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Multiclass Classification of Brain MRI through DWT and GLCM Feature Extraction with Various Machine Learning Algorithms

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Abstract—This study delves into the domain of medical diagnostics, focusing on the crucial task of accurately classifying brain tumors to facilitate informed clinical decisions and optimize patient outcomes. Employing a diverse ensemble of machine learning algorithms, the paper addresses the challenge of multiclass brain tumor classification. The investigation centers around the utilization of two distinct datasets: the Brats dataset, encompassing cases of High-Grade Glioma (HGG) and Low-Grade Glioma (LGG), and the Sartaj dataset, comprising instances of Glioma, Meningioma, and No Tumor. Through the strategic deployment of Discrete Wavelet Transform (DWT) and Gray-Level Co-occurrence Matrix (GLCM) features, coupled with the implementation of Support Vector Machines (SVM), k-nearest Neighbors (KNN), Decision Trees (DT), Random Forest, and Gradient Boosting algorithms, the research endeavors to comprehensively explore avenues for achieving precise tumor classification. Preceding the classification process, the datasets undergo pre-processing and the extraction of salient features through DWT-derived frequency-domain characteristics and texture insights harnessed from GLCM. Subsequently, a detailed exposition of the selected algorithms is provided and elucidates the pertinent hyperparameters. The study's outcomes unveil noteworthy performance disparities across diverse algorithms and datasets. SVM and Random Forest algorithms exhibit commendable accuracy rates on the Brats dataset, while the Gradient Boosting algorithm demonstrates superior performance on the Sartaj dataset. The evaluation process encompasses precision, recall, and F1-score metrics, thereby providing a comprehensive assessment of the classification prowess of the employed algorithms.

Keywords—Brain tumor classification, multiclass classification, machine learning algorithms, Discrete Wavelet Transform (DWT), Gray-Level Co-occurrence Matrix (GLCM), SVM, KNN, DT, Random Forest, Gradient Boosting.

I. INTRODUCTION

In modern medical diagnostics, magnetic resonance imaging (MRI) is a cornerstone for the non-invasive assessment and characterization of brain abnormalities. Brain tumors, a critical subset of neurological disorders, require an accurate and timely classification for effective treatment planning and patient care. The ability to discern between various tumor types and healthy brain tissues from MRI scans holds immense promise in improving clinical outcomes. However, due to the intricate nature of brain tumors with their diverse shapes, sizes, and locations, reliable classification through manual analysis is challenging and time-consuming. This is where machine learning emerges as a formidable ally, capable of swiftly and accurately categorizing complex MRI data.

This paper presents a comprehensive study on the multiclass classification of brain MRI scans using state-of-the-art machine learning algorithms. The fundamental objective is to leverage advanced computational techniques to distinguish between High-Grade Glioma (HGG) and Low-Grade Glioma (LGG) using the BRATS dataset and to classify further Glioma, Meningioma, and No Tumor cases utilizing the Sartaj dataset. The motivation behind this study is rooted in the urgent need for precise, automated tools that aid medical practitioners in making informed decisions for brain tumor management.

The complexity of brain tumor classification and the inherent variability of MRI scans necessitates extracting highly relevant features for accurate discrimination. In this pursuit, we employ the Discrete Wavelet Transform (DWT) to capture frequency and texture information and the Grey-Level Co-occurrence Matrix (GLCM) to quantify spatial relationships within images. These extracted features serve as crucial input for various machine-learning algorithms that underpin our classification framework.

Our approach encompasses a suite of established machine learning algorithms, including Support Vector Machine (SVM), k-nearest Neighbors (KNN), Decision Tree (DT), Random Forest (RF), and Gradient Boosting (GB). Each algorithm is tailored to the unique challenges of multiclass brain tumor classification, offering a diverse ensemble of techniques to address different nuances the data presents.

This paper presents a comprehensive and systematic methodology for brain MRI classification by combining advanced feature extraction methods and powerful machine learning algorithms. Our study contributes to the medical imaging and diagnosis field and provides a blueprint for bridging the gap between cutting-edge technology and real-world healthcare challenges.

The subsequent sections of this paper delve into the detailed methodology, experimental results, and insightful discussions that demonstrate the efficacy of our approach. As the boundaries between medical science and computational technology continue to blur, this research's findings can potentially transform the landscape of brain tumor diagnosis and treatment.

This research significantly contributes to medical imaging and machine learning by presenting a comprehensive framework for the multiclass classification of brain MRI scans. Through the application of advanced feature extraction techniques, namely the DWT and GLCM, and the utilization of a diverse set of machine learning algorithms, including SVM, KNN, DT, RF, and GB, this study not only advances the automation of brain tumor classification but also establishes a benchmark for algorithmic performance. This research can revolutionize brain tumor diagnostics by bridging the gap between medical diagnosis and computational methodologies, aiding medical professionals in timely and accurate decision-making for improved patient care.

II. LITERATURE SURVEY

Machine learning (ML) and deep learning (DL) algorithms have recently been used to detect and evaluate brain tumors in various imaging modalities, especially those collected using MRI. This section contains any related studies and the most recent research on the subject of the publication.

Deep learning (DL) techniques and DWT characteristics have been combined in Mohsen, Heba et al.[1] proposed system for learning. The fuzzy c-mean method was applied in order to perform the segmentation of the brain tumor. The discrete wavelet transform (DWT) was used to each and every identified lesion in order to extract features, which were then entered into the principal component analysis (PCA) in order to reduce the feature dimension. At last, the selected characteristics were introduced into deep neural networks (DNN). According to the numbers, their rate of accuracy is 96.97 percent, and their sensitivity is 97%.

Seetha J. et al. [3] proposed a deep convolutional neural network (CNN)-based technique for automatically classifying brain cancers. The Fuzzy C-Means (FCM) algorithm is the basis for the system's approach to segmenting the brain. The information on texture and form that was retrieved from these segmented regions was sent to classifiers using both SVM and DNN. Based on the findings, it was determined that the method had an accuracy level of 97.5%.

Cheng, Jun et al. [4] improved the classification strategy for brain cancers by using fine ring-form division in conjunction with region-of-interest (ROI) augmentation. These improvements were made to the bag-of-words (BoW), generalized linear classification model (GLCM), and intensity histogram feature extraction approaches. These techniques supply the classifier with feature vectors. According to the results of the experiments, the accuracy of the intensity histogram, GLCM, and BoW all increased from 71.39% to 78.18%, 83.54% to 87.54%, and 89.72% to 91.28%, respectively. .

The genetic technique of feature selection for the dimension reduction of a set of wavelet features was presented by M. Sasikala et al. [5]. The method involves picking the best possible features vector to feed into a particular classifier, such as an artificial neural network. This is done in order to achieve the best possible results (ANN). According to the findings, the genetic algorithm chose only 4 of the 29 features and used those features exclusively in order to attain an accuracy rate of 98%.

