish non-textural or textural image. Equation 12 calculates the Correlation ( $C_{orr}$ ) feature particularly used to measure the intensity of an image is a domain correlation. On the off chance that the image comprises of linear structure the estimation of correlation will be high. Here  $M_x$  and  $\sigma_x$  are mean (arithmetic) and standard deviation in the vertical spatial area. Equation 13 calculates the measure of intensities of dispersion degree in an image as variance. Equation 14 is used in order to calculate homogeneity high values and low values of  $X(x, y)$  in the co-occurrence matrix are combined, thus resulting in a spread of  $X(x, y)$  values in the matrix. Equation 15 is used to calculate the Contrast ( $C_{on}$ ) to evaluate the Image clarity, as well as the distributions of gray levels are measured in contrast.

▪ **Morphological Feature extraction:** After image segmentation is done to binary image, still there is a need of enhancement of tumor region, since segmentation of brain tumors in MRI is troublesome enough due to locations, different shapes of tumor, and intensity of image [37]. The purpose to apply morphological operators is for closing, opening, dilation and erosion that expel the small holes and hurdle from the image. In proposed work, erosion and dilation is used [33]. Dilation adds pixels to limits of item in an image and erosion expels pixels. This addition and removal relies upon the size and state of the organizing component used to process the image, applied by matlab function *imerode* and *imdilate* for erosion and dilation shown by the expression given below:

$$f_e(x, y) = \text{imerode}(f(x, y), E) \quad (16)$$

$$f_e(x, y) = \text{imdilate}(f(x, y), E) \quad (17)$$

Where,  $f(x, y)$  is binary image,  $f_e(x, y)$  is returning the dilated image. The contention E is an organizing component. In this paper seven morphological features were also extracted from the segmented tumor, which is listed below:

$$A_{minor} = p + q \quad (18)$$

$$A_{major} = \sqrt{(p + q)^2 - f^2} \quad (19)$$

$$A_{total} = |X| \quad (20)$$

$$Peri = 4a \int_0^{\frac{\pi}{2}} \sqrt{1 - E^2 \cos^2 \theta} d\theta \quad (21)$$

$$D = \sqrt{\frac{4 * A}{\pi}} \quad (22)$$

$$E = \sqrt{1 - \frac{B^2}{A^2}} \quad (23)$$

$$R = \sqrt{\frac{4 * A}{p^2}} \quad (24)$$

Where, Equation 18 calculate the Minor Axis Length feature which alludes to oval's minor hub length whose standardized second focal minutes have a similar incentive as that of the area thought-about. Where, 'p' and 'q' corresponds to distances of every focus from any point on ellipse. Equation 19 calculates the Major Axis Length feature. This alludes to oval's significant hub length whose standardized second focal minutes have a similar incentive as that of the area considered. Where, f corresponds to the separation between foci, 'p' and 'q' corresponds to distances of every focus from any point on ellipse. Equation 20 calculates the feature Area. This alludes to the number of element in the area through-about.



Where, 'X' indicates the area through-about and |X| is the cardinality of X.

Equation 21, named as Perimeter feature is alludes to the separation around the limit of the sectioned area through-about. Where, 'a' is major axis length, E is eccentricity of ellipse. The vital called elliptic necessary. Equation 22 named as Diameter (D) is used to calculate the worth is equivalent to the measurement of circle whereby the territory of the circle is same as that of the area thought-about. Where, 'A' shows area and 'D' indicates diameter. Equation 23 used to calculate the Eccentricity feature. This alludes to the flightiness of associate oval whose

second-minutes have a similar incentive as that of the area thought-about. The estimation of eccentricity is determined by separating the oval's foci distance to its major axis length. Where, 'A' is semi-major axis length and 'B' is semi-minor axis length. Equation 24 calculates the feature known as Circularity/Roundness. It quantifies how much the state of area is like that of a circle. Where, 'A' shows area and 'P' indicates perimeter/edge of the chosen area. Morphological features like compactness, slenderness, rectangularity are also calculated in this paper Table 1 and Table 2 shows the extracted Statistical texture features and the extracted morphological features of the 6 image out of 982 images.

