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AN IMPROVED CANNY EDGE DETECTION FOR SVM-BASED BRAIN TUMOR IMAGE CLASSIFICATION

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Abstract: *This paper proposes an efficient method for automatic detection and classification of brain tumor. The proposed system incorporates a multi-stage processing that includes preprocessing, segmentation, feature extraction, feature selection, and classification. Preprocessing techniques including median filtering and high pass filtering are employed to enhance image quality; the segmentation process involves Canny edge detection and moving average filtering. Feature ex-traction is performed using Convolutional Neural Network (CNN), and feature selection is conducted using Minimum Redundancy Maximum Relevance (mRMR) to ensure optimal feature representation. Support Vector Machine (SVM) trained on datasets of varying sizes is deployed as a classifier. Evaluation results revealed that the proposed method achieved detection and classification accuracy of 95.83%. The proposed method is expected to facilitate early-detection, improve the accuracy in diagnosis of brain tumors, and ultimately make efficient the work of medical practitioners.*

Key words: Support Vector Machine; Segmentation; CNN; Minimal Redundancy Maximum Relevance; MRI Brain Tumor Detection

1 Introduction

The majority of brain tumors are found in humans, and they are classified as either benign or malignant depending on two features. Brain tumors can appear anywhere, show up in varied imaging intensities, and are available in various shapes and sizes. The infamous ailment known as a brain tumor has ruined and impacted many lives. For several decades now, thousands of researchers worldwide have focused their attention on this illness. Scientists have pooled their expertise and resources from a variety of fields, to get a deeper understanding of the illness and develop better therapies (Mithun & Jawhar, 2024). Currently, MRI scan is the foremost means for tumor detection as well as identifying the position and extent of the tumor for surgical procedure. However, the MRI results are traditionally checked by human experts for existence or absence of tumor (Varuna Shree & Kumar, 2018).

Early and correct detection of brain tumor from MRI is crucial to saving patients' lives. Doctors can miss the ab-normality due to human error, and there is dearth of neurologist at many healthcare facilities in the developing nations, which pose another challenge in the detection and treatment of brain tumor cases (Alam et al., 2019).

MRI is an extensively used technique which facilitates the diagnosis and prognosis of brain tumors in many neurological diseases and conditions. Standard MRI sequences are generally used to differentiate between different types of brain tumors based on visual qualities and contrast structure analysis of the soft tissue (Alfonse & Salem, 2016).

MRI brain tumor report generation by experienced and less experienced examiners may be error-prone because it re-quires deep understanding of the disease. Also, for experienced medical professionals, the task is time-consuming and laborious because it takes at least half an hour to ex-amine an image and write their findings (Ayesha et al., 2021). In order to reduce time consumption and stress by Neurologist, a system for automatic brain tumor detection, classification and report generation in MRI images is re-quired.

Image processing techniques are methods commonly used to improve raw images which are received from formats de-pending on the scanner manufacturer. The most common formats for MRI raw image data: include Digital Imaging and Communications in Medicine (DICOM), Neuroimaging Informatics Technology Initiative (NIfTI), and Medical Imaging NetCDF (MINC) etc. The techniques involve transforming images into digital form, and implementing certain actions on them, for the purpose of generating im-proved images or to extract valuable information there from.

This paper aims to develop a machine learning based detection and classification system for brain tumor from MRI images. It will focus on development of an Improved Canny Edge Moving Average Detection (ICEMAD) as a well-defined technique and a better line drawing algorithm, to detect and classify brain tumor. The system will classify tumors into benign or malignant from brain MRI images obtained from diverse sample of patients of different ages, symptoms, and gender. The system will generate an accurate report which can be used by many potential users, such as radiologist and neurologist.

Section 2 of this paper reviews related literature on auto-mated diagnosis from medical images. In section 3, details of the proposed techniques and methodologies are presented. Section 4 presents the results and discussions and the paper conclude in Section 5.

2 Review of Relevant Literature

Over the decades, there have been growing interest in deploying automation in medical procedures, and the area of detection and analysis of medical images is no exception. In their work on an automatic classification of brain tumor through MRI images (Alfonse & Salem, 2016). The Authors proposed a system that consists of number of phases which include dataset acquisition, preprocessing, segmentation using the expectation maximization (EM) algorithm and adaptive threshold, feature extraction from MRI dataset using Fast Fourier Transform (FFT), feature selection using Minimal-Redundancy-Maximal-Relevance criterion (MRMR) to select most valuable features and finally the classification state in which SVM is used for classification of brain images as normal or abnormal where 98.9% accuracy on the collected dataset was recorded. The system provides an efficient solution as compared to other existing approaches. as a future work aimed to increase the size of the dataset by including more patients of different ages, symptoms and gender (Alfonse & Salem, 2016).

Similarly, in a related work (Gurbină, Lascu, & Lascu, 2019) on tumor detection and classification of brain MRI images, a technique that uses three steps was proposed.

1. Preprocessing (de-noising using different wavelets with different thresholds and levels, feature extraction feature reduction),

2. Training the support vector machines, (linear, kernel);

Submitting new MRI brains images (training sets) to the train SVMs and output obtained prediction. The system was implemented using CWT, DWT and SVMs. The high accuracy part is obtained using CWT. The CWT prevents the loss of edges in segmentation. The result shows that SVMs having the proper set of training data are able to distinguish between abnormal and normal tumor regions and classify them correctly as a benign tumor (non-cancerous), malignant tumor (cancerous) or healthy brain. The result indicates that it is better to use CWT if the interest is mainly for visualization, matching and feature detection. However, if one is interested in denoising, compression, restoration, then DWT is often more appropriate (Gurbină et al., 2019).