Khawaldeh, Saed et al. [6] suggested a method for the non-invasive classification of glioma brain tumors by making use of a modified version of the AlexNet CNN algorithm. The classification method made use of whole-brain MRI scans, and the labels that were put to the pictures were applied at the level of the entire image as opposed to the level of individual pixels. The results of the testing indicate that the procedure obtained a respectable degree of accuracy, which was determined to be 91.16%.

Sajjad, Muhammad et al. [7] proposed a complete data augmentation method that may be used in conjunction with CNN to classify brain cancers. When classifying brain cancers into their many subtypes, it is helpful to make use of segmented MRI images of the patient's tumor. They used a pre-trained VGG-19 CNN architecture for categorization using transferee learning, and they obtained an overall accuracy of 87.38% for data before augmentation and 90.67% for data after augmentation. This was accomplished by obtaining a higher accuracy score for the data after augmentation.

Ozyurt, Fatih et al. [8] diagnose brain tumors using a method that combines CNN with neutrosophic expert maximum fuzzy (NS-CNN) specific entropy. In order to segment the brain tumor, the neutrosophic set-expert maximum fuzzy-sure method was applied. After that, the images were placed into a CNN to have their properties extracted, and then they were given to SVM classifiers to determine whether or not the lesions were benign

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or malignant. They had an overall success rate that was 95.62% on average.

Sakshi Ahuja et al. [9] utilized transfer learning and the superpixel method to detect and segment brain tumors. The model was trained using the VGG 19 transfer learning method, with data from the BRATS 2019 brain tumor segmentation competition. The superpixel technique divided the tumor into LGG and HGG images. Consequently, the average dice index was 0.934, which differed from the actual data.

In their work to segment medical images, Hajar Cherguif et al. [10] made use of U-Net. A sophisticated 2D segmentation network was successfully developed by employing the U-Net design. We put the suggested model through its paces by using the BRATS 2017 data set for our testing and analysis. The new U-Net that has been proposed has a total of 27 convolutional layers, 4 deconvolutional layers, and a Dice coefficient value of 0.81.

Deep learning strategies were utilized by Chirodip Lodh Choudhury et al. [11] in order to get reliable findings from MRI scans. These strategies included the usage of deep neural networks and a model of a convolutional neural network. It was suggested that a three-layer CNN architecture may be connected to a neural network that included full connectivity. Accuracy of 97.33% and 96.05%, respectively, were obtained using the F-score system.

Ahmad Habbie et al. [12] investigated the possibility of a brain tumor by employing a semi-automatic segmentation of MRI T1-weighted images in conjunction with an active contour model. The effectiveness of snake active contours, morphological geodesic active contours, and both morphological active contours with and without edges were investigated and studied. According to the statistics, MGAC performed the most successfully out of the three.

Neelum et al. [13] used a concatenation strategy for the deep learning model in their study to determine the likelihood of developing a brain tumor. Both the discovery and categorization of brain tumors were accomplished through the utilization of two pre-trained deep learning models: Inception-v3 and DenseNet201. The Inception-v3 model was pre-trained to classify tumors in order to extract the characteristics that distinguish them from one another. The classification procedure was finished off by a softmax classifier after that.

Hybrid classifiers were utilized by Ms. Swati Jayade et al [14]. Malignant tumors were categorized separately from benign tumors by pathologists. This research utilized the Gray level Co-occurrence Matrix (GLCM) technique for the purpose of extracting features in order to build the feature dataset. It was suggested that increasing productivity may be accomplished by the use of a hybrid approach to classifiers that included KNN and SVM classifiers.

In the research carried out by Zheshu Jia et al. [15], a fully automatic heterogeneous segmentation was constructed with the use of SVM. For the purpose of training and testing the accuracy of cancer identification in MRI images, a probabilistic neural network classification system was utilized as a classification technique. The model for this work focused on automatically segmenting meningiomas utilizing a multispectral brain dataset as its primary data source.

The Gabor transform, soft and hard clustering, and a technique developed by Drs. Akey Sungheetha et al. [16] were applied in this process in order to locate edges in CT and MRI scans. It was determined that a total of 4,500 MRI scans and 3,000 CT pictures were necessary. K-means clustering was utilized to identify distinct subgroupings based on shared traits. The author provided the images in the form of histogram properties by employing fuzzy-c methods.

Capsule networks and the Bayesian method were utilized by Parnian Afshar et al. [17] in order to classify brain cancers. A capsule network was utilized to improve the accuracy of tumor diagnosis rather than a CNN, which can lead to the loss of important spatial information. CNN is commonly employed to analyze medical images. The BayesCap framework came highly recommended by the group. They evaluated the proposed technique using a standard dataset consisting of patients with brain tumors.

III. FEATURE EXTRACTION TECHNIQUES

This approach extracts the features using DWT and GLCM. Each feature extraction technique is present in this section.

A. DWT

The DWT is a potent signal-processing algorithm that decomposes data or pictures into several frequency components. DWT is frequently used for feature extraction in picture analysis, revealing information about textures, patterns, and other characteristics that may be important for classification tasks such as brain MRI analysis.

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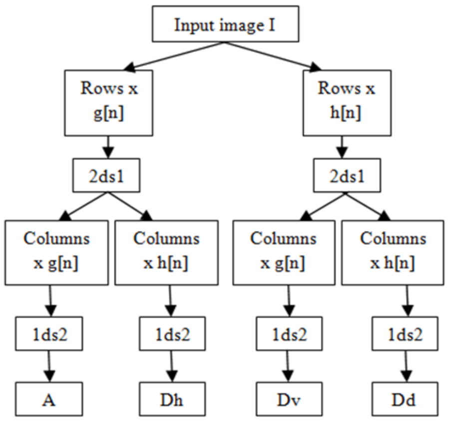

Fig. 1. 2-D DWT Decomposition

The suggested technique uses discrete 2-D wavelet transformations to derive texture features from the region of interest-containing image segment. DWT account for the frequency and unique information of a signal. This property is beneficial for precise texture feature extraction. Information about a signal can be stored using 2-D DWT with fewer coefficients. When processing images, DWT preserves the image as a two-dimensional signal with columns and rows. Wavelet transformations study an image's finer features, such as its horizontal, vertical, and diagonal subbands. Figure 1 depicts the application of 2-D DWT for picture decomposition.

Fig. 1 displays the input image, a high pass filter (h[n]), and a low pass filter (g[n]). When rows are downsampled by 1 and columns by 2, rows are downsampled by 2 and columns by 1. (or 2ds1). This work's key findings are immediately at level one. An approximation coefficient is represented by A. Dh, a vertical coefficient by Dv, and a diagonal coefficient by Dd denotes a horizontal coefficient.

- **Max Value (MaxCoeff):** For each level of DWT decomposition, calculate the maximum value of the detail coefficients. This represents the most prominent feature in that frequency band.

$$MaxCoeff = max(|D_1|, |D_2|, \ldots, |D_n|) \qquad (1)$$

Where $|D_1|$ represents the absolute values of the detail coefficients at level i.

