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An Automated Approach For Brain Tumor Detection And Classification In MRI Using SVM

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Abstract:
Background: *Brain tumors are abnormal and uncontrolled growths within the brain that can disrupt normal brain function and damage surrounding healthy tissues. Early and accurate detection of brain tumors is critical for effective treatment planning and improved patient outcomes. Magnetic Resonance Imaging (MRI) is widely regarded as the most effective imaging modality for visualizing brain structures and identifying tumors. Automated segmentation and classification techniques using machine learning can support radiologists in accurate and timely tumor detection. This study proposes a Fully Automatic Heterogeneous Segmentation using Support Vector Machine for the detection, segmentation, and classification of brain tumors from MRI images.*
Materials and Methods: *In this study, MRI datasets were collected. Preprocessing included grayscale conversion, adaptive contrast enhancement, and skull stripping using a threshold-based method. Tumor regions were segmented using a combination of morphological operations and the Berkeley Wavelet Transform (BWT). A Support Vector Machine (SVM) classifier with a Gaussian kernel was applied to distinguish tumor tissue from normal brain tissues. The system was evaluated using performance metrics including mean, mean square error (MSE), peak signal-to-noise ratio (PSNR), structural similarity index (SSIM), Dice coefficient, sensitivity, specificity, and accuracy.*
Results: *The method achieved accurate segmentation and classification of tumor and normal brain tissues. The Dice coefficient ranged from 0.79 to 0.90 across MRI slices, while classification accuracy ranged from 96.51% to 98.51%. The method demonstrated high sensitivity and specificity compared to existing techniques such as ANFIS, Back Propagation, DWA-DNN, and K-NN classifiers. Early detection of tumors and precise localization were achieved, although processing time was longer due to the high-resolution images and large dataset.*
Conclusion: *The proposed approach enables reliable and accurate detection, segmentation, and classification of brain tumors from MRI images. It provides spatially consistent tumor segmentation, supports clinical decision-making, and outperforms several existing machine learning techniques. Future work can further improve classification accuracy by exploring hybrid classifiers and advanced feature selection methods.*
Keywords: *Brain Tumor; MRI; Segmentation; Support Vector Machine (SVM); Berkeley Wavelet Transform (BWT); Feature Extraction; Classification*

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I. Introduction

Nearly half of global cancer-related deaths could be prevented through effective primary prevention, early detection, and improved treatment strategies. Addressing disparities in cancer outcomes—especially in low- and middle-income countries—requires global efforts to improve access to screening, diagnosis, and advanced medical care. The brain is one of the most complex organs in the human body, composed of billions of interconnected cells that regulate essential physiological and cognitive functions. A brain tumor develops when abnormal and uncontrolled cell division forms a mass within or around the brain. Such abnormal growth can disrupt normal brain activity and damage surrounding healthy tissues.

Brain tumors are broadly classified into benign (low-grade) and malignant (high-grade) types. According to grading systems established by the World Health Organization and the American Brain Tumor Association, tumors are categorized into four grades (I–IV)[1]. Grades I and II tumors are generally slow-growing and considered low-grade, whereas Grades III and IV tumors are aggressive and rapidly progressing. Benign tumors are non-cancerous, slow-growing, and usually well-defined, while malignant tumors are cancerous, invasive, and may either originate in the brain (primary tumors) or spread from other parts of the body (secondary or metastatic tumors). If left untreated, low-grade tumors may develop into high-grade malignant tumors.

Among medical imaging modalities, Magnetic Resonance Imaging (MRI) is widely regarded as one of the most effective techniques for detecting and analyzing brain tumors. MRI produces high-resolution images with excellent soft-tissue contrast, allowing clear visualization of brain structures and abnormalities. Different MRI sequences—such as T1-weighted, T2-weighted, FLAIR, and proton density images—provide complementary diagnostic information [2-5].

