Classification of Brain Tumor in Magnetic Resonance Images using Hybrid Kernel based Support Vector Machine

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ABSTRACT: *Medical image segmentation is a knotty and challenging task. Predominantly, the brain has a complicated structure and its exact segmentation is very essential for identifying the tumors, edema, and necrotic tissues in order to provide proper treatment. In this paper, we have proposed a novel brain tumor classification of MR images using texture features and hybrid kernel based SVM. Our proposed approach comprises the following major steps: i) preprocessing ii) Tumor Region Location iii) Feature Extraction and iv) Final Classification. In preprocessing steps, Anisotropic filtering will be applied to diminish the noise and improved quality of the image for further processing. In the next steps to perform the skull stripping and tumor regions are identified using regionprops algorithm. In feature extraction some specific feature will be extracted using texture using GLCM (Gray Level Co-occurrence Matrix). In the classification stage, the hybrid kernel will be designed and apply to training of support vector machine (SVM) to perform automatic detection of tumor in MRI images. For comparative analysis, our proposed approach is compared with the existing works. The accuracy level (93%) for our proposed approach is proved is good at detecting the tumors in the brain MRI images.*

Keywords: Tumor, Segmentation, Kernel, MRI , SVM, Classification, GLCM, Feature Extraction

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1. Introduction

Magnetic resonance (MR) segmentation used for brain tissues extraction white matter (WM), gray matter (GM) and cerebro-spinal fluids (CSF). These tissues help with many medical image segmentation applications such as radiotherapy planning, clinical diagnosis, treatment planning and Alzheimer disease [1]. Magnetic resonance (MR) imaging suggest more perfect information for medical examination than that of other medical images such as ultrasonic, CT images and X-ray. Especially secondary tumors might be composed of an enormous variety of tissue types depending on the primary tumor site. Its application to several datasets with different tumor sizes, intensities and locations shows that it can automatically detect

and segment very different types of brain tumors with a good quality Sudipta Roy et al., [2]. The quantitative analysis of MRI brain tumor allows obtaining useful key indicators of disease progression.

For the segmentation and identification of pathological tissues (Tumor and Edema), normal tissues (White Matter and Gray Matter) and fluid (Cerebro-spinal Fluid) from Fluid Attenuated Inversion Recovery (FLAIR) magnetic resonance (MR) images of the brain using composite feature vectors comprising of wavelet and statistical parameters, the intracranial brain image has been segmented into five segments using k-mean algorithm, which is based on the combined features of the wavelet energy function and statistical parameters that reflect texture properties. In addition to the tumor, edema has also been characterized as a separate class, which is important for therapy planning, surgery, diagnosis and treatment of tumors [3].

In segmentation stage the structural analysis on both tumorous and normal tissues has been performed. The local textures in the images could disclose the normal 'regularities' of biological structures. Therefore, the textural features have been extracted using co-occurrence matrix approach. The analysis of level of correlation has permitted to reduce the number of features to the only significant component. The classification has been performed by employing an artificial neural network and fuzzy c-means. They have designed in order to examine the differences of texture features between macroscopic lesion white matter (LWM) and normal appearing white matter (NAWM) in magnetic resonance images (MRI) from patients with tumor and normal white matter (NWM) [4]. After segmenting the brain the suspicious areas have been selected with respect to the approximate brain symmetry plane and fuzzy classification for tumor detection [5].

In order to improve robustness of automated image segmentation, especially in the field of brain tissue segmentation from 3D MRI towards classical image deteriorating including the noise and bias field artifacts that arise in the MRI acquisition process, Caldairou et al., propose to integrate into the FCM segmentation methodology concepts inspired by the Non-Local (NL) framework [6]. The key algorithmic contributions of this article were the definition of an NL data term and an NL regularization term to efficiently handle intensity inhomogeneity and noise in the data. The resulting energy formulation was then built into an NL/FCM brain tissue segmentation algorithm. Experiments were performed on both the synthetic and real MRI data, leading to the classification of brain tissues into gray-matter, white matter and cerebro-spinal fluid and also indicated significant improvement in performance in the case of higher noise levels, when compared to a range of standard algorithms.

The performances of Seed-Based Region Growing (SBRG), Adaptive Network-Based Fuzzy Inference System (ANFIS), and Fuzzy c-Means (FCM) in brain abnormalities segmentation have been compared by Shafaf Ibrahim et al. [7]. Here, controlled experimental data has been utilized, which designed in such a way that prior information about the size of the abnormalities was known. This was done by cutting several sizes of abnormalities and sticking it onto the normal brain tissues. The normal tissues or the background has been divided into three different categories. The segmentation has been performed with 57 data of each category. Then, the knowledge of the size of the abnormalities by the number of pixels has been compared with the segmentation outcomes of three proposed methods. Finally, it has been found that the segmentation performance of ANFIS was excellent in light abnormalities, while the SBRG has performed well in dark abnormalities segmentation.