- **Min Value (MinCoeff):** Calculate the minimum value of the detail coefficients for each level. This captures the least prominent feature in that frequency band.

$$MinCoeff = min(|D_1|, |D_2|, \ldots, |D_n|) \qquad (2)$$

- **Mean Value (MeanCoeff):** Calculate the mean value of the detail coefficients for each level. This represents the central tendency of the image features at different scales.

$$MeanCoeff = \frac{|D_1| + |D_2| + \ldots + |D_n|}{N} \qquad (3)$$

- **Standard Deviation (StdDevCoeff):** Calculate the standard deviation of the detail coefficients for each level. This measures the variability of the image features at different scales.

$$\text{StdDevCoeff} = \sqrt{\frac{\sum D_i - \mu}{N}} \qquad (4)$$

Where μ is the mean value of the samples, and N is the total number of pixels.

- **Skewness (SkewnessCoeff):** Skewness is a measure of the asymmetry of the probability distribution of a real-valued random variable. It indicates how much the data is skewed to the left or right.

$$\text{Skewness} = \sqrt{\frac{\sum_{i=1}^{n} (D_i - \mu_i)^3}{(N-1)\text{StdDevCoeff}^3}} \qquad (5)$$

Where μ is the mean value of the samples, and N is the total number of pixels.

B. GLCM

The texture is the surface's quality. It is defined by the geographical distribution of grey levels in a neighborhood. Texture displays its characteristics through pixel placements and pixel values. Hence, there are numerous ways to classify textures. Texture is affected by the scale or resolution at which an image is displayed. A texture having unique features on a small scale can become uniform when exhibited at a larger scale.

In statistical texture analysis, the distribution of pixel intensities at a particular place conveys texture qualities. Based on the number of pixels or dots in each combination, it generates first-order, second-order, and higher-order statistics. An image can be evaluated as a texture using second-order statistics for feature extraction based on GLCM.

The GLCM table displays the frequency of a given combination of pixel brightness values inside an image. As depicted in Figure 2, the GLCM of a four-level image is calculated at a distance of 1 and a direction of 0°.

0	0	1	1	1
0	0	1	1	1
0	2	2	2	2
2	2	3	3	3
2	2	3	3	3

(a)

	0	1	2	3
0	2	2	1	0
1	0	4	0	0
2	0	0	5	2
3	0	0	0	4

(b)

Fig. 2. Example of an image with 4 grey level image b. GLCM for distance 1 and direction 0°.

The statistical data in a picture are known as features. GLCM is a method for extracting unique features from grayscale images.

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Using the provided procedure, the subsequent GLCM characteristics are obtained.

- **Contrast:** The local differences in the GLCM are measured using contrast.

$$Contrast = \sum_{i,j} |i-j|^2 p(i,j) \quad (6)$$

- **Homogeneity:** Homogeneity is measured by the closeness of the element distribution in GLCM to the GLCM diagonals.

$$Homogeneity = \sum_{i,j} \frac{1}{1+(i-j)^2} p(i,j) \quad (7)$$

- **Energy:** It measures the uniformity among the pixels.

$$Energy = \sum_{i,j} p(i,j)^2 \quad (8)$$

- **Dissimilarity:** Dissimilarity is a metric that describes how different grey-level pairings in an image vary.

$$Dissimilarity = \sum_{i,j} |i-j| p(i,j) \quad (9)$$

Where, $p(i,j)$ = image pixel to be processed

- **ASM:** It represents the uniformity of the image's grey-level distribution.

$$ASM = \sum_{i=1}^{G} \sum_{i=1}^{G} (P(i,j))^2 \quad (10)$$

IV. MACHINE LEARNING ALGORITHMS

In the proposed approach, three distinguished deep learning algorithms are used. This section presents a detailed explanation of SVM, KNN, Decision Tree, Random Forest, and Random Forest algorithm.

A. SVM

SVM is a potent and widely deployed machine learning technique frequently applied to classification and regression applications. Due to its effectiveness with complicated datasets, it is a popular choice for various applications, including image classification, text categorization, and medical diagnostics, such as brain MRI classification. Finding the ideal hyperplane that best separates data points of distinct classes in a high-dimensional space is the primary function of SVM. This hyperplane optimizes the difference between classes, increasing generalization and performance on unseen data.

In a binary classification scenario, the SVM seeks a hyperplane that most effectively divides the data points of two classes. The margin is the distance between the hyperplane and each class's closest data point. SVM attempts to optimize this margin to improve the classification precision of new data.

SVM can apply the kernel approach when data are not linearly separable in the original feature space. Kernels permit SVM to implicitly map the data into a higher-dimensional space where separation may be possible. Linear, polynomial, radial basis function (RBF), and sigmoid are typical kernel functions.

The regularisation parameter C strikes a balance between maximization of margin and minimization of classification error on training data. A minor C permits a more significant margin but may lead to certain misclassifications. A more excellent C lowers misclassification but may narrow the margin. These are the closest data points near the decision boundary (hyperplane). They are essential in determining the hyperplane and are the origin of the term "Support Vector Machine." SVM is a binary classifier, but it can be extended to multiclass classification using One-vs.-Rest (OvR) or One-vs.-One approaches (OvO).

SVMs are renowned for their capacity to handle high-dimensional data, efficiency with small datasets, and generalizability. Additionally, they are less prone to overfitting. The performance of SVM can be affected by the kernel selection and its parameters, as well as the scaling of input characteristics. Moreover, SVMs may not perform effectively when classes are highly unbalanced.

B. KNN

KNN is a simple yet effective machine-learning method for classification and regression tasks. It is intuitive and straightforward, making it a popular choice for various applications, including picture categorization, recommendation systems, and anomaly detection. KNN is a non-parametric algorithm, which means it makes no assumptions about the distribution of the underlying data. KNN assumes that related data points belong to the same class. Given a new data point, the algorithm determines the k-nearest neighbors in the training dataset and assigns to the new data point the class that is most prevalent among these neighbors.

Here's an overview of how KNN works:

- **Distance Metric:** The choice of distance metric, such as Euclidean distance or Manhattan distance, plays a crucial role in determining the similarity between data points. The distance metric defines the "closeness" of two points in the feature space.

- **Parameter k:** The parameter "k" represents the number of neighbors to consider when making a prediction. A small k can lead to noisy results, while a large k can result in over-smoothing and might not capture local patterns well.

- **Weighted Voting:** In specific variants of KNN, it is possible to assign weights to the neighbors based on their proximity to the new data point. Closer neighbors may have a more significant impact on the final prognosis than their more distant counterparts.

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- **Choosing k:** Selecting the correct value of k is essential. A small k can make the algorithm sensitive to noise, while a large k might lead to overgeneralization. Cross-validation or other validation techniques can help determine an appropriate value of k.
- **Multiclass Classification:** KNN can be extended to multiclass classification using majority or distance-weighted voting techniques. For each class, the number of instances of that class among the k-nearest neighbors is tallied, and the class with the most significant count is assigned to the new data point.