Accurate segmentation of pathological and healthy brain tissues, including gray matter (GM), white matter (WM), and cerebrospinal fluid (CSF), is a crucial step in tumor analysis. Image segmentation involves dividing MRI images into meaningful regions based on characteristics such as intensity, texture, contrast, and boundaries.[6] This process helps clinicians determine tumor size, location, and its impact on surrounding tissues, which is essential for effective treatment planning.With advancements in information technology and e-healthcare systems, automated medical image analysis has become increasingly important. Traditional machine learning methods such as Support Vector Machine (SVM) and Neural Networks (NN) have demonstrated strong performance in medical image classification tasks.[7] Although deep learning approaches have recently gained attention due to their ability to model complex patterns, classical machine learning algorithms like SVM remain highly effective, particularly when working with limited datasets.

This study focuses on the automated segmentation of meningioma tumors from multi-spectral brain MR images. Meningioma is one of the most common benign tumors occurring in the brain region [8]. Accurate identification of these tumors is essential for determining appropriate surgical interventions, particularly in elderly patients with intracranial meningiomas [9]. In recent years, Support Vector Machine (SVM) techniques have demonstrated strong performance in MRI segmentation tasks aimed at identifying various neurological disorders [10]. Segmentation plays a crucial role in medical image analysis as it enables the detection and isolation of abnormal tumor tissues from medical imaging modalities [11]. It involves partitioning an image into several meaningful regions that share similar characteristics such as gray-level intensity, texture, color, contrast, boundaries, and brightness [12].

In this study, an automated framework for brain tumor detection and classification using MRI images is developed. The methodology consists of image preprocessing, segmentation, feature extraction using the Discrete Wavelet Transform (DWT), and classification using SVM. The proposed system aims to distinguish between normal brain tissues and different tumor types, thereby improving diagnostic accuracy and supporting clinical decision-making. Early and accurate detection of brain tumors significantly increases patient survival rates [13]. Therefore, the development of reliable automated systems for tumor segmentation and classification plays a vital role in enhancing medical diagnosis, treatment planning, and overall patient outcomes.

The rest of the paper is organized as follows: Section 2 presents the related works, Section 3 describe the steps of the proposed methodology, Section 4 presents the results and discussion, the conclusion and future work in section 5.

II. Related Works

Medical image segmentation for brain tumor detection from Magnetic Resonance (MR) images and other medical imaging modalities is a crucial step in determining appropriate and timely treatment. Numerous techniques have been developed for brain tumor classification, including fuzzy C-means (FCM), Support Vector Machines (SVM), Artificial Neural Networks (ANN), knowledge-based approaches, and Expectation–Maximization (EM) algorithms. The following section presents an overview of recent and significant research contributions in this area.

P. Mohamed Shakeel et al. [14] proposed a machine learning–based Backpropagation Neural Network (MLBPNN) for brain tumor classification. Their approach follows standard biopsy image processing steps—image acquisition, enhancement, segmentation, feature extraction, and classification—and was evaluated using infrared sensor imaging. The system also integrates a wireless infrared sensor to transmit tumor data for remote monitoring, though performance may decline when subsystem components degrade. Ali and Hanbay [15] proposed an Extreme Learning Machine with Local Receptive Fields (ELM-LRF) for brain tumor detection and classification. Their method uses noise reduction preprocessing, followed by MR image classification into malignant or benign cases and tumor segmentation, achieving an accuracy of 96.2% and demonstrating improved performance compared to recent approaches.

Zanaty [16] proposed a hybrid brain tumor segmentation method combining Fuzzy C-Means (FCM), seed region growing, and the Jaccard similarity coefficient to segment gray and white matter from MR images, achieving an average segmentation score of 90% under moderate noise levels. Kong et al. [17] also studied automatic brain tissue segmentation from MR images using discriminative clustering with feature selection techniques.