An autonomous brain segmentation of the MRI images was proposed in (Alam et al., 2019). The System uses three steps for efficient processing of brain tumor detection from MRI images. Those are data preprocessing with DWT, Feature reduction with PCA to reduce over fitting and tumor detection by feature selection process with KSVM. The preprocessed images are passed through SVM to predict the output and identify if tumor exists or not, the process was divided into abnormal regions identification, identified tumor and detected malignant and benign. The approach for the identification of brain tumors from MRI images shows a high rate of accuracy. The technique extracts the tumor section fully. An additional phase, which involves calculating the grey-scale threshold value, binarize the image and getting rid of blobs, ensures the algorithm to deliver a more reliable outcome (Alam et al., 2019).

In another work on detection and classification of brain tumor in MRI images by (Ansari, Mehrotra, & Agrawal, 2020), wavelet and support vector machine were used to put forward an analytical course of action for the recognition of brain tumors. The work focuses on the eradication of noise, features extraction based on grey-level co-occurrence matrix (GLCM) and BT segmentation based. The system classification is done using SVM. The size of image taken is 256x256 in JPG/JPEG format. The SVM classification technique used gives a high precision. Their method provides enhanced results comparatively proficient with 98.91% exactness.

A modified canny edge detection technique for identifying endpoints was proposed in (Kieu, Bade, & Hijazi, 2022). The technique enhances canny edge detection by adding a fifth step. The traditional canny edge detection technique has a total of four steps, namely; Gaussian blurring, intensity gradient calculation, non-maximum suppression and hysteresis thresholding. The fifth step identifies endpoints. Canny edge detection leaves discontinued edges. The step attempts to identify and fix the edges, first by identifying endpoints. This is done by checking the neighbourhood of the surrounding pixels, focusing on pinpointing the edge endpoints, and connecting the endpoints, without employing deep learning. The technique deals with the discontinued edges problem of the traditional canny technique. The problem was solved by the developed algorithm, where a straight line was used to connect the endpoints. Also, the mean square error (MSE) test result of the method was found to be lower than traditional Canny. The authors conclude that the technique works well if the discontinued edges are straight, but a better line drawing algorithm that can draw curves could be developed further because some dis-continued edges are most at times nonlinear (Kieu et al., 2022).

In a similar work of brain tumor detection and classification by MRI images using deep learning techniques (Mangla & Chetna, 2022), the authors proposed implementing a four-phase system that includes: Data Collection and Image Pre-processing, Features Extraction using HOG, Tumor Detection using CNN and Tumor Classification using SVM. An approach based on a combination of the feature extraction algorithm (HOG), CNN, and SVM for tumor identification and classification from brain pictures is provided. The most important aspect of the proposed work was how to use a CNN to detect the presence of a tumor and a HOG to extract features from brain tumor MRI images, followed by a classification method, SVM, to classify brain tumors into benign and malignant. The tumor screenings were divided into two categories: normal and patient. The proportion of sick to healthy subjects was proportionate to the proportion of image categorization in two classes. After pre-processing, the images were fed into the CNN. CNN's accuracy is 87.02 % for appropriately categorizing images into two normal and patient classes. The accuracy of the proposed algorithm increased to 96.35 % on the test data while using the proposed approach of feature extraction and using SVM for categorization into benign and malignant tumors.

As stated above, many different approaches have already been proposed for the detection of the tumor from brain MRI using various techniques, over the last decade. The rapid development of technology leads to new ideas that make improvement on the previous methods. These pre-ceding reports were able to classify tumor into benign, malignant or normal brain, they however call for creation of more dataset for patients across different age groups, symptoms and gender. This will improve the efficiency in the detection and classification of brain tumor. Furthermore, it would address the weakness of edge-based segment such as noise sensitivity, failure to produce boundary of objects and sensitivity of expanding the edges between important regions. This would be done by identifying end-points and connecting the endpoints of tumor for obtaining precise tumor boundary for better classification of the tumor.

3 The Proposed Method

The proposed method consists of a number of phases as depicted in Figure 1. It begins with dataset acquisition of MRI images from across various sources, preprocessing is then applied to standardize the obtained images. Image segmentation is carried-out using Improved Canny Edge Moving Average Detection (ICEMAD) method, feature extraction from MRI dataset using CNN (ResNet-50), feature selection using Minimal-Redundancy-Maximal- Relevance criterion (MRMR) to select most valuable features and finally the classification stage in which SVM is used for classification of tumors in brain images as benign or malignant.