KNN is easy to comprehend, does not presuppose any underlying data distribution, and can perform well with complex and non-linear decision limits. The performance of KNN can be affected by the distance metric chosen, the number of neighbours (k), and the data distribution. It can be computationally expensive for large datasets because it needs computing distances to all training locations.

For proposed research involving multiclass classification of brain MRI scans, KNN could be a valuable algorithm to experiment with. Its simplicity and lack of assumptions about the data distribution might make it effective in capturing complex patterns in the MRI images. However, remember that pre-processing the data and optimizing k and distance metrics are crucial for achieving good results with KNN.

C. DT

A Decision Tree is a flexible and interpretable machine-learning technique for classification, regression, and feature selection problems. Each internal node represents a decision based on a feature, and each leaf node represents a class label (in the case of classification) or a forecast value (in the case of regression).

Here's an overview of how Decision Trees work:

- **Splitting Criteria:** The algorithm finds the optimal feature to partition the data at each internal node. The "best" characteristic is determined using criteria such as Gini impurity (for classification) or variance reduction (for regression). The feature that results in the most significant separation between classes or the most considerable reduction in variance is selected.
- **Recursive Partitioning:** Once a feature is selected for splitting, the data is subdivided based on the feature's values. The process is then continued recursively on each subset until a stopping requirement, such as reaching a maximum depth, having a minimum amount of samples in a node, or obtaining pure classes, is reached (homogeneous target values).
- **Decision Rules:** The resulting tree structure forms a set of decision rules that can be easily understood and interpreted. Each path from the root to the leaf symbolizes a series of decisions leading to a final forecast.
- **Overfitting:** Decision Trees are susceptible to overfitting, which occurs when the model collects noise and irrelevant patterns from the training data. Techniques like pruning (removing parts of the tree) and setting a maximum depth are commonly used to mitigate this.
- **Handling Categorical Data:** Decision Trees can handle both categorical and numerical features. Based on the available categories, the tree can perform binary or multiway splits for categorical features.

Decision Trees can capture non-linear relationships in data, are easy to understand and interpret, and require minimal data pre-processing. They are also less sensitive to feature scaling. Decision Trees can suffer from instability (small changes in data can lead to different tree structures) and might not perform well on complex tasks without proper regularization.

Decision Trees could be valuable for this research on multiclass classification of brain MRI scans due to their interpretability and the potential to capture relevant features understandably. It can control the trade-off between model complexity and generalization performance by tuning hyperparameters, such as the maximum depth and splitting criteria. Additionally, considering ensemble methods like Random Forest could further enhance the accuracy of your classification tasks.

D. RF

Random Forest is a potent ensemble learning method for classification, regression, and machine-learning applications. It is an extension of Decision Trees and leverages the concept of creating multiple decision trees to make more accurate predictions and improve generalization.

Here's an overview of how Random Forest works:

- **Ensemble of Decision Trees:** Random Forest generates a collection of several Decision Trees, each trained on a distinct subset of data. These subsets are obtained through bootstrapping, where random samples (with replacement) are drawn from the original dataset.
- **Random Feature Selection:** Besides using different data subsets, Random Forest introduces randomness in feature selection for each Decision Tree. A random subset of features is evaluated at each tree node to determine the optimal split. This unpredictability helps to prevent overfitting and enhances tree diversity.
- **Voting or Averaging:** Random Forest combines the forecasts of all individual trees for classification tasks using

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majority voting. For regression tasks, it averages the predictions of all trees. This ensemble approach produces more robust and accurate predictions than a single Decision Tree.

- **Bagging and Aggregation:** Bagging generates numerous decision trees using bootstrapping and merging their predictions (bootstrap aggregation). Aggregating the predictions reduces the variance and can lead to improved overall performance.
- **Out-of-Bag (OOB) Samples:** Since each Decision Tree is trained on a different subset of data, some data points are not included in the training set of specific trees. These out-of-bag samples can be used to estimate the performance of the Random Forest without the need for cross-validation.
- **Hyperparameters:** Considerable hyperparameters include the number of trees in the forest, the maximum depth of each tree, the number of characteristics examined at each split, and the splitting criterion (e.g., Gini impurity or entropy).

Random Forest offers several benefits, including reduced overfitting, improved generalization, resistance to noise, and the ability to handle high-dimensional data. It's also capable of handling both numerical and categorical features. While individual Decision Trees are interpretable, the ensemble nature of Random Forests makes them less interpretable. However, techniques like feature importance can provide insights into which features are most influential for making predictions.

Random Forest could be a valuable algorithm for this research on multiclass classification of brain MRI scans due to its ability to handle complex relationships within the data, reduce overfitting, and provide a reliable prediction framework. You can fine-tune the Random Forest model for optimal performance on your specific classification tasks by tuning hyperparameters and analyzing feature importance.

E. GB

Gradient Boosting is a potent ensemble learning technique that excels in classification and regression tasks. Like Random Forest, Gradient Boosting combines the predictions of numerous weak learners (usually decision trees) to generate a robust predictive model. Gradient Boosting constructs trees consecutively, with each successive tree focusing on repairing the mistakes of the prior tree. In contrast to Random Forest, which constructs trees individually, Gradient Boosting constructs trees consecutively. Each successive ensemble is educated to remedy the faults of the prior ensemble.

Here's how Gradient Boosting works:

- **Loss Function:** A loss function quantifies the disparity between expected and actual target values. The Gradient Boosting algorithm aims to minimize this loss function in each iteration by adding a new decision tree to the ensemble.
- **Gradient Descent:** Gradient Boosting employs gradient descent optimization to find the direction and magnitude of the changes needed for the new tree to minimize the loss function.
- **Learning Rate:** A learning rate parameter determines the contribution of each new tree to the overall ensemble. A lower learning rate makes the model more robust but might require more trees for optimal performance.
- **Weak Learners:** Decision trees are often used as weak learners in Gradient Boosting. However, these trees are shallow (limited depth) to avoid overfitting and ensure better generalization.
- **Weighted Data:** Gradient Boosting assigns weights to data points during each iteration. Misclassified or poorly predicted data points receive higher weights, guiding subsequent trees to focus on these challenging cases.
- **Additive Training:** Trees are added sequentially, with each new tree focusing on the mistakes of the ensemble up to that point. This additive approach gradually improves the model's performance.
- **Stopping Criteria:** Gradient Boosting stops when a predefined number of trees is reached or when the improvement in the loss function becomes negligible.
- **Hyperparameters:** Important hyperparameters include number of trees, learning rate, maximum depth of each tree, and loss function.
- **Regularization:** To prevent overfitting, Gradient Boosting can incorporate regularization techniques, such as subsampling (using only a portion of the data for each tree) and shrinkage (reducing the contribution of each tree).

