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Enhanced Brain Tumor Classification: A Hybrid Classifier Approach

Abstract: - Early detection of brain tumors is crucial for enhancing patient survival rates and treatment effectiveness. Analyzing magnetic resonance imaging (MRI) images by manually is a difficult task. Therefore, there is a requirement for digital techniques to improve the accuracy of tumor diagnosis. Study of this work was to enhance the performance of Machine Learning classifiers rather than move to deep learning. Machine Learning classifiers are advantageous compared to deep learning methods because of their ability to train on small datasets, low computing time complexity, affordability, and ease of adoption by individuals with less expertise The proposed methodology encompasses image processing, segmentation, feature extraction, feature reduction, and classification, leveraging techniques such as Otsu's thresholding, GLCM, BWT, and PCA to extract pertinent information while minimizing dimensionality. By integrating a hybrid classifier that combines SVM, DT, and KNN, along with ensemble techniques, significant improvements in classification accuracy and robustness are achieved. Experimental results on the TCGA-GBM dataset showcase accuracy of 96.9%, with high specificity (95.14%) and sensitivity (97.14%) for classify normal tumors (benign tumors) and cancerous tumors (malignant tumors). Furthermore, the proposed methodology demonstrates efficiency with relatively low execution time, rendering it suitable for real-world application***s.***

Keywords:SVM,KNN,DT,Otsus,GLCM,BWT.

I. INTRODUCTION

In the year 2023, brain tumors emerged as the tenth most prevalent type of tumor among the Indian population, with over 38,000 cases reported annually, resulting in more than 34,000 fatalities, according to data from the International Association of Cancer Registries (IARC).Magnetic Resonance Imaging (MRI) plays a pivotal role in understanding human anatomy, offering excellent spatial resolution and strong soft tissue contrast without radiation exposure Brain tumors are broadly classified into malignant and benign types. To aid in early diagnosis, an automated system holds promise for analyzing tumor images and pin pointing tumor localization..

Accurate segmentation and classification of brain tumors are crucial for guiding treatment decisions, such as surgical planning, radiation therapy, and chemotherapy. Precise delineation of tumor boundaries helps surgeons remove tumors more effectively while minimizing damage to healthy brain tissue.

In recent times, numerous methods have been presented for the purpose of automatically classifying brain tumors. These approaches can be categorized into two main classes. Machine learning (ML) [1] and deep learning (DL) utilize distinct methods for feature selection and learning. These classifications are based on the selection of features and the learning process. While DL techniques, particularly Convolutional Neural Networks (CNNs), have demonstrated high levels of accuracy and are widely employed in medical image analysis, they come with several limitations compared to traditional ML methods.

One of the key challenges with DL techniques [2] is their heavy reliance on large datasets for training, leading to increased time complexity and computational resources. This poses a significant barrier, especially in scenarios where access to extensive datasets is limited. Furthermore, DL methods often require expensive GPUs for efficient computation, resulting in higher costs for users and healthcare providers. Additionally, the complexity of selecting appropriate DL architectures, along with the need for expertise in optimizing various parameters and training methodologies, further complicates their implementation and adoption in clinical settings.

On the other hand, traditional ML approaches have been widely utilized in medical imaging with notable success. These methods offer advantages such as the ability to perform well with smaller datasets, lower computational requirements, and ease of interpretability. However, despite their effectiveness, there remains a need to explore and develop novel ML techniques [3] that can address the specific challenges posed by brain tumor classification, particularly in scenarios where DL methods [4] may not be feasible or practical. Given these considerations, there is a clear research gap in the development of ML-based approaches for brain tumor classification that can offer comparable accuracy to DL methods while addressing the limitations associated with dataset size, computational complexity, and expertise requirements

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The primary objective of this study is to identify solutions for the challenges associated with restricted datasets, feature extraction, high computational complexity, and accuracy in order to automate the process of brain tumor classification using machine learning.

The major contributions of this article are as follows:

1. Integrating powerful methods Otsu's thresholding, Gray-Level Co-occurrence Matrix (GLCM), Berkeley Wavelet Transform (BWT), and Principal Component Analysis (PCA)—for comprehensive feature extraction and dimensionality reduction.
2. Integrating ML techniques Support Vector Machine (SVM), Decision Tree (DT), and K-Nearest Neighbors (KNN) algorithms into an ensemble approach can harness the unique strengths of each method to achieve improved predictive accuracy.