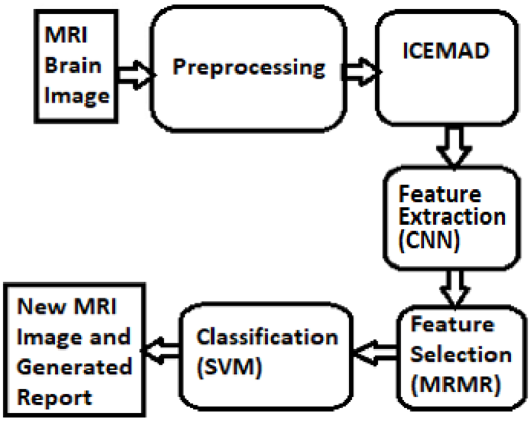


Figure 1: The Architecture of the Proposed System

3.1 Data Acquisition

To develop and test the system, MRI brain images were collected from multiple reliable sources (See Figure 2 for samples), including Radiopaedia, Kaggle, Brain Atlas, and Katsina Orthopaedic Hospital, Katsina State, Nigeria. These sources provided a diverse range of data, ensuring that the dataset was comprehensive and suitable for both training and testing of the system.

Figure 2: Katsina Orthopaedic Hospital MRI Machine

3.1.1 Method of Data Collection

As stated above, the method involves sourcing data from online databases for MRI image dataset as well as onsite collection of MRI data from a clinic in Katsina state, Nige-ria. The online source is downloaded from the following databases.

i. **Radiopaedia (Online):** A collection of MRI scans was accessed from Radiopaedia, a well-known educational platform for radiology images: Radiopaedia. (2024, May 18). This ensured access to high-quality, labelled medical images.

ii. **Kaggle (Online):** The Kaggle platform provided publicly available datasets specifically curated for brain tumor research: Kaggle. (2024, June 24), offering a diverse set of images for both benign and malignant cases.

iii. **Brain Atlas (Online):** Brain Atlas contributed anatomically detailed MRI scans: Harvard Medical School. (2024, June 22). Whole brain atlas, aiding in robust feature extraction and classification tasks.

iv. **Katsina Orthopaedic Hospital (Onsite):** Locally sourced data from Katsina Orthopaedic Hospital included region-specific MRI scans, adding to the dataset's variability and practical applicability.

3.1.2 Dataset Composition

The online dataset were collected from the already mentioned websites by visiting the sites and downloading the available MRI brain tumor images the onsite were also collected by visiting the hospital. The composition is summarized in Table 1.

Table 1: Break and Composition of Acquired MRI Dataset

Aspect	Category/Class Labels	Number
Dataset Size	Online Dataset	204
	Onsite Dataset	35
	Total	239 MRI Scans
Class Labels	Benign Tumors	76 Cases
	Malignant Tumors	163 Cases

i. **Training Set:** One Hundred and Sixty-Seven (167) out of 239 images were used for the training (about 70%) of the MRI images, representing a diverse subset to avoid over fitting.

ii. **Testing Set:** An extensive test was conducted with the remaining 30% of 239 MRI brain tumor im-ages to ensure the system's generalizability and robustness.

3.2 Pre-processing

A total of 239 brain tumor images we gathered came in a variety of shapes, sizes, and orientations. The images were each preprocessed. The preprocessing involves removing of noise and image reconstruction (Sudhakar, Bethanney Janney, Haritha, Juliet Sahaya, & Parvathy, 2017). An im-age is converted from RGB to Greyscale followed by median filtering and high pass filtering to enhance image quality. The median filtering removes noise without blurring and preserves edges so also the high pass filtering which sharpen edges and enhance texture. It is important to conduct pre-processing to remove any unnecessary items from the MRI images. After removing unnecessary artefacts, the image can be processed successfully.
The input image is further enhanced as usually medical images appear inhomogeneous and of poor contrast. In this work, the MRI images are enhanced using median, and high pass filters in order to remove noise and to clean-up the background of the image (Alfonse & Salem, 2016) (see Figures 3 and 4).

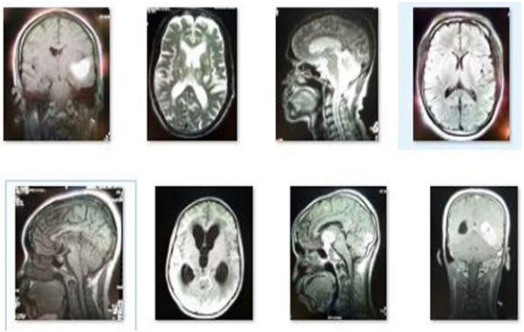
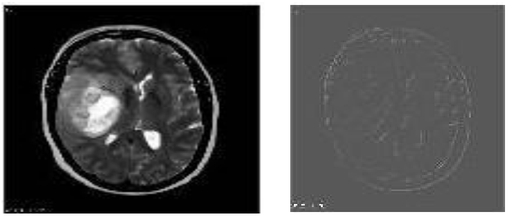


Figure 3: Sample MRI Images collected from Katsina Orthopaedic Hospital

As the name suggests, high pass filter passes high frequencies and attenuates frequencies lower than the cut off frequency. For the noise removal, the cut off frequency was empirically selected, starting with a low initial value typically present in high frequencies.

$$Hhp = 1 - Hlp \quad (1)$$

where Hhp represents the high-pass filter, which allows high frequencies to pass while attenuating frequencies below the cut-off. Hlp is the low-pass filter, allowing low frequencies to pass while attenuating higher ones, with the relationship $Hhp = 1 - Hlp$. The function $Hlp(u,v)$ is defined as 1 if the distance $D(u,v)$, calculated as $\sqrt{(u - u_0)^2 + (v - v_0)^2}$, is less than or equal to the cutoff frequency D_0, and 0 otherwise. Here,u_0 and v_0 represent the center of the frequency domain, $D(u,v)$ is the Euclidean distance from the center, and D_0 is the cut-off frequency that determines the boundary between passed and attenuated frequencies.