Gradient Boosting often achieves higher predictive accuracy than individual Decision Trees or Random Forests. It can handle complex relationships and noisy data well. For this research on multiclass classification of brain MRI scans, Gradient Boosting could provide a robust predictive model due to its ability to sequentially correct errors and adapt to complex patterns in the data. By tuning hyperparameters and controlling the learning rate, you can ensure that the model converges effectively and produces accurate results for your classification tasks.

V. PROPOSED SYSTEM

The block diagram of the proposed system is shown in Fig. 1. It consists of an Input dataset, Pre-processing, dataset Feature extraction, training and classification.

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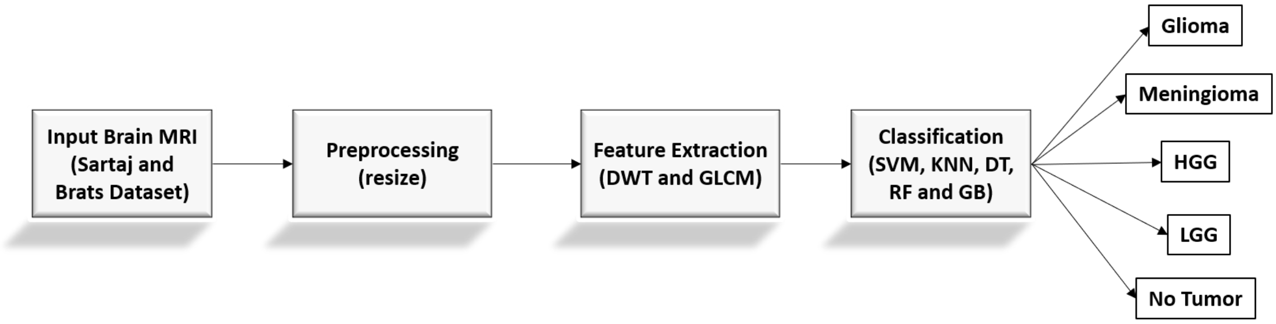
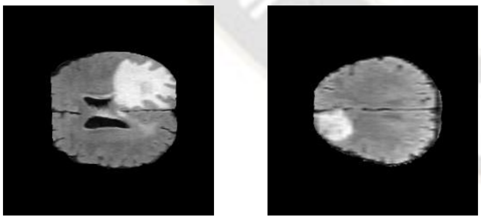


Fig. 3. Block diagram of the proposed system

A. Dataset Preparation

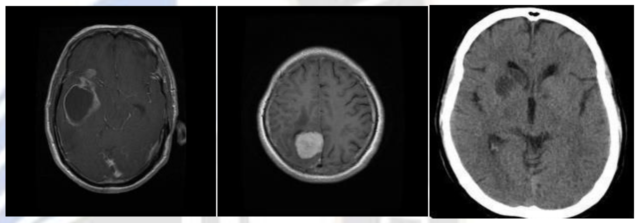
Brain Tumor Segmentation (BTATS) and Sartaj datasets are used for evaluation in this approach. The BRATS (Brain Tumor Segmentation) dataset is a frequently utilized standard for brain MRI analysis and classification, particularly emphasizing brain tumour segmentation. It consists of a comprehensive set of multimodal brain MRI scans, including T1-weighted, T1-weighted contrast-enhanced, T2-weighted, and fluid-attenuated inversion recovery (FLAIR) images, as well as the ground truth tumour segmentation labels that correspond to each image. The MRI scans used to compile the BraTS dataset came from various organizations. These images were acquired using T1-weighted (T1), T1-weighted with contrast enhancement (T1ce), T2-weighted (T2), or Fluid Attenuated Inversion Recovery (FAI) modalities (FLAIR). These modalities capture many aspects of brain architecture and pathology, and as a result, they provide helpful information for categorizing tumours. The 2018 version of the BraTS dataset consists of a training set and a validation set with 285 instances in total. Each example includes the four MRI modalities and the corresponding tumour segmentation masks. Different tumour grades are represented in the training set by high-grade gliomas (HGG) and low-grade gliomas (LGG). Fig. 4 depicts an example image of the Brats dataset.



(a) (b)

Fig. 4. Dataset samples of Brats 2018 Dataset (a) HGG (b) LGG

The SARTAJ data collection consists of magnetic resonance (MR) pictures of three types of brain cancer (glioma, meningioma, and pituitary), as well as images of normal brain tissue (no tumor). The collection contains 3264 photographs in RGB JPG format. The dataset contains two issues: an unequal distribution of classes and unpredictable splitting ratios. The number of photographs with "no tumor" is relatively low in comparison to the number of photographs with tumors, which are as follows: 500 photographs with no tumor, 937 photographs with meningioma tumors, 901 photographs with pituitary tumors, and 926 photographs with glioma tumors. Consequently, this distinction creates classification difficulties that result in an imbalance in which the classifier may prefer tumor scans. In addition, the train-test splitting ratio of the images linked with "Pituitary Tumor" differs from that of the other images. The dataset, therefore, excludes the pituitary class from this method. Fig. 5 depicts an example image of the SARTAJ dataset.



(a) (b) (c)

Fig. 5. Dataset samples of Sartaj Dataset (a) Glioma (b) Meningioma (c) No tumor

A training dataset comprises 80% of the total dataset, whereas a validation dataset comprises 20%. Table I summarises the distribution of the image datasets Brats 1018 and SARTAJ used for the proposed system.

Table I: Dataset distribution

Dataset	Classes	Training	Validation
Brats	HGG	7148	1786
	LGG	4623	1155
SARTAJ	Glioma	1321	300
	Meningioma	1339	306
	No tumor	1595	405

B. Data pre-processing

This image has been pre-processed to facilitate its manipulation. Filtration is a crucial component of the pre-processing operation. The median filter is a non-linear filter that removes noise and smooths images. Widespread use has resulted from its ability to minimize noise while preserving edges. It excels at evading sounds like salt and pepper. As it advances from pixel to pixel, the median filter iteratively applies itself to an image, replacing each value with the neighborhood median value. Calculating the median requires sorting the window's

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pixel values in numerical order and then replacing the window's central pixel with the pixel value indicating the median.

C. Feature Extraction

The feature extraction process for brain MRI images involves two fundamental techniques: the DWT and the GLCM. Using DWT, images are decomposed into different frequency components across various scales, from which statistical features like maximum, minimum, standard deviation, skewness, and mean values of detail coefficients are calculated. In parallel, GLCM captures textural information by quantifying the occurrence of pixel value pairs with specific offsets and angles, subsequently yielding features such as contrast, energy, homogeneity, entropy, and ASM. These extracted DWT-based and GLCM-based features comprehensively represent frequency-related patterns and texture characteristics within the MRI images. The culmination of this dual approach results in a fused feature set that encapsulates essential information for subsequent classification tasks. This combined feature set is the foundation for training and evaluating machine learning algorithms, ultimately enabling accurate and nuanced classification of brain MRI scans into distinct categories.