**Table 1: Statistical Texture feature extraction through GLCM of Tumor**

Extracted feature	Input image					
	Image 1	Image 2	Image 3	Image 4	Image 5	Image 6
Mean	0.4868	0.5196	0.6720	0.6032	0.5795	0.6030
Entropy	0.9995	0.9989	0.9129	0.9690	0.9817	0.9692
Kurtosis	1.0028	1.0061	1.5368	1.1781	1.1039	1.1772
Standard Deviation	0.4999	0.4997	0.4695	0.4893	0.4937	0.4893
Skewness	0.0530	-0.0784	-0.7327	-0.4220	-0.3223	-0.4209
Energy	0.4555	0.4488	0.5304	0.4703	0.4689	0.4804
Inverse Difference Moment	138.5865	88.1866	319.5767	153.4883	133.7741	159.3366
Correlation	0.9065	0.8882	0.9236	0.8786	0.9006	0.9028
Variance	0.1909	0.1764	0.1293	0.1661	0.1575	0.1749
Homogeneity	0.9766	0.9721	0.9833	0.9712	0.9759	0.9769
Contrast	0.0468	0.0557	0.0334	0.0577	0.0482	0.0462

**Table 2: Morphological features/measure of Tumor**

Extracted feature	Input image					
	Image 1	Image 2	Image 3	Image 4	Image 5	Image 6
Area	2132	2229	15150	4003	4277	3859
Perimeter	318	421	1000	514	538	450
Compactness	0.0211	0.0126	0.0152	0.0152	0.0148	0.0191
Slenderness	0.8088	0.6849	0.8025	0.9367	0.9059	1
Diameter	57.9114	56.7684	141.5600	72.4259	76.4339	70.9757
Eccentricity	1.7842	1.5757	1.3487	1.0694	1.3920	1.1217
Circularity	0.7487	0.7966	0.8611	0.9670	0.8476	0.9442
Rectangularity	0.5701	0.6107	0.7194	0.6847	0.6535	0.6860

**D. Classification Methods used by Machine Learning**

Arrangement is the procedure in which given input is classified by training it with a classifier. The algorithms used for classification are k-Nearest Neighbor, Decision Tree, Support Vector Machine and Artificial Neural Network.

▪ **Support Vector Machine:** Support Vector Machine (linear model for categorization and regression problems), does classification by creating a line or a hyper plane separating the data into classes. Now algorithm finds the points close by to the line from both the classes. These points are known to be support vectors and the span is called the margin. SVM tries to make a decision boundary by separating the two classes as wide as possible. SVM is independent algorithm in respect to dimensionality and attribute space. It changes the input space to a higher measurement highlighted space, via a non-direct mapping function, and afterward develops an isolating hyper plane with most extreme separation from the nearest points of the training set. A set of mathematical function known as kernel functions are used by SVM algorithm. It is found that kernel function transforms non linear spaces into linear space. Several non linear kernels exists in SVM ranging from simple

polynomial basis function to sigmoid function which can perform its functionality by being selected and the software itself transforms the data, classify the data and retransforming the output back into the initial space.

➤ **Linear kernel (LK):** is the simplest kernel and is defined by the Eq. (25).

$$K(x_i, x_j) = (x_i x_j) \tag{25}$$

➤ **Multilayer Perceptron kernel (MLP):** also known as Hyperbolic Tangent kernel or Sigmoid kernel and is defined by the Eq. (26).

$$K(x_i, x_j) = \tanh(\gamma x_i x_j + r) \tag{26}$$

➤ **Gaussian Radial Basis Function (RBF):** It is a common purpose kernel used when no prior knowledge is provided about the data. It is defined by the Eq. (27).