(a) Raw MRI image (b) Median filtered

Figure 4: (a & b): Enhanced 4 x 4 square neighbourhood MRI images (Jibo, 2019)

$$Hlp(u,v) = \begin{cases} 1 \ if \ D(u,v) \le D_0 \\ 0 \ if \ D(u,v) > D_0 \end{cases} \quad (2)$$

Input images are converted into greyscale by adjusting contrast and brightness so that images are blurred to eliminate noise. To ensure effective edge detection, noise in the main image was filtered using Gaussian filter [8]. Gaussian filter reduces high-frequency components (like random noise), while keeping the low-frequency parts (like important structures and edges) relatively intact and it is defined by:

$$G(x,y) = \frac{1}{2\pi\sigma^2} exp^{\left(\frac{x^2+y^2}{2\sigma^2}\right)} \quad (3)$$

where y is the distance from the origin in the vertical axis, x is the distance from the origin in the horizontal axis and σ is the standard deviation of the Gaussian distribution σ.

3.3 Segmentation

Segmentation involves partitioning the image into a set of homogeneous and meaningful regions such that pixels be-longing to each region share the same properties or attributes. This process generally rests on the detection of abrupt changes in grey levels, hence enhancing the representation of the lines and edges of an image. The edges, lines, and points detected represent essential ingredients for describing the structure of the image and the objects it contains (Gurbină et al., 2019). Canny edge detection was used in segmentations because it possesses an immunity to noise with low errors and can locate more accurate true edge points. It uses the key approaches in Canny algorithms, including: Gaussian filtering, Intensity Gradient Computation, Non-Maximum Suppression, Double Thresholding and Hysteresis Edge Tracking. Additionally, the Canny algorithm utilizes four filters to calculate edges along diagonal, vertical, and horizontal directions in the blurred image. The edge direction angle is rounded to one of four principal angles 0°, 45°, 90°, and 135° (Sekehravani, Babulak, Foundation, & Masoodi, 2020). To estimate the first derivatives in the vertical and horizontal directions. This process ensures the detection of edges where the intensity of the grey level changes most significantly. By maximizing the signal-to-noise ratio and minimizing false responses to single edges, the Canny method effectively removes noise-corrupted edges and provides a robust solution for edge-based segmentation (Jo, Lee, & Oh, 2019)

3.3.1 Edge Refinement

The sequence of data points characterized as a smooth curve, which roughly follow the expected form, but contain some irregularities in the curve is assumed to have some kind of noise. This noise is removed from the data, so as to obtain a closer representation to the expected smooth curve by using a moving average filter. Its design involves looping through all the points in the signal and averaging the values of successive pairs of points, thereby replacing each pixel with an average of all the values in its neighbourhood.

$$y = \frac{1}{M} \sum_{j=0}^{M-1} x_{i+j} \quad (4)$$

where x is the input signal, y is the output signal, and M is the number of points in the average (Filters, 1999).

3.4 Feature Extraction

Feature extraction and reduction is necessary for image processing to reduce the complexity, data, memory and time. The extracted features are used as the input of image selection. It calculates features on the basis of which image can easily be classified as benign or malignant. The following features are extracted:

- Greyscale
- Texture
- Symmetry

In this paper CNN, a class of deep learning models that finds widespread application in computer vision tasks, is employed for future extraction. CNNs are specifically de-signed to autonomously learn and extract meaningful features from input images. CNNs have innate ability to autonomously learn and extract meaningful features from images and can significantly advance the capacities of computer systems in comprehending and interpreting visual information (Ali et al., 2025).

The Convolutional Neural Network (CNN) employed in this work is based on the ResNet-50 architecture, which is a deep residual learning framework consisting of 50 layers, including convolutional, pooling, fully connected, and shortcut (residual) connections that address the vanishing gradient problem in very deep networks. ResNet-50 integrates convolutional filters of size 7×7 in the initial stage, followed by multiple bottleneck blocks with 1×1, 3×3, and 1×1 convolutions, enabling efficient feature extraction while maintaining computational feasibility.

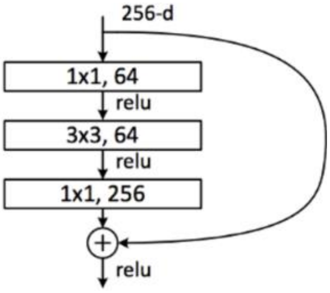


Figure 5: *ResNet50-architecture (He et al., 2016)*

This architecture is widely recognized for its ability to capture hierarchical and discriminative features from complex medical images such as MRI brain scans. In this work, ResNet-50 was used for feature extraction after the pre-processing stage, where an improved Canny edge detection technique was applied to enhance tumor boundary visibility and reduce noise. The extracted deep features were subsequently refined using Minimum Redundancy Maximum Relevance (MRMR) feature selection method, and finally classified using Support Vector Machines (SVM). The com-bination of improved Canny for robust preprocessing and ResNet-50 for deep feature representation significantly enhanced the accuracy and reliability of brain tumor detection and classification.