D. Training and classification

The training and classification phase of our study involves the application of diverse machine learning algorithms, namely SVM, KNN, DT, RF, and GB, on the extracted feature sets from brain MRI images. Each algorithm brings unique strengths to the classification task. SVM constructs an optimal hyperplane to separate different classes, utilizing a kernel trick to handle non-linear boundaries effectively. KNN uses the proximity of data points in feature space to make predictions, assigning class labels to the k-nearest neighbors. By recursively partitioning data based on feature values, DT generates a decision tree structure that is interpretable and capable of capturing complex relationships. RF constructs an ensemble of decision trees through bootstrapped data and random feature selection, promoting robustness and reducing overfitting.

Conversely, GB sequentially builds decision trees to correct the errors of its predecessors, enhancing predictive accuracy. By training each algorithm on our fused feature set and employing cross-validation techniques, we assess their performance and fine-tune hyperparameters for optimal results. This comprehensive analysis will guide the selection of the most suitable algorithm or combination of algorithms for accurately classifying brain MRI images, ultimately contributing to improved medical diagnostic capabilities.

E. Evaluation

Our classification models are evaluated through a comprehensive set of metrics, including precision, recall, F1 score, and accuracy. These metrics collectively provide insights into our trained models' performance and ability to classify brain MRI images accurately.

- **Precision:** Precision is the fraction of accurately predicted positive cases (true positives) relative to the total number of positive instances predicted by the model. It represents the model's capacity to avoid false positives, making it especially useful when false positives are expensive. Mathematically, precision is calculated as:

$$Precision(P) = \frac{TP}{TP + FP}$$

- **Recall:** Recall, also known as sensitivity or true positive rate, is the proportion of true positive occurrences accurately detected by the model out of the total number of positive instances. It highlights the model's ability to capture all relevant positive instances. Mathematically, recall is given by:

$$Recall\ (R) = \frac{TP}{TP + FN}$$

- **F1 Score:** The F1 score is the harmonic mean of precision and recall, measuring a well-balanced model's performance. It considers both false positives and false negatives and is particularly beneficial when class distribution is unequal. The F1 score is calculated as follows:

$$Recall = \frac{2 \times P \times R}{P + R}$$

- **Accuracy:** Accuracy is the proportion of instances accurately predicted (including true positives and true negatives) relative to the total number of instances in the dataset. Accuracy is essential, but it may not be the optimal metric when dealing with imbalanced datasets where one class considerably exceeds the other.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

In the context of problems involving classification, samples can be separated into groups labelled True Positive (TP), False Positive (FP), True Negative, and False Negative(FN), respectively.

VI. RESULT

This section presents the results of the proposed brain MRI classification using a machine learning algorithm with DWT and GLCM feature extraction techniques.

A. Results of Brain MRI Classification into Glioma, Meningioma and No Tumor using ML algorithm on Sartaj Dataset

In this study, we aimed to classify brain MRI images into three distinct categories: Glioma, Meningioma, and No Tumor. We employed a variety of machine learning algorithms, leveraging

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the power of feature-rich DWT and texture-based GLCM features extracted from the Sartaj Dataset. The results of our classification experiment are outlined below:

a) DWT

The analysis of different machine learning classifiers on DWT features of Sartaj Dataset for classification of brain MRI into Glioma, meningioma and no tumor classification is presented in Table II.

Table II: Comparative analysis of different ML algorithms with DWT features on Sartaj Dataset

Classifiers	Attributes	Precision	Recall	F1_Score	Accuracy
SVM	linear	0.75	0.74	0.74	0.7394
	rbf	0.79	0.79	0.79	0.7934
	poly	0.76	0.67	0.68	0.6737
KNN	k=3	0.83	0.83	0.83	0.8286
	k=5	0.82	0.82	0.82	0.8192
	k=7	0.83	0.83	0.82	0.8262
DT		0.75	0.76	0.76	0.7582
RF		**0.84**	**0.84**	**0.84**	**0.8427**
GB		0.82	0.82	0.82	0.8169

Table II shows that the RF algorithm achieved the highest accuracy of 84.27% compared to other algorithms on DWT features.

b) GLCM

The analysis of different machine learning classifiers on GLCM features with 0º,45º,90º, and 135º of Sartaj Dataset for classification of brain MRI into Glioma, meningioma and no tumor classification are presented in Table III, IV, V, and VI.

Table III: Comparative analysis of different ML algorithms on GLCM features with 0º on the Sartaj Dataset

GLCM 0 degree					
Classifiers	**Attributes**	**Precision**	**Recall**	**F1_Score**	**Accuracy**
SVM	linear	0.72	0.71	0.72	0.7112
	rbf	0.77	0.76	0.77	0.7629
	poly	0.75	0.64	0.64	0.6384
KNN	**k=3**	**0.88**	**0.88**	**0.88**	**0.8826**
	k=5	**0.88**	**0.88**	**0.88**	**0.8826**
	k=7	0.87	0.87	0.87	0.8685
DT		0.84	0.84	0.84	0.8427
RF		0.86	0.86	0.86	0.8638
GB		0.82	0.81	0.81	0.8098

Table III shows that the KNN algorithm with K=3 and K=5 achieved the highest accuracy of 88.26% than other algorithms on GLCM features with 0º.

Table IV: Comparative analysis of different ML algorithms on GLCM features with 45º on the Sartaj Dataset

GLCM 45 degree					
Classifiers	**Attributes**	**Precision**	**Recall**	**F1_Score**	**Accuracy**
SVM	linear	0.72	0.72	0.72	0.718309
	rbf	0.77	0.76	0.76	0.760563
	poly	0.74	0.62	0.63	0.622065
KNN	k=3	0.86	0.86	0.86	0.861502
	k=5	0.86	0.86	0.86	0.863849
	k=7	0.86	0.86	0.86	0.863849
DT		0.81	0.81	0.81	0.814553
RF		**0.87**	**0.87**	**0.87**	**0.870892**
GB		0.82	0.81	0.81	0.809859

Table IV shows that the RF algorithm achieved the highest accuracy of 87.08% compared to other algorithms on GLCM features with 45º.

Table V: Comparative analysis of different ML algorithms on GLCM features with 90º on the Sartaj Dataset

GLCM 90 degree					
Classifiers	**Attributes**	**Precision**	**Recall**	**F1_Score**	**Accuracy**
SVM	linear	0.74	0.73	0.73	0.730046
	rbf	0.75	0.75	0.75	0.748826
	poly	0.74	0.62	0.62	0.61737
KNN	k=3	0.87	0.87	0.87	0.870892
	k=5	**0.88**	**0.88**	**0.88**	**0.884976**
	k=7	0.88	0.88	0.87	0.875586
DT		0.82	0.82	0.82	0.819248
RF		0.87	0.87	0.86	0.866197
GB		0.82	0.81	0.81	0.812206

Table V shows that the KNN algorithm with K=5 achieved the highest accuracy of 88.49% compared to other algorithms on GLCM features with 90º.