Kumar and Vijayakumar [18] proposed a brain tumor segmentation and classification method using PCA feature reduction with an RBF-kernel SVM classifier. Their approach achieved a similarity index of 96.2%, overlap fraction of 95%, extra fraction of 0.025%, and a tumor classification accuracy of 94%.Mallick et al. [19]

suggested the Deep wavelet Auto Encoder and Deep Neural Network (DWA-DNN) for Brain Magnetic Resonance image classification for cancer recognition. This paper proposes a Deep Wavelet Auto Encoder (DWA) image compression technique, which combines the Auto Encoder essential feature extraction function with the transform wavelet image decomposition method. The mixture of both has a tremendous impact on the reduction of the feature set to continue to identify with DNN. The suggested DWA-DNN image classifier was reviewed, and a brain picture dataset was taken.

This study proposes an automatic brain tumor segmentation method using a supervised Support Vector Machine (SVM) approach. Treating segmentation as a classification problem, the method analyzes multiple MRI modalities and demonstrates fast processing, strong generalization ability, and effective handling of volumetric data for accurate tumor detection.

III. Proposed Methodology

This study presents an Automatic Segmentation using Support Vector Machine (SVM) method for brain tumor detection and segmentation. The overall architecture of the proposed approach, illustrated in Figure 1, outlines each stage from data acquisition to final tumor segmentation. Magnetic Resonance Imaging (MRI) is employed as the primary diagnostic modality for analyzing brain anatomy and identifying abnormalities. Increased tumor vascularity leads to greater uptake of contrast agents, thereby enhancing tumor visibility relative to surrounding normal tissues. Moreover, dynamic and repeated contrast administration enables assessment of temporal contrast uptake patterns, which supports differentiation between malignant and benign tumors.

The proposed methodology was applied to real MRI datasets with image dimensions of 512 × 512 pixels. All images were converted to grayscale prior to further processing. Subsequent stages include preprocessing, feature extraction, and SVM-based segmentation, thereby establishing a fully automated framework for accurate brain tumor detection and tissue segmentation.

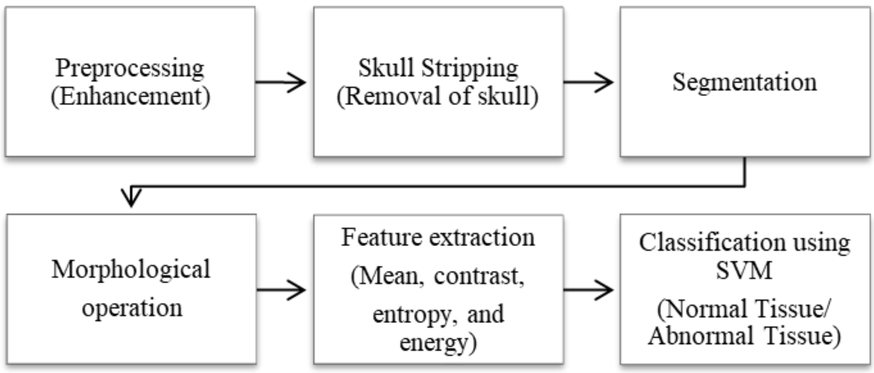

Figure 1: Proposed Algorithm

Preprocessing

Preprocessing is an essential step that improves the quality of MRI images and prepares them for accurate analysis by human observers or computer vision systems. It begins by enhancing key image parameters, such as increasing the signal-to-noise ratio, improving visual clarity, removing unwanted background noise and irrelevant details, smoothing internal regions, and preserving important edges. In this work, adaptive contrast enhancement using a modified sigmoid function is applied to the raw MRI images to improve SNR and overall image quality, ensuring that the images are better suited for subsequent segmentation and classification processes.

Skull Stripping

Skull stripping is a crucial step in biomedical image analysis and is essential for accurate examination of brain tumors from MRI images [20-23]. This process involves removing all non-brain tissues from the MRI scans, such as the skull, skin, and surrounding fat, to isolate only the brain region for further analysis. Effective skull stripping improves the performance of subsequent steps like segmentation and classification by eliminating irrelevant information.