The ResNet-50 was trained by optimizing the network parameters through back propagation and gradient descent, enabling the network to minimize the disparity between its predictions and the true labels in the training data.

$$(f \times w)[i,j] = \sum_{m,n} f[m,n] \times w[i-m, j-n] \quad (5)$$

As shown in (5), the Convolution layers utilized can be observed as follows. The output value at the position (i, j) after applying convolution to the input data f using the convolutional kernel w is represented as$(f \times w)[i,j]$. The convolution operation involves summing the products of the input data and the corresponding elements of the kernel over the spatial dimensions. This process applies the kernel to the relevant receptive field for each output position.

3.5 Feature Selection

Feature selection is the process of identifying a subset of relevant features (variables or attributes) from a high-dimensional dataset that best serve the purpose of analysis. High-dimensional datasets often contain thou-sands or even tens of thousands of features, many of which may be redundant or irrelevant. The goal of feature selection is to identify a set of features that are most relevant to the analysis of particular events or phenomena.

In this work, the Minimum Redundancy Maximum Relevance (MRMR) (Xie et al., 2022). Algorithm is used. MRMR is a supervised feature selection algorithm that evaluates the relevance of features based on their correlation with the class information while minimizing redundancy among selected features. Maximal relevance and minimal redundancy (MRMR) is a filter feature measurement criterion, which calculates the redundancy between features and the correlation between features and class based on mutual information I(x;y). It selects the features that are most relevant to the category and have the least redundancy with other features from the raw feature set. The mutual information I(x;y) is defined in equation (6)

The mutual information estimation between two given discrete random variables x and y is determined in terms of their individualistic probabilities P(x), P(y) and their joint probability P(x, y), as shown in Equation (Rabiu, Saripan, Mashohor, & Marhaban, 2012).

$$I(x;y) = \sum_{x \in X} \sum_{y \in Y} P(x,y) \, log \frac{P(x,y)}{P(x)P(y)} \quad (6)$$

Where $p(x,y)$ is the joint probability density of random variables x and y, and $p(x)$ and $p(y)$are the marginal probability densities of x and$y$, respectively. Given a sample feature set $S = [f_1, f_2, \dots f_n]$ and a sample class c. The relevance between S and c is the mean of all mutual information between each feature f_1 and class c.

The method combines relevance and redundancy metrics based on mutual information to optimize the selected features. The MRMR method seeks features with maximal relevance $D_{s,c}$ and minimal redundancy R_s, described by the criterion:

$$MRMR = max\left(D_{s,c} - R_s\right) \qquad (7)$$

Steps in the MRMR Algorithm:

Initialization:

- Compute the mutual information $I(X_i;\, C)$between each feature $X_{i1}$and the class label C.
- Initialize the selected feature set S as empty.

Relevance Calculation:

- For each feature X_{i1}, calculate its relevance $D_{S,c}$ to the class label CC using mutual information

$$D_{S,c} = \frac{1}{|S|}\sum_{X_i \in S} I(X_i;\, C) \qquad (8)$$

Redundancy Calculation:

- Compute redundancy RSR_S among the selected features:

$$R_s = \frac{1}{|S|}\sum_{X_i, X_j \in S} I(X_i; X_j) \qquad (9)$$

Selection Criterion:

- At each iteration, add the feature that maximizes the MRMR criterion

Stopping Condition:

- Stop when the desired number of features is selected or the MRMR value does not improve significantly.

By iteratively applying this process, the MRMR algorithm selects an optimal subset of features that are highly relevant to the target class while minimizing redundancy among features. This ensures a compact and informative feature set that improves the accuracy and efficiency of subsequent analysis (Xie et al., 2022).

3.6 Classification using SVM Algorithm

A support vector machine (SVM) is a supervised learning algorithm based on statistical learning theory. In order to classify the input image as benign or malignant, we applied SVM. The SVM is trained using the selected features given as an input. During training, the SVM finds the suitable margins between two classes (Alfonse & Salem, 2016).

A support vector machine is a pattern recognition technique grown up from statistical learning theory. The basic idea of applying SVMs for solving classification problems can be stated briefly as follows:

a) Transforming the input space to higher dimension feature space through a non-linear mapping function.

b) Constructing the separating hyper plane with maximum distance from the closest points of the training set. In the case of linear separable data, the SVM tries to find among all hyper planes that minimize the training error, the one that separates the training data with maximum distance from their closest points (Isselmou, Zhang, & Xu, 2016).

c) Data Used for Training: The training dataset con-sists of MRI images labelled as either benign or malignant, with each image represented by a set of features extracted from the image (e.g., intensity, edges, texture, etc.). These features serve as input to the SVM. The dataset is split into a training set and a test set. The training set contains a majority of the labelled samples, which the SVM uses to learn the decision boundary, while the test set is reserved for evaluating the model's performance on unseen data. Details of the dataset are presented in Table 1.

Given a labelled data set (training set):

$$D = \{x\ data\ sample, y\ class\ label\},$$

an SVM tries to compute a mapping function f such that $f(x) = y$ for all samples in the data set. This mapping function describes the relationship between the data samples and their respective class labels; and is used to classify new unknown data. Classification in the context of SVMs is done using the following classification decision function (a process called the feed-forward phase) (Sudeep, Naidu, Girish, Nikesh, & Sunanda, 2022). Feed-forward process refers to the process of using the trained model to make predictions on new, unseen data.

$$D(z) = sign\left(\sum_{I=1}^{N} \alpha_i\, y_i\, K(z, s_i) + b\right) \qquad (10)$$

where α_i are the alpha coefficients, are the class levels of the support vectors, s_I are support vectors, z is the input vector, $K(z, I)$ is the chosen kernel function, and b is bias.