Table VI: Comparative analysis of different ML algorithms on GLCM features with 135º on the Sartaj Dataset

GLCM 135 degree					
Classifiers	**Attributes**	**Precision**	**Recall**	**F1_Score**	**Accuracy**
SVM	linear	0.74	0.73	0.73	0.727699
	rbf	0.76	0.75	0.75	0.748826
	poly	0.73	0.61	0.62	0.610328
KNN	k=3	0.86	0.86	0.86	0.859154
	k=5	0.88	0.88	0.88	0.880281
	k=7	**0.87**	**0.87**	**0.87**	**0.873239**
DT		0.82	0.82	0.82	0.816901
RF		0.86	0.86	0.86	0.859154
GB		0.79	0.78	0.78	0.78169

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Table VI shows that the KNN algorithm with K=7 achieved the highest accuracy of 87.35% than other algorithms on GLCM features with 90°.

This experiment demonstrates that each machine learning algorithm performs differently, classifying brain MRI images into Glioma, Meningioma, and No Tumor categories. KNN and Random Forest algorithms stand out with higher accuracy, precision, recall, and F1 scores than other algorithms, indicating their efficacy in this task. This comprehensive analysis aids in identifying the most suitable algorithm for accurate and reliable brain tumor classification, contributing to enhanced medical diagnostics and patient care.

B. Results of Brain MRI Classification into HGG and LGG using ML algorithm on Brats dataset

In this study, we aimed to classify brain MRI images into two distinct categories: HGG and LGG. We employed a variety of machine learning algorithms, leveraging the power of feature-rich DWT and texture-based GLCM features extracted from the Brats 2018 Dataset. The results of our classification experiment are outlined below:

a) DWT

The analysis of different machine learning classifiers on DWT features of Sartaj Dataset for classification of brain MRI into Glioma, meningioma and no tumor classification is presented in Table VII.

Table VII: Comparative analysis of different ML algorithms with DWT features on Brats Dataset

Classifiers	Attributes	Precision	Recall	F1_Score	Accuracy
SVM	linear	0.73	0.73	0.71	0.727828
	rbf	0.76	0.75	0.74	0.752973
	poly	0.78	0.73	0.69	0.727149
KNN	k=3	0.74	0.74	0.74	0.740061
	k=5	0.75	0.75	0.74	0.748558
	k=7	0.76	0.76	0.76	0.763506
DT		0.72	0.72	0.72	0.716955
RF		**0.77**	**0.77**	**0.77**	**0.77268**
GB		0.76	0.76	0.75	0.75739

Table VII shows that the RF algorithm achieved the highest accuracy of 77.26% compared to other algorithms on DWT features.

b) GLCM

The analysis of different machine learning classifiers on GLCM features with 0°,45°,90°, and 135° of Sartaj Dataset for classification of brain MRI into Glioma, meningioma and no tumor classification is presented in Table VIII, IX, X, and XI.

Table VIII: Comparative analysis of different ML algorithms with DWT features on Sartaj Dataset

GLCM 0 degree					
Classifiers	**Attributes**	**Precision**	**Recall**	**F1_Score**	**Accuracy**
SVM	linear	0.77	0.77	0.77	0.772823
	rbf	0.8	0.79	0.79	0.794479
	poly	0.78	0.76	0.74	0.758386
KNN	k=3	0.79	0.79	0.79	0.793205
	k=5	0.8	0.81	0.8	0.80552
	k=7	0.81	0.81	0.81	0.809766
DT		0.76	0.75	0.76	0.754989
RF		**0.81**	**0.81**	**0.81**	**0.810615**
GB		0.79	0.79	0.78	0.78811

Table VIII shows that the RF algorithm achieved the highest accuracy of 81.06% compared to other algorithms on GLCM features with 0°.

Table IX: Comparative analysis of different ML algorithms with DWT features on the Sartaj Dataset

GLCM 45 degree					
Classifiers	**Attributes**	**Precision**	**Recall**	**F1_Score**	**Accuracy**
SVM	linear	0.79	0.79	0.78	0.787685
	rbf	0.81	0.8	0.8	0.802972
	poly	0.79	0.77	0.75	0.7707
KNN	k=3	0.8	0.8	0.8	0.797452
	k=5	**0.81**	**0.81**	**0.81**	**0.810191**
	k=7	**0.81**	**0.81**	**0.81**	**0.810191**
DT		0.75	0.75	0.75	0.75414
RF		0.81	0.81	0.81	0.808492
GB		0.79	0.79	0.78	0.786411

Table IX shows that the KNN with k=5 and k=7 algorithms achieved the highest accuracy of 81.01% than other algorithms on GLCM features with 45°.

Table X: Comparative analysis of different ML algorithms with DWT features on the Sartaj Dataset

GLCM 90 degree					
Classifiers	**Attributes**	**Precision**	**Recall**	**F1_Score**	**Accuracy**
SVM	linear	0.78	0.78	0.78	0.782165
	rbf	0.81	0.8	0.8	0.802972
	poly	0.79	0.77	0.75	0.770276
KNN	k=3	0.79	0.79	0.79	0.794479
	k=5	0.81	0.81	0.81	0.808492
	k=7	**0.81**	**0.81**	**0.81**	**0.809341**
DT		0.75	0.75	0.75	0.748619
RF		0.8	0.8	0.8	0.798301
GB		0.79	0.79	0.79	0.792356

Table X shows that the KNN algorithm with K=7 achieved the highest accuracy of 80.93% than other algorithms on GLCM features with 90°.

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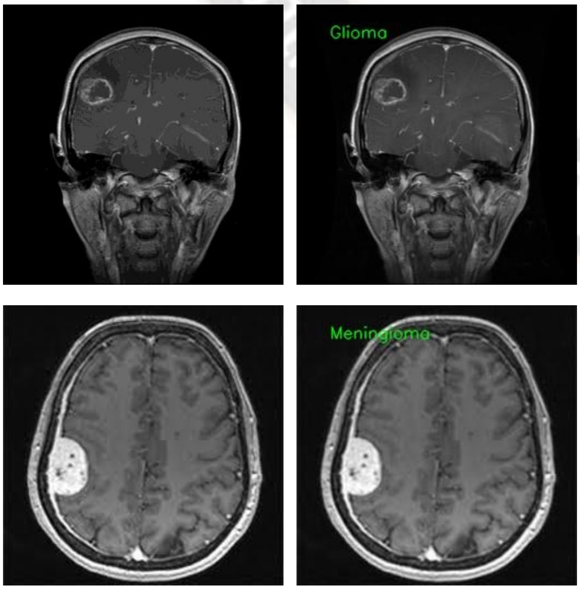
Table XI: Comparative analysis of different ML algorithms with DWT features on Sartaj Dataset

GLCM 135 degree					
Classifiers	**Attributes**	**Precision**	**Recall**	**F1_Score**	**Accuracy**
SVM	linear	0.78	0.78	0.78	0.782165
	rbf	0.81	0.8	0.8	0.802972
	poly	0.79	0.77	0.75	0.770276
KNN	k=3	0.79	0.79	0.79	0.794479
	k=5	0.81	0.81	0.81	0.809341
	k=7	**0.81**	**0.81**	**0.81**	**0.809766**
DT		0.75	0.75	0.75	0.750318
RF		0.8	0.8	0.8	0.8
GB		0.79	0.79	0.79	0.793205

Table XI shows that the KNN algorithm with K=7 achieved the highest accuracy of 80.97% than other algorithms on GLCM features with 90^o.