Several techniques exist for skull stripping, including automatic methods based on image contours, approaches using segmentation combined with morphological operations, and methods relying on histogram analysis or thresholding. In this study, skull stripping is performed using a threshold-based technique to remove skull tissues. The algorithm demonstrates how the thresholding operation effectively separates brain tissues from non-brain structures, such as the skull and surrounding tissues, while preserving essential anatomical details required for accurate tumor detection and analysis.

Algorithm: Skull Stripping Procedure
Step 1: Read the input MRI image.
Step 2: Convert the input image into a grayscale image.
Step 3: Convert the grayscale image into a binary image using an appropriate thresholding technique.
Step 4: Identify and count the connected components (objects) in the binary image.
Step 5: Select the object corresponding to the brain region and create a mask by assigning:
1 to pixels inside the brain region
0 to pixels outside the brain region
Step 6: Multiply the generated mask with each MRI modality (T1, T2, and FLAIR images).
Step 7: Obtain the skull-stripped MRI images for all modalities.

Segmentation and Morphological Operations

The segmentation of infected brain MR regions is performed through a sequence of thresholding, morphological processing, and wavelet-based analysis. Initially, the preprocessed MRI image is converted into a binary image using a fixed threshold value of 128. Pixel intensities greater than the threshold are mapped to white, while those below it are mapped to black, resulting in distinct regions corresponding to tumor and non-tumor tissues. This binary separation facilitates isolation of the infected region.

In the next step, a morphological erosion operation is applied to remove unwanted white pixels and refine the segmented regions. Erosion eliminates boundary pixels based on a defined structuring element, thereby reducing noise and small artifacts. The eroded image and the original binary image are then divided into two equal regions, and the black pixel region obtained after erosion is considered as the brain MRI mask. Morphological operations, including dilation and erosion, are particularly suitable for binary images because they manipulate the spatial arrangement of pixels rather than their intensity values. Dilation adds pixels to object boundaries, whereas erosion removes pixels from boundaries, both depending on the selected structuring element. These operations are used to extract accurate boundary regions of brain tissues.

For effective segmentation, the Berkeley Wavelet Transform (BWT) is employed. A wavelet is a function defined over a finite interval with an average value of zero, enabling signal decomposition into different frequency components. Wavelet transformation allows image data to be analyzed at multiple resolutions by separating it into frequency sub-bands. All wavelets are generated from a fundamental function known as the mother wavelet, represented as:

$$\Psi_{s,\tau} = \frac{1}{\sqrt{s}} \Psi\left(\frac{t-\tau}{s}\right)$$

where s and τ denote the scale and translation parameters, respectively.

The Berkeley Wavelet Transform is a two-dimensional triadic wavelet transform used for image processing. Similar to other wavelet families, BWT converts spatial image data into the frequency domain, providing a complete orthonormal representation. The mother wavelet in BWT is a piecewise constant function, and its scaled and translated versions are generated across different pixel positions in a two-dimensional plane. The transformation function is expressed as:

$$\beta_\theta^\varphi(\tau, s) = \frac{1}{s^2} \beta_x^\varphi(3^s s(x - i), 3^s(y - j))$$

where τ and s represent translation and scale parameters, andβ_θ^φdenotes the Berkeley mother wavelet function. A single constant term is sufficient to represent the mean value of the image, given by:

$\beta_0 = \frac{1}{\sqrt{9}}\left[u\left((\frac{x}{3}, \frac{y}{3}\right)\right]$

The experimental results demonstrate successful segmentation of white matter (WM), gray matter (GM), cerebrospinal fluid (CSF), and tumor regions. The Dice overlap coefficient is calculated to evaluate segmentation performance by comparing the algorithm output with the ground truth. The fully automatic heterogeneous segmentation results are illustrated for axial, coronal, and sagittal views, confirming the effectiveness of the proposed approach in accurately extracting tumor and brain tissue region.