The training of an SVM involves learning the optimal hyper plane that best separates the two classes (benign and malignant tumors) in the feature space. The process follows these steps:

1. **Preprocessing**
   - First, the MRI images undergo feature extraction and selection (such as using mRMR or Canny edge detection), ensuring that the most relevant features are used for classification.
   - The features are normalized or standardized if necessary, ensuring that all input data is within the same scale for optimal SVM performance.
2. **SVM Model Training**
   - Using the training data (a set of feature vectors with corresponding class labels), the SVM algorithm finds the best hyperplane (or decision boundary) that maximizes the margin between the two classes. This is done by minimizing the classification error and maximizing the distance between the separating hyperplane and the nearest data points from each class, called support vectors.
   - The SVM attempts to find the function $f(x) = y \text{ where } x$ is the feature vector of a sample and y is the corresponding class label (benign or malignant)

4 Results and Discussion

This section discusses the experimental setup, including the dataset formation, preprocessing techniques, and the methodologies used for tumor classification. It also presents comparisons between previous existing works and the proposed method.

4.1 Experimental Setup

A diverse dataset of MRI images was collected from multiple sources. The dataset was categorized into three classes: benign tumors, malignant tumors, and tumor-free images.

The simulation was implemented in MATLAB 2021b, with input images acquired in various formats such as JPEG, PNG, and JPG. As the collected MRI images came in different shapes, sizes, and orientations, the images were re-shaped and converted into greyscale when for RGB images.

4.2 Training and Testing

Moving to the testing phase, One Hundred and Sixty-Seven (167) out of 239 images were used for the training (70%) of the available MRI images.

Testing Set: The test conducted for 30% of 239 MRI brain tumor images yielded a decent performance. The precision of 95.65% means out of all the tumors predicted as malignant 95.65% were actually malignant. The recall of 97.92% shows the model could identify all actual malignant cases. Figures 8 and 9 summarise the performance of the system.

4.3 Results

Original MRI Image: Figure 4a shows the original MRI image, representing the initial input before any preprocessing.

Enhanced MRI Image: Figure 4b displays the result after median filtering, where noise is removed, and the image is smoothed to enhance further processing.

Processed MRI Images: Figures 6 and 7 show the three (3) key stages in the processing of the MRI images:

a) Illustrates the moving average filtered image, where a moving average filter is applied to smooth the image and eliminate noise, enhancing the structural features.

b) Presents the tumor outline, obtained through edge detection techniques, emphasizing the boundaries of the tumor for further analysis.

c) Shows the tumor alone, isolated from the back-ground after segmentation, allowing for focused analysis and accurate classification of the tumor type (benign or malignant).

These stages, from initial image preprocessing to tumor segmentation, collectively enhance the accuracy and reliability of the SVM-based classification system for brain tumor detection.

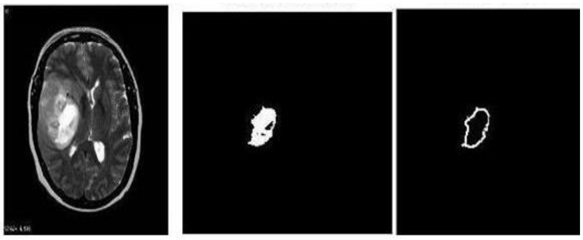

(a) (b) (c)

Figure 6: Malignant Brain Tumor Result (a) Moving Average Filtered (b) Tumor alone (c) Tumor outline


(a) (b) (c)

Figure 7: Benign Brain Tumor: (a) Moving Average Filtered (b) Tumor alone (c) Tumor outline

4.4 Evaluation Metrics

In this study, we employed the accuracy, precision, and recall to assess the performance of Support Vector Ma-chine (Jibon, 2019). The performance evaluation using confusion matrix technique for abnormality classification and brain tumor classification of proposed method are shown in the Table 2.

Table 2: Break and Composition of Acquired MRI Dataset

N = No. of Cases	Target Class Benign Output (0)	Target Class Malignant Output (1)
Non-Tumor Input (0)	True Negative (TN)	False Positive (FP)
Tumor Input (1)	False Negative (FN)	True Positive (TP)

All the performance metrics were computed as follows.

i. **Accuracy:**

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}\ x\,100 \quad (11)$$

If the count of True Positives (TP) and True Negatives (TN) are high then the system depicts high accuracy.

ii. **Recall:** measures the system's ability to correctly classify abnormal/tumor instances as abnormal/ tumor. It is calculated as:

$$Recall = \frac{TP}{TP + FN}\ x\,100 \quad (12)$$

iii. **Precision:** When the system correctly classifies normal/benign as normal/benign then it is called precision and true negative rate is calculated as follows,

$$Precision = \frac{TP}{TP + FP}\ x\,100 \quad (13)$$

iv. **Specificity:** measures how many of the actual negatives the model correctly identified.

$$F1_{score} = \frac{2 \times (Precision \times Recall)}{(Precision + Recall)} \quad (14)$$

These metrics provides a quantitative assessment of the model's competency in classifying instances accurately, enhancing its accuracy and reliability in classifying tumor MRI images.