Dr. H. B. Kekre et al. [8] have proposed a vector quantization segmentation technique to identify a cancerous mass from MRI images. In order to improve the radiologists' diagnostic performance, computer-aided diagnosis (CAD) scheme has been introduced to enhance the recognition of primary signatures of this disease: masses and microcalcifications. As well, to tackle the class distinguishability as well as feature space sparseness and solution space intricacy problems in multivariate image segmentation, a Markov random field (MRF) based multivariate segmentation algorithm called "multivariate iterative region growing using semantics" (MIRGS) has been proposed by A. K. Qin, and David A. Clause [9]. In MIRGS, the impact of intra-class variation and computational cost has been minimized by means of the MRF spatial context model integrated with adaptive edge penalty and applied to regions. To restrain the initialization sensitivity, a region-level means (RKM) based initialization technique has been utilized, which always provides exact initial conditions at low computational cost. Experiments have demonstrated the pre-eminence of RKM relative to two frequently used initialization techniques.

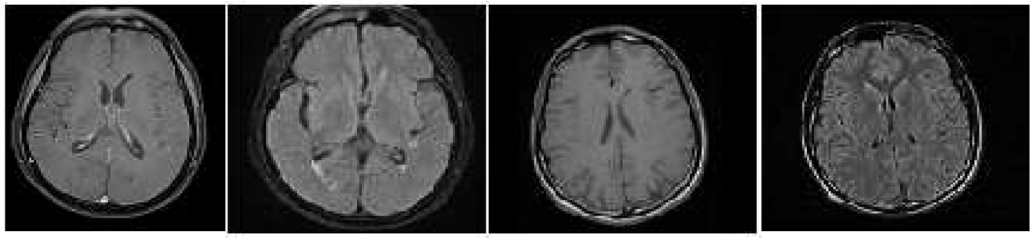
In our proposed technique, initially the input MRI image is pre-processed in order to eliminate the noise and make the image fit for the rest of the process. Here we use the Anisotropic filter in the preprocessing stage. Subsequently, the pre-processed image is segmented using the morphological operator and tumor location is identified using regionprops algorithm. After segmentation process, the features are extracted from the regions using Intensity based Histogram and GLCM Then the extracted features are given to the Hybrid kernel based support vector machine for training. In the final stage the image is classified as tumorous or normal with the help of the trained HKSVM. Finally, the degree of severity analysis using Jaccard and the dice

coefficient will be included.

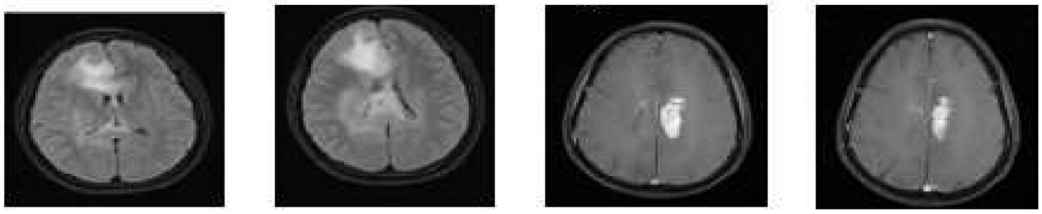
The rest of the paper is organized as follows: The description about the MRI image is presented in the Section 2. The proposed technique is presented in the section 3. The detailed experimental results and discussions are given in the Section 4. and the conclusions are summed up in Section 5.

2. MRI Image Dataset Description

For our proposed method, we have collected the various tumor and non tumor MRI images from south Indian area severity analysis which are undergone for processing the images. This image dataset contains 80 brain MRI images. In which, a total of 60 T1-weighted gadolinium enhanced MR images were tumorous. These 3D DICOM real images were obtained from Government Medical College Hospital, Tirunelveli, Tamilnadu, India with verified intracranial tumors using SIEMENS 1.5 Telsa MR unit and the other 20 brain images are without tumor. The sample images are shown in the Figure 1.



Normal Images



Tumor Images

Figure 1. T1- weighted tumors and Non-tumor images

In our proposed method the Brain image dataset is divided into two sets such as, (1) Training dataset (2) Testing dataset. To segment the brain tumor images the training data set is used and to analyze the performance of the proposed technique the testing dataset is used. In this method, the 50 images (40-tumor and 10-non-tumor) are utilized for the training purpose and the remaining 30 images (20-tumor and 10-non tumor) are utilized for testing purpose.