$$K(X_i, X_j) = \exp(-\gamma \|X_i - X_j\|^2) \tag{27}$$

For  $\gamma > 0$  and sometimes parameterized using  $\gamma = \frac{1}{2\sigma^2}$  SVM is a supervised learning methodology based on the theory of statistical learning. On a given labeled dataset (training set),  $DS = \{x, y | x \rightarrow$

data sample,  $y \rightarrow$  class label}, SVM computes a mapping function  $f(x) = y$  for every dataset. The mapping function shows the relationship among dataset and their corresponding class labels, and thus used for classifying unknown data. In SVM classification is done through the following classification decision function shown below in Eq. (28), which is also a process known as feed-forward phase.

$$D(z) = \text{sign}(\sum_{i=1}^N \alpha_i \gamma_i K(z, s_i) + b) \quad (28)$$

Here,  $\alpha_i$  are coefficients of alpha,  $\gamma_i$  are class labels of support vectors,  $z$  is input vector,  $s_i$  is support vectors,  $K(z, s_i)$  is chosen kernel function,  $b$  is bias.

▪ **Decision Tree:** Activity of any calculation depends on choice of tree is straightforward, and depends on the system of separation and overcome. As a rule it depends on the progressive division of the issue in a few sub issues with fewer measurements, except if and until an answer for every one of the less difficult issues is discovered. In light of this, decision tree discover approaches to separate the universe by making hubs containing the individual tests until each tending to just a single class or till one of the type showing dominant majority without supporting up and coming divisions, creating a leaf comprising the class larger part. The characterization is done just to pursue the way, managed by the progressive test set along the tree till it found a leaf containing the class [38]-[40]. Though the working approach of all the classifiers relying on decision tree is same, there are many permutations for its construction.

Steps involved are:

- The best attribute  $\rightarrow$  I, of the dataset is set at the base of the tree i.e. the NODE.
- Assign I as the decision (test case) attribute of the NODE.
- For every value of I, new descendant NODE is created.
- Arrange the samples (training) to its appropriate leaf node.
- If samples are perfectly classified, end of steps else recapitulate over new leaf nodes.

Assumptions while creating Decision Tree.

- Firstly, the entire preparing set is considered as the root.
- Feature esteems are wanted to be absolute. If quantities are incessant, at that point they are discretized before the structuring of the model. Distribution of records is done recursively in accordance to attribute values.
- Order of placing attributes as a root hub of the tree is done by using a statistical approach.

▪ **Artificial Neural Network:** In Artificial Neural Network, input of a specific hub is the weighted sum of output of all the hubs connected to it. The output value is a non linear function known as activation function. The weight is the multiplicative weighing factor between input and output node. ANN is adaptive non-linear, that is parameter are changed during training phase and after training parameters are fixed for solving the problem. The following work used Feed-Forward, Cascaded Feed-Forward, and Pattern Recognition Neural Network.

➤ **Feed-Forward Neural Network-** The data passes from the input hubs and is released on the output hubs. It may not possess or may have hidden layers. It has a front

engendered wave and no back-propagation by utilizing a grouping enactment work usually.

➤ **Cascaded Feed-Forward Neural Network-** Cascade-forward systems are like feed-forward systems, however it incorporates an association from the information and each past layer to the comparing layer. Rather than modifying the loads in a system having fixed topology [41]. Cascaded-Correlation starts with a negligible system, at that point consequently prepares and includes new shrouded units consistently, making a multi-layer structure. When another shrouded unit is added to the system, its information estimate loads are solidified. This unit at that point turns into a perpetual component finder in the system, accessible for creating yields, progressively complex element indicators. Favorable instances of Cascade-Correlation design is that it adapts rapidly, holds the structure it has manufactured regardless of whether the preparation set changes and requires no back proliferation decides its own size and topology.