The subsequent sections of the paper are structured as follows: Section II presents an extensive review of pertinent literature, Section III outlines the methodology employed in this study, Section IV delves into the analysis and discussion of the results, and Section V concludes the paper with final remarks

II. LITERATURE REVIEW

The prevalence of brain tumors in the Indian population, as highlighted in the introduction, underscores the pressing need for accurate and efficient methods for tumor segmentation and classification. In recent years, the field of medical image analysis has witnessed a surge in research efforts aimed at developing automated approaches for brain tumor classification, with a particular emphasis on machine learning (ML) and deep learning (DL) techniques. [5]

DL methods, notably Convolutional Neural Networks (CNNs), have garnered significant attention for their remarkable performance in medical image analysis tasks, including brain tumor classification. Studies such as Akkus et al [6] and Pereira et al. [7] have demonstrated the efficacy of CNN-based models in accurately segmenting and classifying brain tumors from MRI images. However, while DL techniques excel in achieving high levels of accuracy, they often face challenges related to the need for large datasets, computational resources, and complex model architectures.

Conversely, traditional ML approaches [8] offer advantages such as interpretability, reduced computational demands, and performance with smaller datasets. Research by Menze et al. [9] and Cheng et al. [10] has explored the application of ML algorithms, including Support Vector Machine (SVM), Decision Tree (DT), and K-Nearest Neighbors (KNN) [11], in brain tumor classification. These studies have demonstrated the potential of ML techniques to achieve competitive performance with fewer computational requirements and greater interpretability compared to DL methods. [12]

Despite their respective strengths, both DL and ML approaches face challenges that hinder their widespread adoption in clinical settings. DL methods require extensive datasets for training, which may not always be readily available, particularly in the context of rare diseases or specific patient populations. Moreover, DL architectures often lack transparency, making it difficult to interpret model predictions and understand the underlying decision-making process.

On the other hand, while ML techniques offer greater interpretability and efficiency with smaller datasets, they may struggle to capture complex patterns and nuances present in medical images. Additionally, selecting appropriate features for classification and optimizing model parameters remain challenging tasks in traditional ML approaches

To address these challenges and advance the field of brain tumor classification, recent research has focused on integrating ML-based approaches with advanced feature extraction techniques. Methods such as Otsu's thresholding, Gray-Level Co-occurrence Matrix (GLCM), Berkeley Wavelet Transform (BWT), and Principal Component Analysis (PCA) [13] have been proposed for comprehensive feature extraction and dimensionality reduction . By combining these techniques with ML algorithms, researchers aim to enhance classification accuracy while mitigating the limitations associated with dataset size, computational complexity, and expertise requirements.

Overall, while DL techniques [14] have shown promise in achieving high accuracy levels, there remains a need for complementary approaches that offer interpretability, efficiency, and robust performance with limited data. By leveraging advanced feature extraction methods and ML algorithms, researchers can develop hybrid approaches that bridge the gap between DL and traditional ML techniques [15], ultimately advancing the field of brain tumor classification and improving patient outcomes.

III. METHODOLOGY

The proposed methodology for brain tumor classification involves a systematic approach comprising several key steps. Initially, the MRI images of brain tumors undergo thorough image processing and preprocessing to enhance their quality, eliminate noise, and normalize intensity levels. Following this, segmentation techniques are applied to delineate the tumor regions accurately, utilizing methods such as Otsu's thresholdingto define tumor boundaries effectively.Subsequently, feature extraction is conducted to capture pertinent information from the segmented tumor regions. This involves the utilization of Gray-Level Co-occurrence Matrix (GLCM) and BWT..Principal Component Analysis (PCA)[16] is then implemented to reduce the feature space while retaining essential information.The next phase involves the integration of a hybrid classifier, which combines multiple conventional classifiers such as Support Vector Machine (SVM), Decision Tree (DT), and K-Nearest Neighbors (KNN). Ensemble techniques[17] like voting or stacking are explored to leverage the complementary strengths of these classifiers, thereby improving classification accuracy and robustness.