3. Tumor Detection using Glcm and Improved K-SVM

Segmentation has extensive application in the field of bio-medical image processing .The result of image segmentation is a set of segments that collectively cover the entire image, or a set of contours extracted from the image [10]. As the segmentation of brain tissue has the most complex structure, it is an imperative step of the proposed method. Our proposed method consists of three phases namely, Tumor Region Location, feature extraction and final classification. In this method, Tumor Region identification is done using pre-processing and segmentation process. In pre-processing, applying anisotropic filtering is done to remove the noise. In segmentation phase, brain tissues segmentation process is done using Skull Stripping. The steps involved in the proposed technique for skull stripping are: (i) Binarization (ii) Morphological operations. Subsequently, we use GLCM for feature extraction phase. In the final classification, we use the kernel based improved Support vector machine classifier is used to detect whether a tumor is present or not. The Block diagram of the proposed technique is shown schematically in Figure 2.

3.1. Tumor Region Location Identification

3.1.1 Preprocessing

It is very much essential to carry out the pre-processing on the input image, so that the image gets transformed to be relevant

to the further processing because the proposed technique, MRI brain images cannot be given directly as the input. The pre-processing technique is carried out to reduce the noise present in the input image by loading the input MRI images to the MATLAB environment. The input image is passed through an anisotropic filter which diminishes the noise and the quality can also be improved so that we can obtain a better quality image for further processing.

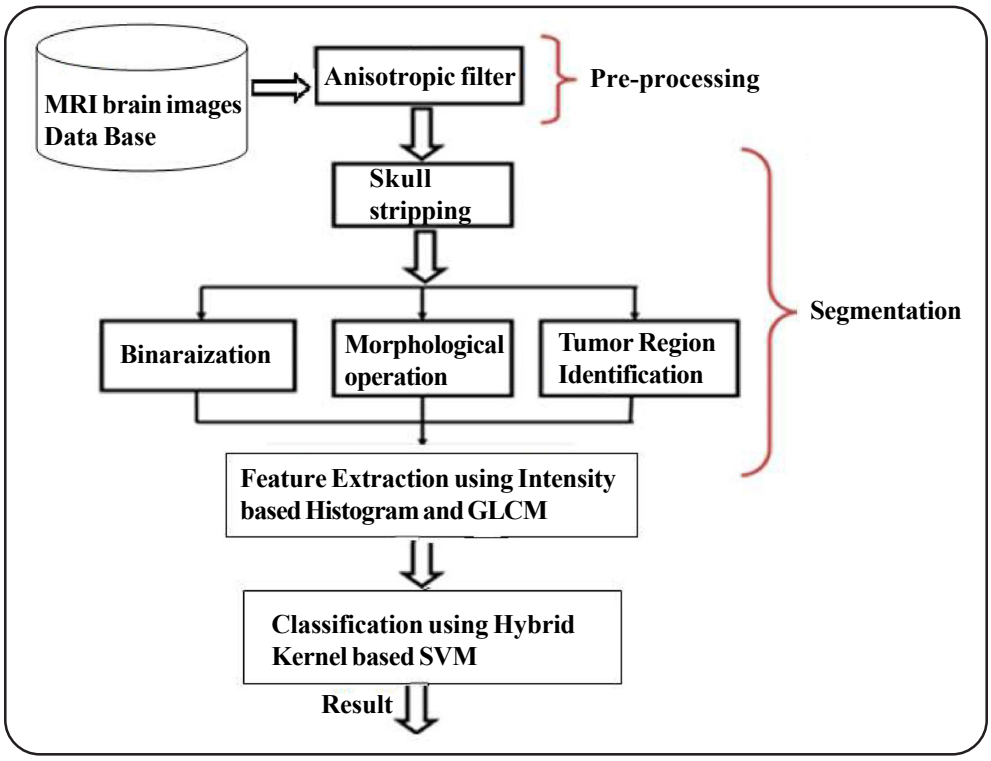


Figure 2. Overall block diagram of our proposed approach

Anisotropic Filter: Anisotropic Filter is a technique aiming at reducing image noise without removing significant parts of the image content, typically edges, lines or other details that are important for the interpretation of the image. It is also enhancing the image quality of textures on surfaces of computer graphics that are at oblique viewing angles with respect to the camera where the projection of the texture (not the polygon or other primitive on which it is rendered) appears to be non-orthogonal (thus the origin of the word: "an" for *not*, "iso" for *same*, and "tropic" from tropism, relating to direction; anisotropic filtering does not filter the same in every direction) [11].