➤ **Pattern Recognition Neural Network-** Pattern acknowledgment systems are feed-forward systems that groups contributions as indicated by target classes. The objective information for pattern acknowledgment systems should comprise of vectors, of every one of all zero values with exception for a 1 in element  $i$ , where  $i$  is the class to be represented. Pattern coordinating can recognize the class of info flag or examples. Pattern coordinating ANN is prepared utilizing directed learning procedures. If the input symbol does not match the accepted pattern, the system raises a warning flag which indicates a potential problem.

Training the network: For training the network train ratio is 70/100, validate ratio is 15/100, and test ratio is 15/100. The learning process demands an error function  $E$  that finds out the performance, that is non similar between the computed output of the perceptron  $o$  and the true value for an input  $\vec{x}$  over a set of multiple input-output pairs  $(\vec{x}, y)$ . This error function is the mean squared error (MSE), which is described by a set of  $N$  input-output pairs. The Eq. (29) listed below shows MSE.

$$X = \{(\vec{x}_1, y_1), \dots, (\vec{x}_N, y_N)\} \text{ as}$$

$$E(X) = \frac{1}{2N} \sum_{i=1}^N (o_i - y_i)^2 = \frac{1}{2N} \sum_{i=1}^N (g(\vec{w} \cdot \vec{x}_i + b - y_i))^2 \quad (29)$$

Where  $o_i$  denotes the output of the perceptron on input  $\vec{x}_i$  having activation function  $g$ . The factor of  $\frac{1}{2}$  is included in order to calculate the derivative later. Thus  $E(X) = 0$  when  $o_i = y_i$  for every and each input-output pairs  $(\vec{x}_i, y_i)$  in  $X$ , so prominent objective is to attempt to change  $\vec{w}$  and  $b$  such that  $E(X)$  is as nearer to zero as possible. Thus, minimizing  $E(X)$  with  $\vec{w}$  and  $b$  to yield a better classification limit.

▪ **k-Nearest Neighbor (KNN):** k-Nearest Neighbor algorithm is a type of classifier or regressor which stores all available data and classifies new occurrences based on similar features. Whenever any prediction is done for a concealed information case, the KNN classification will look through the entire preparing dataset for the k-most comparable occurrences. The output prediction of the most comparable occurrences is summarized and then reverted as the prediction for the new instance. Similarity measure of data relies upon class of information itself.



If the information is real-valued, the Euclidean span can be used and for other variant of data like binary or categorical, Hamming span can be used. For the instance of relapse issues, the normal of the anticipated characteristic might be returned. On account of order, KNN returns the most prevalent class.

KNN: Step by Step.

- Handles the data- Complete dataset splits into test and train dataset.
- Similarity- Distance between two data instance is calculated. Once the distance is calculated, pinning of neighbors is done.
- Neighbors- After that locating the K most similar data instances from a new point is done.
- Response- A response is generated from a set of data instance. This decides to class to which the dataset belong.
- Accuracy- Finally accuracy is obtained.

**E. K-fold stratified cross validation**

Since the classifier is set up by a provided dataset, thus it would achieve high order exactness only for this readiness dataset, not yet different self-sufficient datasets. To maintain a strategic distance from this over fitting, Incorporation of cross validation has been made. Cross validation won't increment to the ultimate classification accuracy, anyway it will build the classifier more reliable and might be summarized to alternative free datasets.



**Fig.4: A 5-fold Cross validation**

Cross validation/approval strategies comprise of three kinds: K-fold cross validation, Random sub-sampling, and leave-one-out validation. The K-fold cross validation is connected because it has characteristics as straightforward, basic, and utilizing all information for preparing and approval. The whole dataset is divided into K-fold segment, rehash K times to utilize K-1 folds for preparing and staying for approval, and then average the error rates of K experiments. The setting of approval images and training images is appeared in the systematic chart of 5-fold cross validation in above shown Fig. 4.

In this way, stratified K-fold cross validation was used, wherever every overlay has practically comparable class disseminations [42]. Another check is to choose the amount of folds. If K is set excessively enormous, the inclination of the authentic error rate estimator will be close to nothing, however the variance of the estimator will be enormous and the computation will be time taking. One the other hand, if K is set close to nothing, the figuring time will diminish, the difference of the estimator will be small, yet the base of the estimator will be huge [43]. During this research, observationally K is chosen as 5 through the experimental technique. At last selection of the optimal K value relating to the most prominent classification accuracy is carried out.