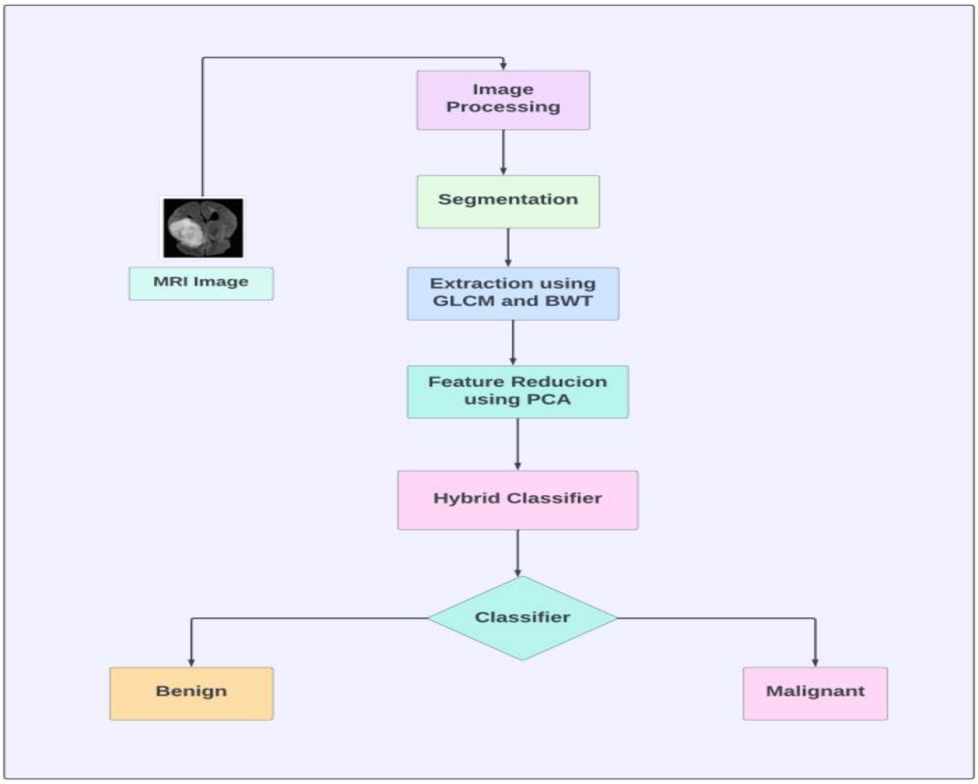


Fig1: Proposed Method

A. Segmentation

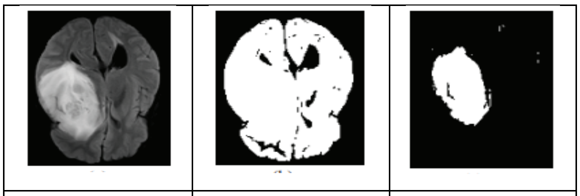
Otsu thresholding:

Using a single threshold value, the Otsu technique automatically divides images into foreground and background categories. By maximizing the variance across classes and decreasing the variance within classes, this threshold is determined. Statistical significance attained by minimizing intra class variance and adding the variances of two classes

$$\sigma_w^2(T) = \omega_1(T)\sigma_1^2(T) + \omega_2(T)\sigma_2^2(T) \qquad (1)$$

Where

The averages of the background class and the foreground class are represented by μ_1(T) and μ_2(T) respectively. The optimal threshold T is then determined by maximizing σ_B^2which typically involves iterating over all possible threshold values and selecting the one that yields the maximum value of σ_B^2. Once the optimal threshold is found, it can be used to convert the input grayscale image into a binary image.



(a)Brain Image (b) Threshold image (c) Image Segmentation

Fig2: Otsu Thresholding

B. Feature Extraction

GLCM (Gray-Level Co-Occurrence Matrix)

In our research, we employed GLCM statistical features [18] to analyze textures present in brain images. By computing GLCM matrices and extracting relevant features

1. Contrast: Measures the local variations in the gray-level co-occurrence matrix.

$$\mathrm{Contrast} = \sum_{i,j} (i - j)^2 \cdot P(i,j) \qquad (2)$$

Where P (i,j) is the probability of co-occurrence of intensity levels i and j.

2. Correlation: Measures the linear dependency between the gray-level co-occurrence matrix and the pixel correlation image.

$$\mathrm{Correlation} = \sum_{i,j} \frac{(i - \mu)(j - \mu) \cdot P(i,j)}{\sigma^2} \qquad (3)$$

Where μ is the mean and σ 2 is the variance of the GLCM.