3.1.2. Segmentation using Skull Stripping

In medical image Processing, segmentation is an important and challenging factor. It is the process of partitioning a digital image into multiple segments (sets of pixels, also known as super pixels). The goal of segmentation is to simplify and/or change the representation of an image into something that is more meaningful and easier to analyze. It has an extensive application in the medical field. From intricate medical images, pertinent information can be extracted. Categorization of volumetric data into gray matter, white matter, and cerebro-spinal fluid tissue types are the primary task in brain MRI segmentation.

Skull stripping is a vital process in brain image analysis, which involves removal of the scalp tissue, skull, and Dura. In the proposed technique, skull stripping is used for the segmentation of brain tissues.

The steps involved in the skull stripping process are:

- *Binarization via Thresholding*
- *Morphological Operation*

• *Tumor region identification*

i. MRI image is covert into a binary image by thresholding

Initially, the MRI image is transformed into a binary image. An image of up to 256 gray levels is translated to a black and white image using the threshold value. The gray level value of every pixel in the improved image is considered at this stage. All the pixels with values above the threshold are set as white and the remaining pixels are set as black in the image during the binarization process. In this paper, the threshold value is selected based on the contrast of the image.

$$Binarized\ Image,\ B_{Binary}(k,y) = \begin{cases} 0, & if \quad B_{grey}(k,y) = < Threshold \\ 1, & Otherwise \end{cases}$$

ii. Sharpening the region using Morphological Operation

After transforming into binary images, the morphological process is applied for sharpening the regions and filling the gaps. The main processes of the morphological operations are opening, closing, erosion and dilation. In this paper, erosion operation is applied for removing the hurdle, noise and enhances the image.

Erosion: In the erosion operation on an image F having labels 0 and 1 with structuring element Y, the value of pixel i in F is changed from 1 to 0, if the result of convolving Y with F, centered at i, is below some predefined value. We have set this value to be the area of Y, which is principally the number of pixels that are 1 in the structuring element itself. The structuring element, also known as the erosion kernel, finds out the details of how particular erosion thins boundaries.

$$IE = imerode\,(F, Y)$$

iii. Tumor Area Identification

After the morphological operation, the tumor regions are identified via a regionprops algorithm. The regions of the tumor are marked out based on their area properties. The regionprops algorithm measures the properties of image regions. Using the actual number of pixels in the region, the tumor region's area is segmented. This value is slightly different from the value returned by *bwarea,* which weights diverse patterns of pixels in a different way. The regionprops calculates the area by measuring the distance between each neighboring pair of pixels around the border of the region.

3.2 Feature Extraction

Feature is the significant information about the image. The transformation of an image into its set of features is known as feature extraction. There are many techniques for feature extraction such as texture features [23], Zernike moments [23], features based on wavelet transform. In this paper statistical feature based on intensity histogram like mean, variance, skewness, kurtosis [26] and features from gray level co-occurrence matrices (GLCM) [24] [25] are used to investigate the adequacy for the discrimination of normal and abnormal brain slices.

3.2.1 Intensity Histogram based Features

In Tumor identification the objects are classified based on similar technique. In our proposed method the similarity matrix is constructed using the texture features such as business, skewness, coarseness and standard deviation. Also the color feature contrast is extracted to identify the tumor.

Skewness: It is a measure of the asymmetry of the data around the sample mean. If the value is negative, the data are spread out more to the left of meaner than to the right. If the value is positive, the data are spread out more to the right. The sickness of the normal distribution (or any perfectly symmetric distribution) is zero. The skewness of a distribution is defined as

$$Y = E\,(x-\mu)^3/\sigma^3$$

Where μ is the mean of x, σ is the standard deviation of x, and $E(t)$ represents the expected value of the quantity t.

The autocorrelation function of an image can be used to evaluate the quantity of promptness as well as the excellence of the texture present in the image, denoted as $f(\delta_i, \delta_j)$. For a n x m image is defined as follows:

$$f(\delta_i, \delta_j) = \frac{1}{(n-\delta_i)(m-\delta_j)} \sum_{i=0}^{(n-\delta_i)} \sum_{j=0}^{(m-\delta_j)} I(i,j)\, I(i+\delta_i, j+\delta_j)$$

Here $1 \le \delta_i \le n$ and $1 \le \delta_j \le m$. δ_i and δ_j represent a shift on rows and columns, respectively.