**IV. RESULT AND DISCUSSION**

The algorithm method was successfully applied in MATLAB in combination with image processing. MATLAB is a high level language having an interactive environment for programming, numerical computing and representation. Here data can be analyzed, algorithm can be developed, models and application can be built. The built-in math function, tools, and language empower us to investigate different methodologies and arrive at an answer quicker in comparison to spreadsheets or programming languages like C, C++ and Java. MATLAB's two and three dimensional diagrams are entity-oriented. The operator can generate personal modified tasks and packages (well-known as M-files) in MATLAB program. MATLAB is quicker than another outdated encoding. It is simple to adjust the tasks meanwhile maximum of the M-files can be unlocked and changed. For safeguarding high presentation, the MATLAB software has been printed in enhanced C and is implicit in assembly language. Environmental setup is recorded below in Table 3.

**Table 3: Environmental Setup**

HARDWARE AND SOFTWARE SPECIFICATION	CONFIGURATION
Processor	Intel(R) Core(TM) i3-3217U CPU @ 1.80GHz
Operating System	Windows 8
Random Access Memory	4.00 GB
System Type	64-bit Operating System
Developing Environment	MATLAB

**A. Data Set**

The datasets of T1 weighted contrast enhancement magnetic resonance image was obtained from [32] and is available publically. Total number of slices used for the experimental analysis is 982. The proposed strategy is completely founded on 2D slices. Every data set is 512x512 pixels. Downloaded slices are in Matlab data format (.mat file) which was converted to joint photographic expert group format (.jpg file) before using it through MATLAB environment.

**B. Performance measure**

The The KNN algorithm's effectiveness can be assessed in wording of accuracy, specificity, and sensitivity. The confusion matrix characterizes the terms TP, FP, TN, and FN from the expected outcome and ground truth result for the estimation of accuracy, specificity, and sensitivity are appeared in Table 4.

**Table 4: Confusion matrix**

Expected outcome	Ground truth		Row total
	Positive	Negative	
Positive	TP	FP	TP+FP
Negative	FN	TN	FN+TN
Column total	TP+FN	FP+TN	TP+FP+FN+TN



# Segmentation and Detection of Brain Tumor by using Machine Learning

Where TP is the quantity of true positive, which is utilized to show the complete number of unusual cases accurately characterized. TN is the quantity of true negative, which is utilized to show normal cases accurately classified.

FP is the quantity of false positive, and it is utilized to demonstrate wrongly recognized or characterized abnormal instances. When they are really typical cases and FN is the quantity of false negatives, it is utilized to show wrongly ordered or distinguished normal instances, when they are really abnormal cases [44]. These result parameters are determined using the absolute number of tests analyzed for the recognition of tumor.

The confusion matrix is one of the straightforward metrics used for detecting the exactness and accuracy of the model. It is used for classification problem where machine predict, the chance of the image, benign or a malignant image. The confusion matrix by itself is never a performance criterion, regardless almost all of the performance metrics are rooted on confusion matrix, and the value inside the matrix [45], [46]. Table 5 demonstrates the recipes to figure accuracy, specificity, and sensitivity.

Table 5: Accuracy, specificity, and sensitivity calculation.