3. Energy (Angular Second Moment): Represents the sum of squared elements in the GLCM.

$$\mathrm{Energy} = \sum_{i,j} P(i,j)^2 \qquad (4)$$

4. Entropy: Measures the randomness or uncertainty in the GLCM

$$\mathrm{Entropy} = -\sum_{i,j} P(i,j) \log\left(P(i,j)\right) \qquad (5)$$

5. Mean: Represents the average gray-level value of the GLCM

$$\mathrm{Mean} = \sum_{i,j} i \cdot P(i,j) \qquad (6)$$

6. Standard Deviation: Measures the spread or dispersion of the gray-level values in the GLCM.

$$\mathrm{Standard\ Deviation} = \sqrt{\sum_{i,j} (i - \mathrm{Mean})^2 \cdot P(i,j)} \qquad (7)$$

7. Kurtosis: Measures the peakedness or flatness of the gray-level distribution in the GLCM

$$\mathrm{Kurtosis} = \frac{\sum_{i,j} (i - \mathrm{Mean})^4 \cdot P(i,j)}{(\mathrm{Standard\ Deviation})^4} \qquad (8)$$

8. Skewness: Measures the asymmetry of the gray-level distribution in the GLCM

$$\mathrm{Skewness} = \frac{\sum_{i,j} (i - \mathrm{Mean})^3 \cdot P(i,j)}{(\mathrm{Standard\ Deviation})^3} \qquad (9)$$

BWT (Berkeley Wavelet Transformation):

We employed the Berkeley Wavelet Transform (BWT) to analyze the preprocessed brain images in our research. Specifically designed for two-dimensional images, the BWT is a triadic wavelet transform that facilitates the decomposition of spatial data into the temporal frequency domain. This transformation is particularly well-suited for image analysis tasks due to its ability to capture both spatial and frequency information simultaneously β_θ^φ

$$\beta_{s,\tau}(x,y) = \beta(x - s, y - s) - \varphi_\theta(x,y) \qquad (10)$$

Where $\beta_{s,T}(x,y)$represents the substitute wavelet at position (x, y) with scale s and translation τ $\beta(x - s, y - s)$ is a mother wavelet,$\varphi_\theta(x,y)$ is another wavelet

The wavelet transformation's scale parameter is s and its translation parameter is τ.

C. Feature Reduction

Principal Component Analysis (PCA):

To reduce the dimensionality of the high-dimensional feature vectors while retaining as much data variance as possible, we employed principal component analysis (PCA) [19]. This involved computing the covariance matrix of the dataset and conducting eigen value decomposition. The resulting eigenvectors represent the principal components of the data, capturing the directions of maximum variance in the original feature space. These principal components serve as new, lower-dimensional representations of the original data, allowing us to effectively summarize and retain the most significant information from the original feature set.

Mean of the dataset $\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i$

Co variance Matrix C== $\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})\ (x_i - \bar{x})^2$

Eigen value decomposition of the covariance matrix: C $v_k=\lambda_k v_k$

Support Vector Machine (SVM)

SVMs aim to find the hyper plane that best separates the classes in the feature space, maximizing the margin between them. By finding this optimal hyper plane, SVMs [20]can effectively classify data points into different categories with high accuracy

We are given a training dataset of n points of the form(x_1, y_1) … … … (x_n, y_n)

$$w^T\ x - b = 0$$

Wherew^T is the normal vector to the hyper plane,The parameter $\frac{b}{||w||}$determines the offset of the hyperplane from the origin along the normal vector w

$$w^T\ x - b \geq 1 \text{ if } \ y_i = 1$$

$$w^T\ x - b \leq 1 \text{ if } \ y_i = -1$$

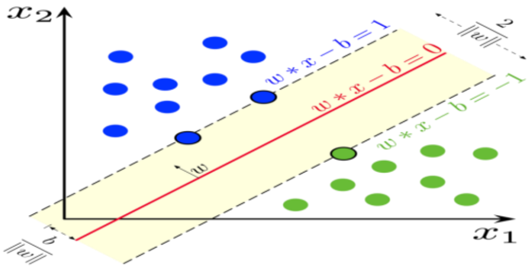


Fig3: SVM Hyperplane

Decision Tree:

A Decision Tree T[21] forms a directed acyclic graph consisting of nodes and edges. Each branch in the tree represents a potential outcome of a decision rule based on a feature f, such as split(n) indicating a decision rule. In the feature space X, with possible class labels or target values represented by Y, a leaf node l in the tree corresponds to a region $R_l$in X, and is associated with a prediction $y_l$in Y.