Coarseness: The Coarseness is calculated based on the Shape. This value is not equal to zero then the segmented area has been affected by the tumor, otherwise the tumor does not affect the segmented area. It is the average number of maxima in the autocorrelated images and original images. The coarseness (Cs) is calculated as follows

$$C_s = \frac{1}{0.5 * \left(\frac{\sum_{i=1}^{n} \sum_{j=1}^{m} Max(i,j)}{n} + \frac{\sum_{i=1}^{n} \sum_{j=1}^{m} Max(i,j)}{m} \right)}$$

Busyness: It is calculated based on connectivity, how much the pixels are connected is calculated that is above 5 then the segmented area has a tumor. The business' value is below 5 the segmented area does not have a tumor. The Busyness value is depending on Coarseness .If the value of Coarseness is high, the It is related to coarseness in the reverse order, that is when the business is low.

$$B_s = 1 - C_s^{1/\alpha}$$

Standard Deviation: It shows how much variation or exists from the expected value i.e., the mean. The data points tend to be very close to the mean results low standard deviation and the data points are spread out over a large range of values results high standard deviation. It is the average value of all the segmented area pixels.

Sl. no	Coarseness	Busyness	Contrast	Standard deviation	Skewness
1	3.2735	11.8	0.0527	7.2209	1.9945
2	0.7417	6.9044	0.0125	1.9794	2.3452
3	2.5308	9.6144	0.0445	4.1905	1.1379
4	3.4828	13.2448	0.0552	5.719	1.0794
5	0.8507	7.6284	0.0104	2.5882	2.9365
6	0	4.9987	0	0	0
7	0	4.9987	0	0	0
8	0	4.9987	0	0	0
9	0	4.9987	0	0	0
10	0	4.9987	0	0	0

Table 1. Various Feature extraction value of 10 images

3.2.2 Gray Level Co-Occurrence Matrix

GLCM contains the second-order statistical information of neighboring pixels of an image. In our proposed method, Gray Level Co-occurrence Matrix (GLCM) -based feature extraction process are performed.. It is estimated of a joint probability density function (PDF) of gray level pairs in an image [12].

It can be expressed in the following equation

$$P_{\mu}(i,j)\,(i,j=0,1,2,\ldots N-1)$$

Where i, j indicate the gray level of two pixels, N is the gray image dimensions, μ is the position relation of two pixels. Different values of μ decides the distance and direction of two pixels. Normally Distance (D) is 1, 2 and Direction (θ) is 0^0, 45^0, 90^0, 135^0 are used for calculation [13].

Texture features can be extracted from gray level images using GLCM Matrix. In our proposed method, five texture features energy, contrast, correlation, entropy and homogeneity are experiments. These features are extracted from the segmented MR images and analyzed using various directions and distances.

Energy expresses the repetition of pixel pairs of an image

$$k1=\sum_{i=0}^{N-1}\sum_{j=0}^{k-1} p^2{}_{\mu}(i,j)$$

Local variations present in the image is measured by Contrast. If the contrast value is high means the image has large variations.

$$k2=\sum_{i=0}^{N-1} t^2\left\{\sum_{i=0}^{N-1}\sum_{j=0}^{N-1} P_{\mu}(i,j)\right\}$$

Correlation is a measure linear dependency of gray level values in co-occurrence matrices. It is a two dimensional frequency histogram in which individual pixel pairs are assigned to each other on the basis of a specific, predefined displacement vector.

$$k3=\sum_{i=0}^{K-1}\sum_{j=0}^{K-1}\frac{(i,j)\,p\,(i,j)-\mu_1\mu_2}{\sigma_1{}^2\sigma_2{}^2}$$

Where μ_1, μ_2, σ_1 ,σ_2 are mean and standard deviation values accumulated in the x and y directions respectively.

Entropy is a measure of non-uniformity in the image based on the probability of Co- occurrence values, it also indicates the complexity of the image

$$k4=-\sum_{i=0}^{K-1}\sum_{j=0}^{K-1} p_{\mu}(i,j)\,log\,(p_{\mu}(i,j))$$

Homogeneity is inversely proportional to contrast at constant energy whereas it is inversely proportional to energy

$$k5=\sum_{i=0}^{k-1}\sum_{j=0}^{k-1}\frac{p_{\mu}(i,j)}{1+(i-j)^2},\ i\neq j$$

3.3 Feature Classification

In our proposed method, we perform the final classification step. Here we use the Hybrid kernel based Support Vector Machine classifier to classify the image into tumors or not. In 1995, Support Vector Machine (SVM) has been developed, which is an effective supervised classifier and accurate learning technique. It is derived from the statistical theory invented by Vapnick in 1982 [14]. It produces successful classification results in several application domains, for e.g. medical diagnosis [15, 16]. SVM follows the structural risk minimization principle from the statistical learning theory. Its kernel is to control the practical risk and classification capacity in order to broaden the margin between the classes and reduce the true costs [17]. A support vector machine searches an optimal separating hyper-plane between members and non-members of a given class in a high dimension feature space [18]. The decision boundary and margin of Linear SVM is shown in Figure 3.