Feature Extraction

Feature extraction involves deriving higher-level image information such as shape, texture, color, and contrast to facilitate effective analysis and classification. Texture analysis, in particular, plays a crucial role in both human visual perception and machine learning systems, as it enables the identification of discriminative patterns that enhance diagnostic accuracy. By selecting prominent and informative features, the performance and reliability of automated diagnosis systems can be significantly improved.

One of the most widely adopted approaches for texture-based image analysis was introduced by Robert M. Haralick through the Gray Level Co-occurrence Matrix (GLCM) method. The GLCM-based technique for medical image feature extraction is generally performed in two stages. In the first stage, the GLCM is constructed to represent the spatial relationship between pairs of gray-level pixels within the image. In the second stage, statistical texture features are computed from the generated GLCM to quantitatively describe the image texture.

In brain Magnetic Resonance (MR) images, extracting meaningful features is particularly challenging due to the complex anatomical structure and the presence of diverse tissue types such as White Matter (WM), Gray Matter (GM), and Cerebrospinal Fluid (CSF). Accurate characterization of these tissues is essential for identifying abnormalities. Textural analysis contributes substantially to tumor detection, tumor staging, and therapy response assessment by capturing subtle variations in tissue intensity and spatial distribution.

By incorporating both first-order and second-order statistical features derived from intensity distributions and GLCM matrices, the extracted descriptors provide a comprehensive representation of brain MR images. These mathematical formulations of statistical and textural features serve as the foundation for subsequent classification and diagnostic processes.The statistics feature formula for some of the useful features is listed below.

Mean (M): Average intensity of the image.

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

Standard Deviation (SD): Measures intensity variation or inhomogeneity

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

Entropy (E): Quantifies randomness in texture.

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

Skewness (S_k): Measures asymmetry of intensity distribution.

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

Kurtosis (Kurt): Describes the peakedness of intensity distribution.

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

Energy (En): Angular Second Moment: Measures pixel pair repetition.

$$En = \sqrt{\sum_{x=0}^{m-1} \sum_{y=0}^{n-1} f^2(x, y)}$$

Contrast (Con): Measures intensity difference between a pixel and its neighbor.

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

Inverse Difference Moment (IDM) / Homogeneity: Evaluates local homogeneity.

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

Directional Moment (DM): Captures texture orientation and alignment.

$$DM = \sum_{x=0}^{m-1} \sum_{y=0}^{n-1} f(x, y) \, |x - y|$$

Correlation (C_{orr}): Represents spatial dependency between pixels.

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

where M_x and σ_x are the mean and standard deviation in the horizontal spatial domain and M_y and σ_y are the mean and standard deviation in the vertical spatial domain.

Coarseness (C_{ness}): Measures texture roughness; larger values indicate coarser textures.

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

In addition to texture features, image quality assessment ensures reliable evaluation of MRI analysis results:

Structural Similarity Index (SSIM): Measures perceptual similarity, capturing luminance, contrast, and structure preservation: a perceptual metric that signifies that the degradation in image quality may be caused by data compression or losses in data transmission or by any other means of the image processing. It is defined as

$$SSIM = \left(\frac{\sigma_{xy}}{\sigma_x\, \sigma_y}\right)\left(\frac{2\bar{x}\bar{y}}{\bar{x}^2 + \bar{y}^2 + c_1}\right)\left(\frac{2\sigma_x\sigma_y}{(\sigma_x)^2 + \left(\sigma_y\right)^2 + c_2}\right)$$

Higher SSIM values indicate better quality.

Mean Square Error (MSE): Quantifies fidelity between original and processed images.

$$MSE = \left(\frac{1}{M \times N}\right)\sum\sum(f(x,y) - f^R(x,y))^2$$

Peak Signal-to-Noise Ratio (PSNR): Evaluates reconstruction quality.

$$PSNR\ in\ dB = 20\log_{10}\frac{2^n - 1}{MSE}$$

Dice Coefficient: Measures overlap between the algorithm-predicted tumor region.

$$Dice(A,B) = 2 \times \frac{|A_1 \wedge B_1|}{(|A_1| + |B_1|)}$$

where $A \in \{0,1\}$ is tumor region extracted from algorithmic predictions and $B \in \{0,1\}$ is the experts ground truth. Values range from 0 (no overlap) to 1 (perfect overlap).