This experiment demonstrates that each machine learning algorithm performs differently in classifying brain MRI images into Glioma, Meningioma, and No Tumor categories. KNN and Random Forest algorithms stand out with higher accuracy, precision, recall, and F1 scores than other algorithms, indicating their efficacy in this task. This comprehensive analysis aids in identifying the most suitable algorithm for accurate and reliable brain tumor classification, contributing to enhanced medical diagnostics and patient care.

Figure 6 depicts the qualitative analysis of the proposed system on the Sartaj dataset for the classification of Glioma, Meningioma, and No tumour. Figure 7 depicts the qualitative analysis of the proposed system on the brats dataset for the classification of HGG and LGG.



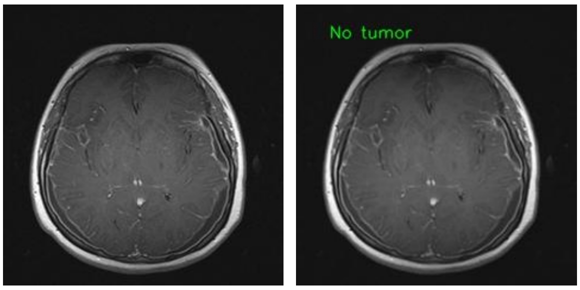


Fig. 6. Testing results of the proposed system on the Sartaj dataset

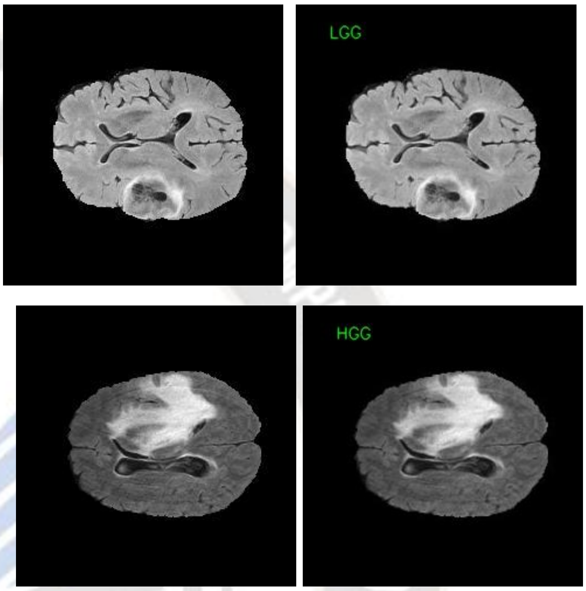


Fig. 7. Testing results of the proposed system on the Brats dataset

In our comprehensive exploration of brain MRI classification, we examined the performance of various machine learning algorithms on two distinct datasets: the BRATS dataset and the Sartaj dataset. Notably, the promising results achieved with the Random Forest and k-Nearest Neighbors algorithms were consistent across both datasets, highlighting their robustness and generalizability.

The Random Forest algorithm's success can be attributed to its ensemble nature, which harnesses the power of multiple decision trees to make accurate predictions collectively. RF demonstrated noteworthy precision, recall, F1 scores, and accuracy on the BRATS and Sartaj datasets. The results clearly reflected its capacity to handle high-dimensional feature spaces and effectively manage overfitting through bootstrapping and random feature selection. The feature importance analysis offered by RF was precious, shedding light on the most influential features in brain MRI classification. This interpretability contributes to the algorithm's utility in medical diagnostics.

The k-Nearest Neighbors algorithm's performance consistency across datasets emphasizes its ability to capture local patterns and nuances within the data. With KNN, the classification decision is heavily influenced by neighboring instances, making it effective when spatial relationships and subtle variations are essential, as is the case with medical images. While the results showed relatively lower precision and recall than RF, KNN's reliability across datasets suggests its stability and adaptability in varying scenarios. Additionally, the straightforward nature of KNN makes it easy to understand and implement, an advantage in the medical domain where interpretability is crucial.

The convergence of promising results with both RF and KNN across the BRATS and Sartaj datasets underscores their potential as strong candidates for brain MRI classification. However, it's essential to recognize that no single algorithm is universally optimal. Factors such as dataset characteristics, class imbalances, computational efficiency, and interpretability must all be weighed when choosing the most appropriate algorithm for a given task. This comprehensive analysis advances our understanding of the suitability of machine learning algorithms in medical image analysis. It highlights the significance of well-informed algorithm selection for accurate diagnosis and patient care.

VII. CONCLUSION

This study delved into the intricate realm of brain MRI classification using a diverse range of machine-learning algorithms on both the BRATS and Sartaj datasets. Through comprehensive analysis, we unearthed valuable insights that can significantly impact medical diagnostics and patient care. The results showcased the effectiveness of various algorithms in accurately categorizing brain MRI images into distinct classes, with notable performances observed for Random Forest (RF) and k-nearest Neighbors (KNN) across both datasets.

Our findings underscore the pivotal role of algorithm selection in achieving accurate classification. SVM, DT, and GB, along with RF and KNN, all demonstrated unique strengths and weaknesses, necessitating careful consideration based on dataset characteristics and clinical requirements. Furthermore, our study emphasized the importance of feature extraction methods, such as DWT, and their synergistic potential with machine learning techniques to create powerful diagnostic tools.

Looking ahead, several exciting avenues for future research emerge from our study. Incorporating advanced deep learning techniques, such as convolutional neural networks (CNNs), could potentially unlock even higher levels of accuracy by harnessing the innate ability of CNNs to learn complex features directly from images automatically. Exploring multimodal datasets, where complementary information from various imaging modalities is combined, might provide a more comprehensive diagnostic approach. Additionally, fine-tuning algorithms to tackle specific subtypes or abnormalities within brain tumors could enhance accuracy in distinguishing between complex cases.

Moreover, expanding the scope of our research to accommodate larger datasets, including diverse demographic information and longitudinal follow-up, could amplify the real-world applicability of our findings. Collaboration with medical professionals could provide valuable clinical insights, ensuring the developed models align with medical needs.

This study is a stepping stone towards integrating advanced machine learning techniques into medical diagnosis. By consistently pushing the limits of research, we foresee a future in which the convergence of cutting-edge technology and medical expertise transforms the healthcare landscape, enabling more accurate and timely diagnoses and eventually enhancing patient outcomes.

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