Quality parameter	Formula
Accuracy	$\frac{TP + TN}{TP + TN + FP + FN}$
Specificity	$\frac{TN}{TN + FP}$
Sensitivity	$\frac{TP}{TP + FN}$

The outcomes acquired from various classifiers with 5 fold cross validation utilizing proposed feature list are appeared in Table 6. The proposed algorithm is compared with three different classifiers having same number of datasets and same MRI mentioned below:

- Support Vector Machine (SVM) with kernel function.
  - Linear
  - Multilayer Perceptron (MLP)
  - Gaussian Radial Basis Function (RBF)
- Decision Tree (DT).
- Artificial Neural Network (ANN).
  - Feed-Forward
  - Cascaded Feed-Forward
  - Pattern Recognition

As delivered from results, KNN classifier obtained the highest accuracy of 97.8%. Likewise an accuracy of 94.4% is achieved from ANN (Feed-Forward), 94.2% from SVM (RBF) kernel, 93.2% from SVM (Linear and MLP) kernel, 87.1% from ANN (Pattern Recognition), 84.8% from ANN (Cascaded Feed-Forward), and 50.3% from DT. This obviously demonstrates KNN performs far better when put next with totally different classifiers for the projected list of capabilities.

Sensitivity gives part of positives that are accurately recognized and specificity gives part of negatives that are accurately identified. All the performance of above mentioned different classifiers are recorded below in Table 6.

Table 6: Performance Metrics for various classifiers using 5-fold cross-validation

CLASSIFIER	CALCULATED PARAMETERS		
	ACCURAC Y (%)	SENSITIVIT Y (%)	SPECIFICIT Y (%)
1 SVM (linear)	93.2	100	95.5
SVM (MLP)	93.2	100	93.5
SVM (RBF)	94.2	99.2	94.8
2 DT	50.3	0	100
3 ANN (Feed-Forward )	94.4	93.9	94.9
ANN (Cascaded Feed-Forward)	84.8	92.5	88.7
ANN (Pattern Recognition)	87.1	92.3	89.7
4 KNN	97.8	62.7	100

The suggested algorithm executes segmentation, feature extraction, and classification of images as is similar to human vision observation, which perceives various objects, various textures, profundity of the image. The performance of the classification techniques by using machine learning is shown in Fig. 5.

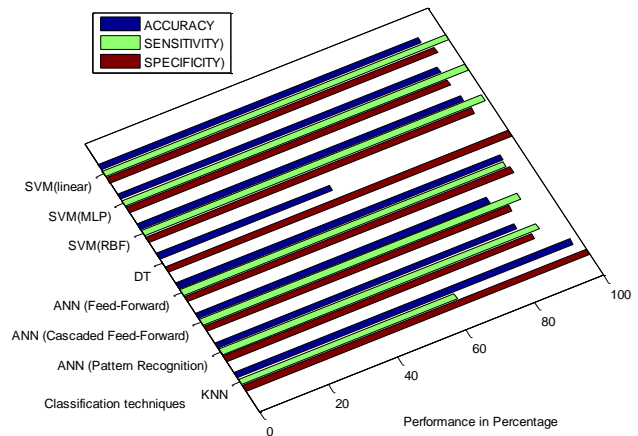


Fig.5: Performance of Classification techniques by using machine learning

## V. CONCLUSION AND FUTURE WORK

The proposed algorithm efficiently classifies the MRI brain tumor. The data collected has been successfully prepared by pre-processing and post-processing operation to make it suitable to detect the tumor. During this assessment, we explore texture based and morphological based features with a generally perceived classifier for the characterization of brain tumor from MRI of brain. From the test results performed on the different MRI, unmistakably the examination for the brain tumor location is rapid and accurate when compared with the manual inquisition executed by radiologists or clinical specialists. The different performance factors additionally show that the proposed algorithm gives better outcome by improving specific parameters, for instance mean, exactness, accuracy, specificity, sensitivity. Consequently, the proposed approach for brain tumor recognition from MRI is significant.



The experimental results accomplished 97.8% accuracy exhibiting the viability of the proposed algorithm for distinguishing benign and malignant tumor from MRI. The obtained outcomes leads to the end that the proposed algorithm is proper for organizing clinical decision choice steady frameworks for basic screening and end by the radiologists or clinical authorities.

Later on, to enhance the accuracy of the order of the current work, we are waiting to research the specific plan of the classification by joining multiple classifier and highlight choice procedures.

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