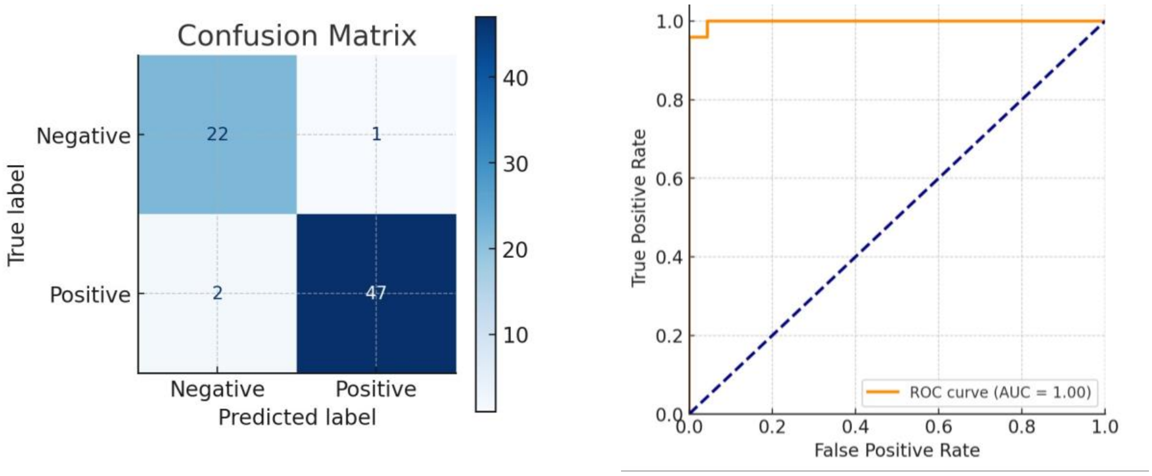
The dataset composition aimed at evaluating the strength of the proposed classification system. Figures: 8 the confusion matrix visualization highlights the minimal number of misclassifications, while the ROC curve (AUC ≈ 0.98) demonstrates excellent discriminative ability between classes. The metric bar chart provides a quick performance snapshot, confirming that the model's predictive power is consistently high across multiple evaluation perspectives. This combination of high precision, high recall, and balanced performance suggests the model is reliable and well-suited for deployment in scenarios where both false positives and false negatives carry significant cost.

Moreover, results from Table 3 show that the model demonstrates strong overall performance across all key classification metrics. The accuracy (95.83%) shows that the majority of predictions are correct, while both precision (97.92%) and recall (95.92%) are high, indicating that the model not only identifies most of the actual positives but also makes very few false positive errors. Other parameters calculated such as specificity (95.65%), NPV (91.67%) confirm that it performs well in recognizing true negatives, though negatives are less common in this dataset. The F1 score (96.91%) reflects an excellent balance between precision and recall, and the Matthews Correlation Coefficient (MCC) of 0.899 shows strong agreement be-tween predictions and actual outcomes even when ac-counting for class distribution.

The results obtained from the diverse and representative dataset, position the proposed classification framework as a promising decision-support tool to augment the expertise of radiologists in the complex task of brain tumor evaluation and diagnosis.

Table 3: Summary of Classification for General Test of Simulated MRI Image.

Number of Training Set (Images)	Benign Images	Malignant Images	No. of cases	TP	TN	FP	FN	Accuracy (%)	Precision (%)	Recall (%)	F1 %
167	76	163	239	47	22	1	2	95.83	97.92	95.92	96.91



(a) (b)