Each decision rule split(n) at node n is defined as a binary split on a feature f, where $f\in F$is a feature and θ is a threshold:

$$split(n)=\{x\epsilon X:x_f\leq\theta\}$$

$\{x\epsilon X:x_f>\theta\}$

Here, xf denotes the value of feature f for instance x and θ is a threshold value.

At each node n, the splitting criterion Impurity(n) measures the impurity of the data in the region defined by the node.

For classification: $Impurity(n)=\sum_{c\in Y}p(c|n)\ (1-p(c|n))$

Where $p(c|n)$is the proportion of instances of class c in the region defined by node n, and $\bar{y}n$ is the mean target value in the region.

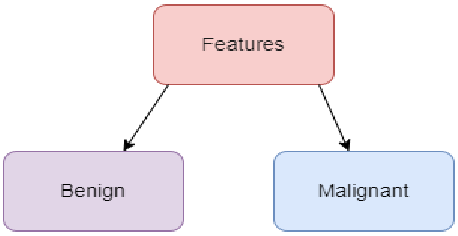


Fig4: DT classification

K-Nearest Neighbor

KNN[22] sorts items into categories based on their distance from other samples. It measures the distance using the Euclidean distance, which is a straightforward and efficient approach. Essentially, when a new data point needs to be classified, KNN looks[23] at the labels of its nearest neighbors and assigns the majority label to the new point. This makes KNN[24][25] easy to understand and implement, yet effective in many classification tasks

$$(x_{i,}y_i) = \sqrt{\sum_{i=1}^{n}(x_i - y_i)^2}$$

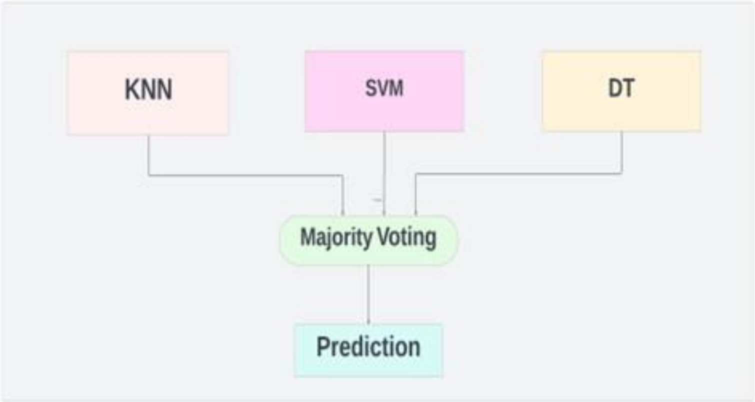


Fig5:Propsed Method classification

Algorithm for proposed framework

```
mod1 ← SVM
mod2 ← KNN
mod3 ← DT
P1 ← Predict from mod1
P2 ← Predict from mod2
P3 ← Predict from mod3
r ← 0
l ← 0
if p1 is "Malignant" then
    r ← r+1
else
    l ← l+1
end
if p2 is "Malignant" then
    r ← r+1
else
    l ← l+1
end
if p3 is "Malignant" then
    r ← r+1
```

```
    else
        $l \leftarrow l+1$
    end
    if $r >= l$ then
        $species \leftarrow$ "Malignant"
    else
        $species \leftarrow$ "Benign"
    end
```

IV. RESULT AND DISCUSSION

A. Dataset Description

The experimental computation of the proposed method is carried out using data gathering from the Cancer Genome Atlas Glioblastoma Multi-forme (TCGA-GBM) data portal [26]

B.Confusion Matrix

Proposed Method confusion matrix is shown in fig. The predicted values are represented on the X-axis, while the actual values are depicted on the Y-axis. The confusion matrix consists of four elements: TN, FP, TP, and FN.[27,28,29]