3.3.1 Linear SVM

The support vector machine (SVM) is a machine learning technique, which originated from the statistical theory and is used for the classification of images. It is one of the a popular tool of classification tasks due to their appealing generalization properties;

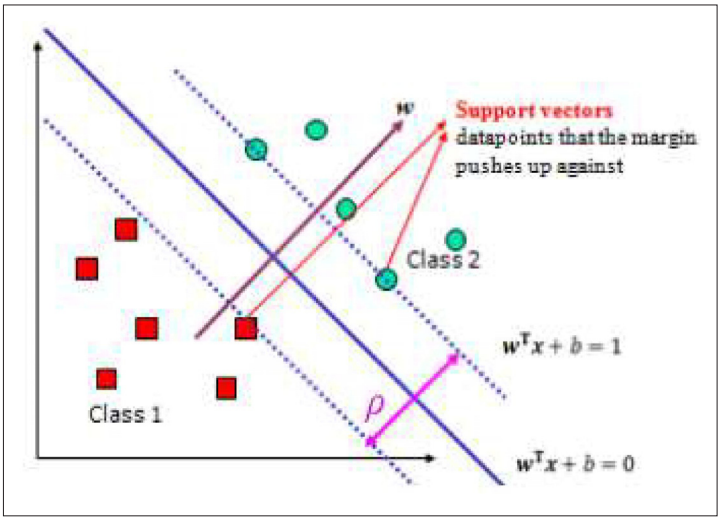


Figure 3. Decision boundary and margin of SVM

this has led several groups to pro-pose using SVMs for brain tumor segmentation. It is derived from the statistical theory invented by Vapnick in 1982. This is the simplest case in which the input patterns are linearly separable. There exists a linear function of the form

$$f(x) = W^T + bx$$

Such that for each training example x_i, the function yields $f(x_i) \geq 0$ for $y_i = +1$ and $f(x_i) < 0$ for $y_i = -1$. Hence, training samples from the two different classes are separated by the hyper plane.

$$f(x) = W^T + bx = 0$$

3.3.2 Non-linear SVM

The linear SVM classifier can be eagerly extensive to a nonlinear classifier by using a nonlinear operator to map the input pattern x into upper dimensional feature space. The non-linear classifier is defined the eqn (11)

$$f(x) = W^T \phi(x) + b$$

In non-linear SVM, the original data set $x \in R^n$ is transformed to upper dimensional data $\phi(x)$, the parameter of the decision function $f(x)$ has satisfied the following minimum criteria

$$min\, J(W, \xi) = \frac{1}{2} \| w \|^2 + C \sum_{i=1}^{l} \varepsilon_i$$

$$\text{Subject to, } y_i (w^1 \phi(X_i) + b) \geq 1 - \varepsilon_i, \varepsilon_i \geq 0; i = 1, 2, 3, ..., l$$

The data with linear separability may be analyzed with a hyperplane and the linearly non separable data are analyzed with kernel functions such as higher order polynomials, Gaussian RBF described as

- Polynomial kernel $k1$ is $K(x_i, x_j) = (x_i^T x_j + 1)^p, \quad p \geq 0$

  Where p is the order of the kernel

- Radial basis function (RBF) $k2$ is: $k(x_i, x_j) = exp\left[\frac{-||x_i - x_j||^2}{2\sigma^2}\right]$

3.3.2 Proposed Hybrid kernels based SVM

In our proposed system, we have developed kernel based SVM for improving the classification process. In most cases, we want to assign an object to one of several categories based on some of its characteristics in our real life situation. For instance, based on the outcome of several medical tests we want to say whether the patient has a particular disease or not. From the existing work [19], we have analyzed the kernel equation and we have used those kernel equations in the proposed work namely, RBF and Polynomial function.

kernel- based Lagrange multipliers $\alpha_i \geq 0 \; \forall_i$

$$L_p = \sum_{i=1}^{n} \alpha_i - \frac{1}{2} \sum_{i=1}^{n} \sum_{i=1}^{n} \alpha_i \alpha_j y_i y_j K(x_i . x_j)$$

Minimize L_p with respect to *w, b* and maximize with respect to α_i.

This is a convex quadratic programming problem. Thus we see that the plane is a nonlinear combination of the training vectors

$$w = \sum_{i=1}^{n} \alpha_i y_i K(x_i)$$

Let k_1 (*RBF*) and k_2 (*polynomial*) be kernels over $\Xi \times \Xi$, $\Xi \subseteq R^p$, and k_3 be a kernels over $R^p \times R^p$. Let function $\varphi : \Xi \rightarrow R^p$. The two kernel based formulation is represented by

$k(x, y) = k_1(x, y) + k_2(x, y)$ is a kernel (i)