Figure 8: Performance Evaluation: (a) Confusion matrix; (b) ROC curve

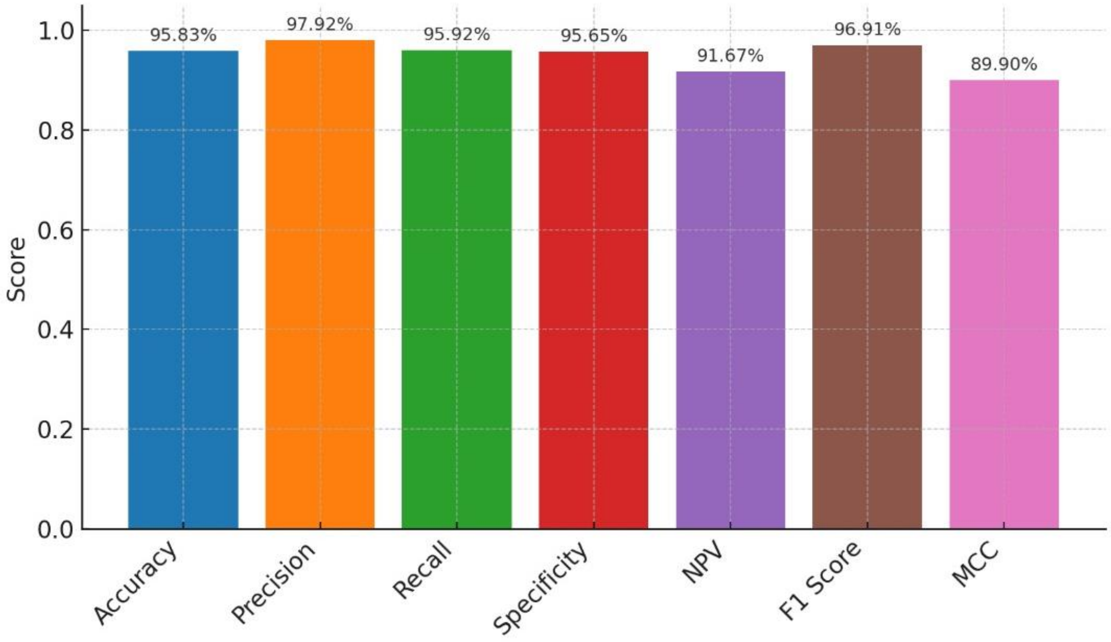


Figure 9: Model performance matrix

4.5 Comparison of Results

Previous research has addressed critical aspects of image analysis and brain tumor classification, yet with notable limitations. One study extended the traditional Canny edge detection algorithm by adding a fifth step to resolve end-point discontinuities; however, its effectiveness was limited to straight edges, failing to handle curved structures commonly present in medical images. Other studies focused on brain tumor segmentation, detection and classification, but lacked demographic diversity, making it less reliable for different types of patients. In contrast, our study presents a more comprehensive solution by enhancing edge detection for both straight and curved boundaries and employing a diverse dataset covering various ages, genders, and symptoms. This comprehensive approach significantly improves segmentation and classification performance, achieving an impressive result of 95.83%, and offering greater clinical relevance and robustness compared to previous works.

The proposed method validates the work in (Kieu et al., 2022). The discontinued edges problem of the traditional Canny technique. See Figures 10 and 11.

But applying moving average filter the endpoints were identified and connected coming up with an edge boundary in Figure 10c and closer representation of smooth tumor boundary in Figure 12a.

Brain tumor detection in MRI images relies heavily on precise boundary detection, which impacts classification accuracy. The results obtained involving various amount of sample images were analysed, which yielded quite an im-pressive result of 95.83%.


(a) Traditional (b) Modified (c) Our Method

Figure 10*(a- c): Canny Edge detection (Kieu et al., 2022)*

Figure 11: *Traditional Canny Method*

The highest accuracy obtained by the previous research is due to selecting dataset which could not have a lot of varieties. Demonstrating that moving average filter leads to better edge continuity, the results from this work have position ICEMAD as an efficient improvement over (Kieu et al., 2022) especially for curved edges.


(a) (b)

Figure 12: *Brain Tumor outline from (a) Canny Edge Detection and (b) Moving Average Filter*

Table 4 shows a comparison between the proposed method and other brain tumour classification techniques.

Table 4: *Comparison of Results*

Author	Methodology	Target	Dataset Used	Accuracy (%)
(Alfonse & Salem, 2016)	FFT + mRMR + SVM	-Automatic Classification using SVM (normal or abnormal)	100	98.9
(Ansari, Mehrotra, & Agrawal, 2020)	DWT +PCA + GLCM + SVM	-Detection and Classification of BT	200	98.91
(Kieu et al., 2022)	GB + IGC + NMS&HT + IEP.	-Improve on discontinued edges	Objects	NA
(Sudhakar, Bethanney Janney, Haritha, Juliet Sahaya, & Parvathy, 2017)	Edge detection (Canny, Robert and Prewitt), segmentation (ROI), GLCM, PNN neural networks	-Automatic Detection and Classification of Brain Tumor	Not Stated	High Accuracy
Proposed Method	ICEMA	-Obtaining Tumor Boundary and Classification	239	95.83

The proposed method validated the work in (Kieu et al., 2022). The discontinued edges problem of the traditional Canny technique by developing a better line drawing algorithm. The highest result obtained by (Ansari, Mehrotra, & Agrawal, 2020) is due to non-inclusion of patients of different ages, symptoms, and gender.

5 Conclusion

In this research, we proposed for an improved Canny Edge Filter using Moving Average for the detection of smoother outlines for better classification of brain tumor in MRI im-ages. The objective was successfully achieved as the system effectively classified brain tumors as benign or malignant with an impressive result of 95.83%. The results demonstrate the potential of the proposed method to significantly improve the reliability and performance of automated brain tumor diagnosis. This performance, achieved on a diverse and representative dataset, position the proposed classification framework as a proficient decision-support tool to extend the expertise of radiologists in the complex task of brain tumor, validation, evaluation and diagnosis.

Although, the proposed improved Canny edge detection (ICEMAD) combined with SVM-based classification achieved high performance on controlled datasets; however, generalizability to low-resolution or noisy MRI data re-mains a challenge. Real-world clinical scans often contain variable contrast, motion artifacts, and reduced spatial resolution, which can distort edge maps and affect SVM decision boundaries. Robustness can be enhanced through preprocessing techniques such as Gaussian smoothing or anisotropic diffusion, resolution normalization, and data augmentation with simulated noise and low-resolution in-puts. In terms of scalability, while the Canny algorithm is computationally efficient, large-scale hospital deployments may require optimized batch or parallel processing and the adoption of linear or approximate SVM variants to handle increased data volumes.

Future work will focus on integrating noise-resilient preprocessing, scalable feature extraction, and adaptive model training strategies to ensure consistent performance across diverse imaging conditions and multi-center datasets. However, the proposed system can be deployed on other forms of binary classification for diseases such as HIV/AIDS, Malaria, Typhoid fever as well as in Forensics.

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