Classification

The Support Vector Machine (SVM) algorithm is a supervised learning technique that can be applied to problems ranging from binary (one-class) classification to multi-class (n-class) classification. The main objective of SVM is to convert a nonlinear classification problem into a linear one through the use of a kernel function. In this study, the Gaussian (Radial Basis Function, RBF) kernel was used for this transformation.

By applying a kernel function, nonlinear data samples are mapped into a higher-dimensional feature space, where they become linearly separable. This transformation enables more efficient and accurate classification of complex data patterns. The SVM algorithm determines an optimal separating hyperplane between two training classes. This hyperplane is defined as

$$\mathrm{f(y)} = Z^T \phi\ (\mathrm{y}) + \mathrm{b}$$

where Z and T are hyperplane parameters and ϕ(y) is a function used to map vector y into a higher-dimensional space. The Gaussian kernel function used for nonlinear SVM is expressed as:

$$k(y_i, y_j) = exp\left[-\gamma\left\|y_i - y_j\right\|^2\right]$$

where y_i and y_j are objects i and j, respectively and γ is a kernel parameter that controls the smoothness of the decision boundary.

Feature selection combined with kernel-based class separability makes SVM a preferred method for brain tumor classification. The performance of the SVM classifier is evaluated using accuracy, sensitivity, and specificity metrics.

Accuracy represents the proportion of correctly classified cases (both normal and abnormal) among all examined samples. Sensitivity measures the classifier's ability to correctly detect tumor cases, while specificity indicates its ability to correctly identify normal cases.

IV. Results And Discussion

This section presents the results of the proposed image segmentation technique using real brain MRI images. The algorithm was implemented in MATLAB 7.14.0 (R2012a) on a Windows 8 platform with an Intel

Core i5 processor and 8 GB RAM. The experimental results obtained from the proposed method are illustrated in Figure 2.

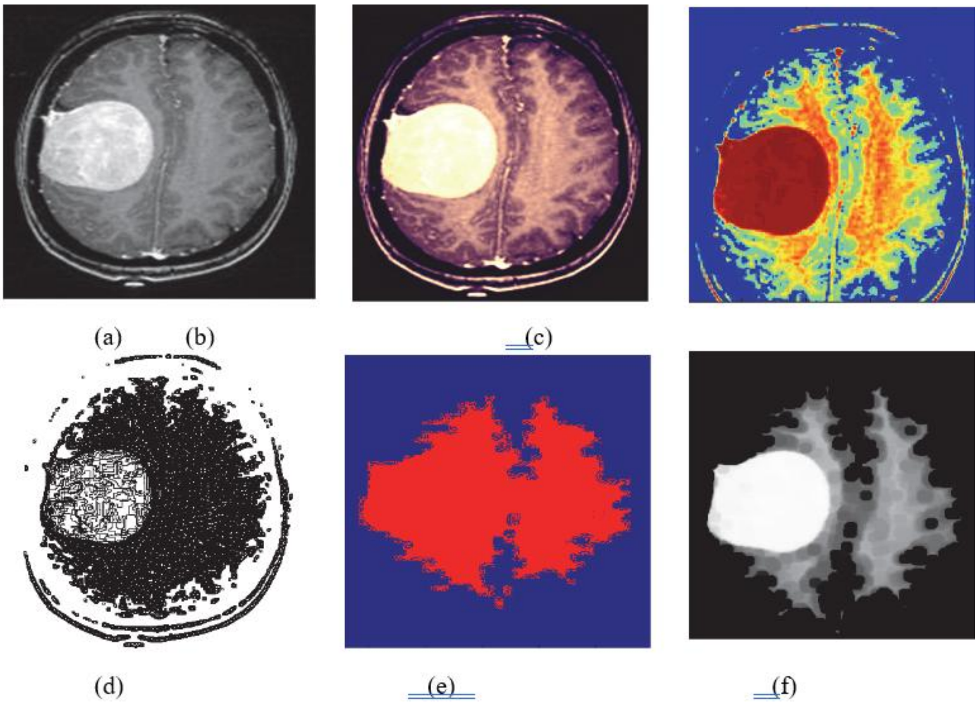

Figure 2: Experimental results (a)Original Image (b)Enhanced Image (c)Wavelet Decompose Image (d)Intense segmented Image (e) Dice overlap Image (f)Tumor region