Substitute the equations (i) in Lagrange multiplier equation, we get

$$L_p = \sum_{i=1}^{n} \alpha_i - \frac{1}{2} \sum_{i=1}^{n} \sum_{i=1}^{n} \alpha_i \alpha_j y_i y_j (k_1(x_i . x_j) + k_2(x_i . x_j))$$

Substitute the theorems in Quadratic function equation, we get

$$w = \sum_{i=1}^{n} \alpha_i y_i (K_1(x_i) + k_2(y_i))$$

***SVM Process*:** To train the SVM classifier, we need some data features to identify the normal brain region and tumor affected brain. The data features will then train the classifier and the classifier will find whether the given MRI image is a tumor or not. The data features which we have chosen for training the SVM classifier five texture features energy, contrast, correlation, entropy and homogeneity (**Detailed in section 3.2**). After computing all the data features, we have to give the result to the SVM classifier. Using these results we can train the classifier to identify the tumor and non-tumor from the given MRI image. After the SVM classifier is trained, we can give a new MRI image to find whether it has a tumor or not. The SVM classifier then compares the values of all the five data features with the stored values of normal and abnormal MRI images. Then identify whether the given MRI image comes under the normal category or abnormal category and give the result to us.

4. Results and Discussion

The proposed method can successfully segment a tumor provided that the parameters are set correctly. The proposed technique is designed for supporting the tumor detection in brain images with tumor and without tumor. The obtained experimental results from the proposed technique are given in Figure 4. The obtained results of the proposed method is evaluated through evaluation metrics namely, sensitivity, specificity and accuracy [20].

$$Sensitivity = TP/(TP + FN)$$

$$Specificity = TN/(TN + FP)$$

$$Accuracy = (TN + TP)/(TN + TP + FN + FP)$$

Where, *TP* stands for True Positive, *TN* stands for True Negative, *FN* stands for False Negative and *FP* stands for False Positive. As suggested by above equations, *Sensitivity* is the proportion of true positives that are correctly identified by a diagnostic test. It shows how good the test is at detecting a disease. *Specificity* is the proportion of the true negatives correctly identified by a diagnostic test. It suggests how good the test is at identifying normal (negative) condition. *Accuracy* is the proportion of true results, either true positive or true negative, in a population. The obtained experimental results of the proposed and existing methods are given in Table 1. By analyzing the results, our proposed approach has a better performance compared to other leading methods.