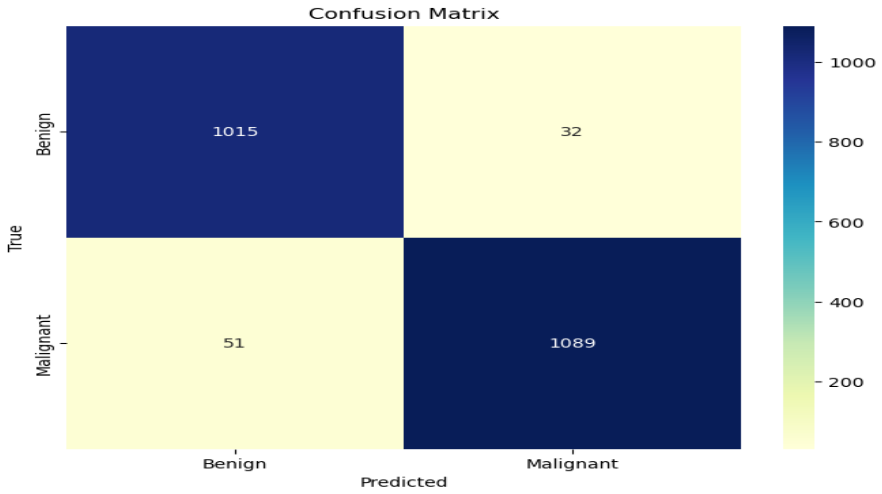


Fig6:Confusion Matrix

C.*Efficiency for the Proposed Methodology*

The experimental results of proposed model as follows

Confusion Matrix

Table1:Efficiency of Proposed Model

Accuracy	96.9%
Specificity	95.14%
Sensitivity	97.14%

Fig7:Efficiency of Proposed Model

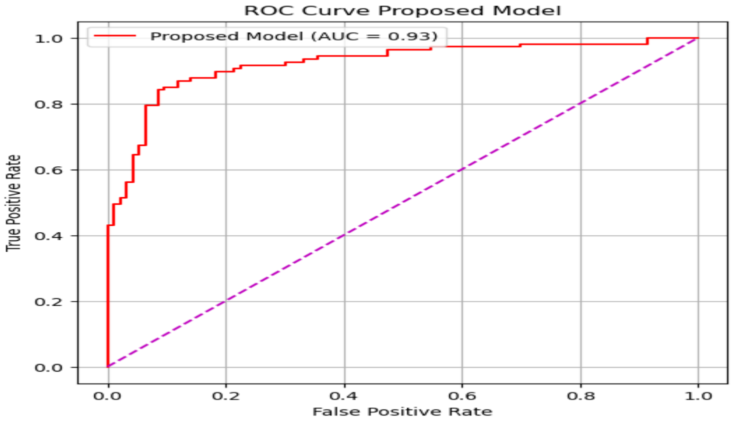


Fig8: ROC Curve of Propsed Model

D.*System Requirements and Execution Time*

The entire implementation of the proposed work is done in Google Colabrun on 13th Gen Intel® Evo™ platform Powered by Intel® Core™ i7 processor, 16GB LPDDR5. One of the most crucial metrics for evaluating a system's efficiency is its execution time. Decomposition takes 0.254 seconds, feature extraction and reduction 0.091 seconds, and classification 0.225 seconds. A total of 0.57 seconds is required for execution, which is significantly less time than human detection.

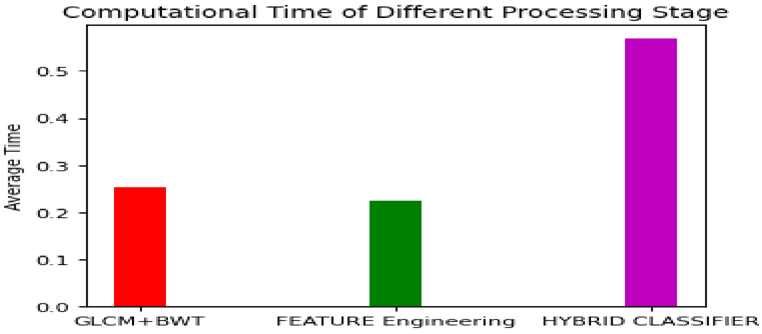


Fig9:Computational Time of Propsed Model

E.GLCM features

Table2.1: Image Features

Image	Contrast	Correlation	Energy	Mean
Image1	0.3301	0.1039	0.7992	0.0035
Image2	0.2375	0.0490	0.7236	0.0034
Image3	0.2339	0.1071	0.7210	0.0048
Image4	0.2417	0.0634	0.7202	0.0039

Image5	0.3101	0.1045	0.7980	0.0036
Image6	0.3469	0.1248	0.8230	0.0051
Image7	0.2458	0.1639	0.7910	0.0025
Image8	0.2321	0.1080	0.7288	0.0035