Table 1 summarizes the performance evaluation using parameters such as mean squared error (MSE), peak signal-to-noise ratio (PSNR), structural similarity index (SSIM), and Dice score. A lower MSE value and a higher PSNR value indicate better image quality and signal-to-noise ratio in the extracted image. The Dice coefficient measures the degree of overlap between the automatic segmentation results and the manually segmented ground truth for the given dataset.

A variety of features, including intensity textures, label lengths, and spatial tissue prior probabilities, are extracted from each image. These features are combined based on the requirements of the classification problem. Using training images, tumor-sampling and non-tumor-sampling maps are generated from classification probabilities. A two-class Support Vector Machine (SVM) classifier is then applied to distinguish tumor tissues from normal tissues. Figure 3 presents the probability detection ratio for the proposed method. A probabilistic neural network classifier was utilized to train and evaluate tumor detection performance using brain MRI images. Early detection of brain tumors is critical for enabling timely and appropriate treatment. However, effective segmentation becomes challenging when feature extraction is limited or when combined features fail to capture sufficient discriminative information. This limitation may lead reduced accuracy in tumor identification and detection.

Table 1: Performance evaluation for segmented tissues

Image	MSE	PSNR(dB)	SSIM	DICE SCORE
1	1.86	55.45	0.894	0.83
2	0.58	68.21	0.902	0.87
3	4.95	56.28	0.970	0.82
4	1.23	58.79	0.8801	0.79
5	5.06	59.65	0.7978	0.90
6	2.14	60.34	0.8856	0.84
7	0.92	66.48	0.9103	0.88
8	3.67	57.91	0.8654	0.81
9	1.74	61.25	0.9037	0.86
10	2.98	59.12	0.8726	0.83
11	0.63	67.84	0.9184	0.89
12	4.12	56.73	0.8542	0.80
13	1.56	62.17	0.8995	0.85
14	2.47	60.08	0.8872	0.84
15	3.35	58.66	0.8617	0.82

Compared with existing techniques, the proposed method demonstrates a lower classification error, as shown in Figure 3. During the feature extraction stage, intensity-based features are calculated to form a characteristic vector for each pixel. The Support Vector Machine (SVM) classifier then develops a model to distinguish between tumor pixels and normal pixels. Using this model, new pixels are classified to identify tumor regions, resulting in the extraction of tumor areas.

The proposed method is particularly effective for brain tumor segmentation because it considers not only local tumor characteristics such as gradients but also global features including tumor size, shape length, and region length. Although the method achieves higher accuracy compared to other segmentation approaches, it has relatively slower processing speed. This is mainly due to the large number of MRI slices and high pixel resolution that must be processed, along with the high number of iterations required to achieve the desired accuracy.