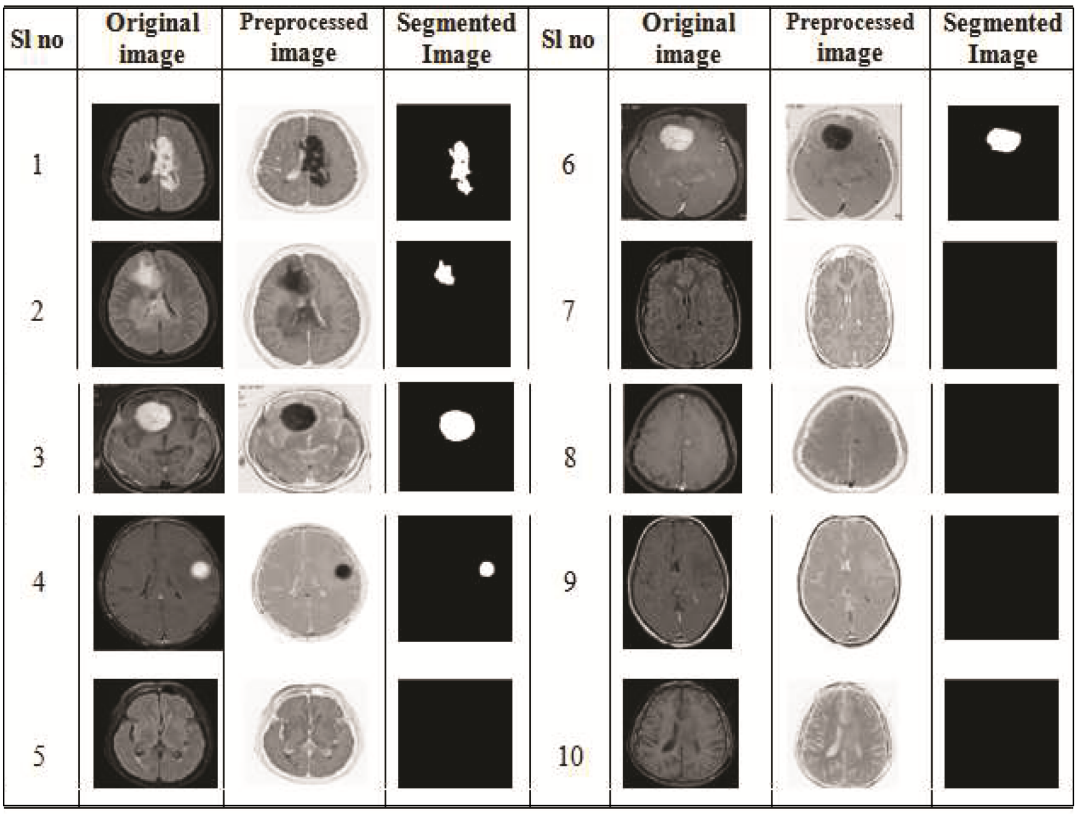


Figure 4. Obtained experimental-results of proposed-method

Evaluation metrics		Kavitha, A.R et al. [21]	Shaheen Ahmed et al.[22]	Our Proposed Approach K1+K2
Input MRI image data set	True Positive(TP)	37	35	38
	True Negative(TN)	8	8	9
	False Positive(FP)	2	2	1
	False Negative(FN)	3	5	2
	Sensitivity	0.925	0.875	0.95
	Specificity	0.73	0.62	0.9
	Accuracy	0.9	0.86	0.94

Table 2. Detection accuracy of the proposed approach in testing data set

4.4. Comparative Analysis

We have compared our proposed tumor detection technique hybrid kernel based SVM against and existing techniques which are Kavitha A, R *et al*. [21], Shaheen Ahmed *et al*. [22]. The performance analysis has been made by plotting the graphs of evaluation metrics such as sensitivity, specificity and the accuracy. By analyzing the plotted graph, the performance of the proposed technique has significantly improved. The evaluation graphs of the sensitivity, specificity and the accuracy graph are shown in Figure 5. Our proposed work is represented by K1+K2. The graph shows that the sensitivity, specificity and accuracy of K1+K2 is almost equal level for every ranges. when comparing the Specificity the graph shows that the specificity of K1+K2 is greater than the existing works. On analyzing the accuracy the graph shows that the accuracy of our proposed work is improved when compared with the existing works.

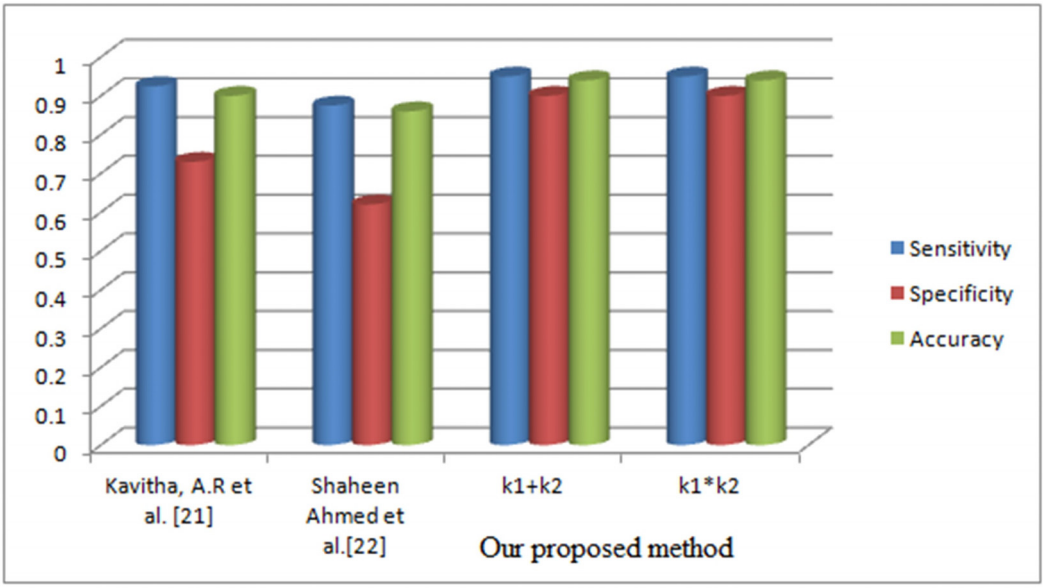


Figure 5. Comparative charts of existing and proposed method

5. Conclusion

In this approach, we have developed a significant tumor detection technique using improved K-SVM. The proposed approach comprises of preprocessing, segmentation, feature extraction and classification. In preprocessing steps, we need to perform skull stripping and then, anisotropic filtering will be applied to make the image suitable for extracting features. In feature extraction, some specific feature will be extracted using texture as well from intensity. In the classification stage, the *hybrid kernel* will be designed and apply to training of support vector machine (SVM) to perform automatic detection of tumor in MRI images. For comparative analysis, our proposed approach is compared with existing works. The accuracy level (94%) for RBF+polynomial based kernel (K1 + K2) proved that the proposed algorithm graph is good at detecting the tumors in the brain MRI images.

Reference

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