Table2.2: Image Features

Image	SD	Entropy	Kurtosis	Skewnes
Image1	0.0869	3.4392	7.8989	1.4789
Image2	0.0869	3.4296	9.0165	0.5487
Image3	0.0869	3.5484	9.5230	0.6204
Image4	0.0870	3.5339	9.5110	0.4889
Image5	0.0869	2.4195	8.4237	1.2638
Image6	0.0870	2.0789	9.1237	0.5839
Image7	0.0869	3.2625	8.1367	1.4702
Image8	0.0870	3.2096	9.3026	0.6523

E.Feature Reduction

When classifying MRI images using features extracted from GLCM (Gray Level Co-occurrence Matrix) and BWT (Block-wise Texture), there's a need to balance between processing time, feature count, and classification accuracy. Lowering the number of features can expedite processing, but it may also diminish accuracy. Hence, it's crucial to strike a balance between the number of features, processing time, and the desired level of accuracy to optimize the classification process effectively

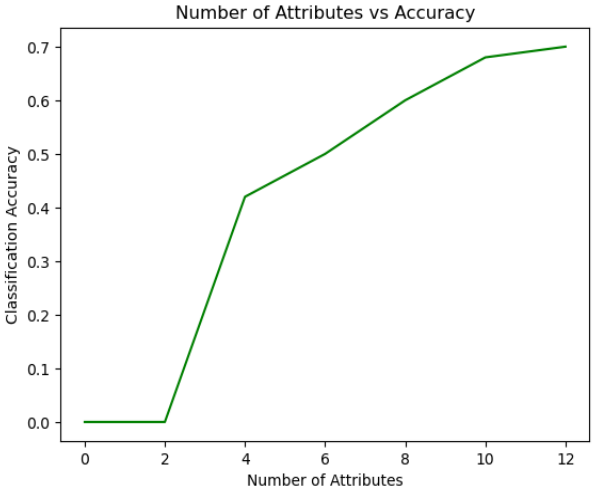


Fig10: Accuracy vs Attributes

F.Comparative Analysis

The table presents the results of the proposed model alongside other machine learning algorithms. The proposed model demonstrates a significant enhancement in classifier accuracy compared to alternative ML models.[30,31]

Table3: Classifier Parameters

Classifier	Accuracy %	Specificity %	Sensitivity %
Proposed Approach	96.9%	95.14	97.14
Naïve Bayes	81.35%	81.85	80.83
DT	93.17%	93.51	92.80
KNN	94.75%	92.76	94.30

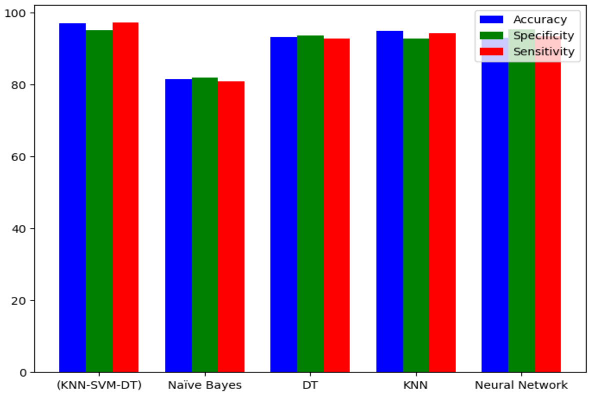


Fig11:Comparision of Various ML models

V. CONCLUSION

This paper introduces a novel binary classification model tailored for brain MRI images, aiming to reduce dimensionality and enhance accuracy. The proposed approach involves image processing, segmentation, feature extraction, feature reduction, and classification, utilizing techniques like Otsu's thresholding, GLCM, BWT, and PCA to extract relevant information while minimizing dimensionality. By integrating a hybrid classifier combining SVM, DT, and KNN, along with ensemble techniques, we achieve significant improvements in classification accuracy and robustness. Experimental results on the TCGA-GBM dataset demonstrate an accuracy of 96.9%, with high specificity (95.14%) and sensitivity (97.14%). Additionally, the proposed methodology exhibits efficiency with relatively low execution time, making it practical for real-world applications. Overall, our work contributes to advancing medical image analysis techniques, providing a valuable tool for early diagnosis and treatment planning in neuro-oncology

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