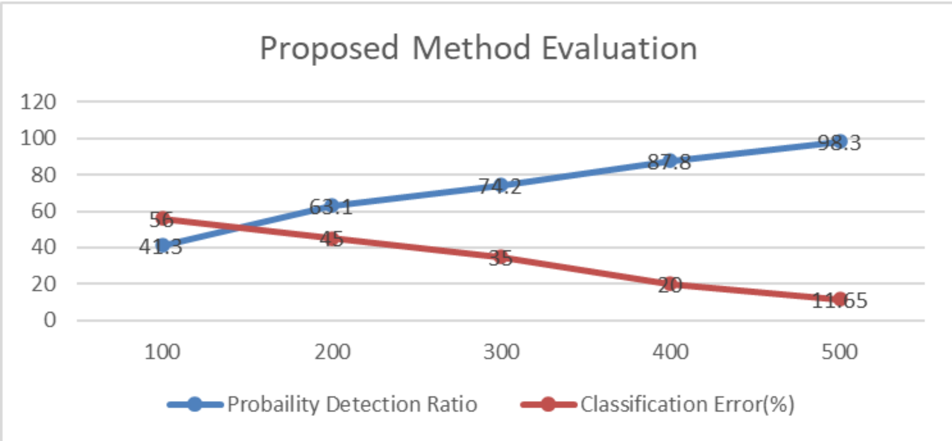

Figure 3. Probability of detection ratio and classification error of proposed method

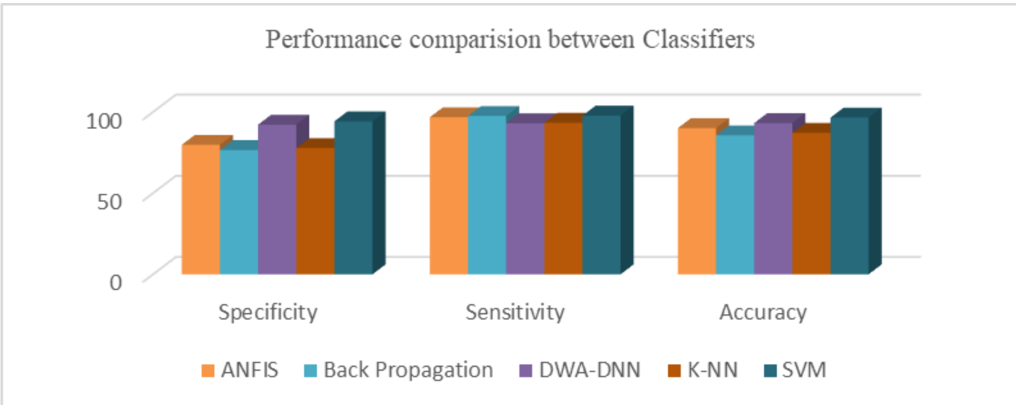

Figure 4: Comparative analysis of different classifiers.

The results obtained using the proposed brain tumor detection technique based on the Berkeley Wavelet Transform (BWT) and Support Vector Machine (SVM) classifier are compared with ANFIS, Back Propagation, DWA-DNN and K-NN classifiers. The comparison is carried out using performance metrics such as sensitivity, specificity, and accuracy. A detailed analysis of these performance measures is presented in Figure 4. The results demonstrate that the proposed methodology significantly improves tumor identification performance compared with ANFIS, Back Propagation, and K-NN based classification techniques.

V. Conclusion

This study proposes an automatic Segmentation and classification using Support Vector Machine for the detection, segmentation and classification of brain tumors from Magnetic Resonance images. The proposed approach integrates image structure hierarchy with statistical classification techniques to accurately identify tumor regions. The segmented tumor areas remain spatially consistent with the image content, thereby providing reliable guidance for the subsequent segmentation process. Experimental results demonstrate that this method achieves high accuracy in detecting and segmenting brain tumors. The system shows improved performance compared with manual detection by radiologists while also reducing processing time. Various performance metrics, including mean, mean square error (MSE), peak signal-to-noise ratio (PSNR), sensitivity, specificity, Dice coefficient, and overall classification accuracy, confirm the effectiveness of the proposed algorithm.

Overall, the proposed approach enables accurate identification of tumor regions and their precise location in MR images. Therefore, this SVM technique can serve as an effective tool for brain tumor detection and can be integrated into clinical decision support systems to assist radiologists and medical professionals in early diagnosis and treatment planning. For future work, the classification accuracy can be further enhanced by exploring hybrid classification models that combine multiple classifiers along with advanced feature selection techniques to improve the robustness and efficiency of the tumor detection system.

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