

Identification of Brain Tumors using a Combined Approach of Discrete Wavelet Transform and Principal Component Analysis

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Submitted: 18/07/2023

Revised: 07/09/2023

Accepted: 25/09/2023

Abstract: A brain tumor diagnosis is a life-changing event that requires the highest degree of skill and competency from the treating physician. Radiologists must use a certain tumor configuration in order to diagnose brain cancers. This study suggests a technique for distinguishing between normal and abnormal MR brain images. In order to improve the output of cataloging, a three-step technique has been proposed that focuses largely on the presentation of a hybrid feature extraction. A 3-level discrete wavelet transform (DWT) is employed in the first phase of the procedure to extract the image's features. Principal component analysis (PCA) is employed in the second step to cut down on the number of dimensions each feature possesses. To make an accurate diagnosis, a feature selection and a random forest classifier (also known as RF) were applied. With a total of 181 MR brain pictures (81 normal and 100 sick), the experiment findings showed an accuracy of 98%, a sensitivity of 99.2%, and a specificity of 97.8%, demonstrating the efficacy of the prospect technique via evaluation of different forms of writing. The results show that 3L-DWT, PCA, and RF tranquility all contribute to the creation of high-quality cataloging outcomes. The predicted method may be used to the subspecialty categorization of brain MRIs, which would help medical professionals determine if a tumor's progression is normal or pathological.

Keywords: Multivariate technique, PCA, DWT, RF.

1. Introduction

For biomedical research and clinical analysis, magnetic resonance imaging (MRI) produces high-quality descriptions of the body's main structural components, particularly the brain [1]–[3]. MRI has been discovered to be the most efficient and appropriate imaging modality for the diagnosis of brain malignancies. Non-invasive MRI allows for the gathering of comprehensive data on the kind, location, and volume of the tumor [4]. In MRI scanners, T2-w images are often utilized for estimate, documenting various tumor types, and separating cancerous from healthy tissues [5-7].

As scanner resolution has increased and segment width has reduced, more segment has been generated, necessitating more patient-specific instances.

Data sampling and training models are

crucial components of effective machine learning algorithms. The majority of models have training error. Malignant brain tumors are still incurable, despite significant advancements in the treatment of other cancer forms. According to the National Cancer Institute, brain tumors are the sixth leading cause of death for females between the ages of 20 and 39. Due to the accurate brain information provided by MRI, glioma confirmation is much easier. Brain MRI sequences including T1, T2, FLAIR, and T2 FLAIR are often used. These sections go into considerable depth about the brain tumor. Radiofrequency (RF) is used to determine the repetition and echo timings (TR and TE) of the MRI scan. Due to the short TR and TE lengths, CSF appears black in T1c and T1 MRI sequences. The brain and spinal cord contain a clear fluid called cerebrospinal fluid (CSF). Due to the longer TR and TE, T2 MRI is the most effective method for assessing CSF. The aberrant region looks dazzling whereas the CSF is dark as a result of the prolonged TR and TE periods that induce flair. T2 is better suitable for dysfunctional areas of the brain where water builds up within the tissues since it is more sensitive to water content. Flair makes it simple to distinguish between the aberrant area and

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the CSF in comparison to other modalities. A group of cells that have undergone four different phases of mutation make up a brain tumor. Brain tumors of grades 1 and 2 develop gradually, but those of grades 3 and 4, which are very aggressive, advance quickly and are incredibly difficult to treat. Preprocessing of the raw image removes noise and non-brain tissues in order to increase accuracy. Outside of the brain, organs may also be removed using the BSE procedure. The fast non-local mean (FNLM), partial differential diffusion filter (PDDF), and Wiener filter are used to lengthen contrast and reduce noise. The most popular techniques for segmenting brain lesions include fuzzy C means, k-means clustering, and the Otsu threshold. The U-Net design, which is also a well-known CNN architecture, has been successfully used to the segmentation of brain lesions.

As a result, the area of automated tumor segmentation and identification has expanded quickly during the last 20 years [8].

The hoped-for method relied on T2-w axial images to characterize brain variations. The wavelet transform's multi-resolution systematic property [9] is used to analyze pictures at various resolutions, and principal component analysis (PCA) was used to invert the feature vector size to improve discriminatory power [10]. One of the most obvious applications of principal component analysis (PCA) is its capacity to reduce data size, which lessens the computational strain associated with analyzing fresh data sets [11].

In the method before, features were extracted from a segmented representation. A more accurate evaluation is produced by extracting the in rank from several MR descriptions using discrete wavelet DWT (Discrete Wavelet Transform) and principal component analysis (PCA). In this study, we collect features that provide the highest accurate classification result possible using a mix of textural data collected from Principal Component Analysis and LL subbands 3-level wavelet decomposition. It is suggested to utilize a Random Forest Classifier (RFC) to determine if an image of the brain is healthy or infected.

A method for analyzing MRI data for the identification and classification of brain tumors using a Support Vector Machine (SVM) and Berkeley wavelet transform (BWT) is provided by Bahadure et al. [12]. Skull debridement, in which all non-brain tissues are removed, may achieve a 95% success rate in identification. Alfonso and

Salem [14] state that the K-means clustering algorithm created by the support vector machine for MR brain image segmentation with morphological filtering for tumor image identification is one automated method for classifying MR images of brain tumors. The recommended technique improved a classifier's accuracy by 98% by employing fast Fourier transform for feature extraction and the most important strategy, nominal redundancy.

A PCA and SVM-based approach that yields 94% accuracy is provided by Kumar et al. A technique to extract texture features using wavelet transformations and support vector machines was proposed by Yao et al. [16]. [15] With an 83% accuracy rate, it is quite accurate.

Mohsen et al. [17] classified 66 images of brain tumors into four categories using a DNN: metastasis, sarcoma, glioblastoma, and tumor-free. The DNN has a 96.97% accuracy rate. With the use of principal component analysis and the Gaussian mixture model applied to wavelet MRI, accuracy of 95% for T1 and T2-weighted and 92% for FLAIR MRI was attained. This thought was first proposed by Chaddad [18]. Sachdeva et al. [19] exhibited feature extraction and enhanced tumor identification for categorizing multiclass MR brain tumor images with an accuracy of 75-80% using principle component analysis-artificial neural network (PCA-ANN) and ANN. This survey provides a thorough overview of the effort carried out to reach that particular site of interest and the extraction method. Only a few of the techniques employed in the recommended methodology include segmentation, k-means clustering, principal component analysis, the discrete wavelet transform, and the Random Forest Classifier.

2. Literature Review

(Including but not limited to) Hemanth (G), Janardhan (M), and Sujihelen (L). In order to ascertain tiny 3x3 kernels, CNN are used as part of an automatic segmentation technique. In addition to its use for classification, this method may also be put to use for segmentation. The CNN that was created from NN employs a classification method based on layers. Data collection, pre-processing, segmentation, feature extraction, convolutional neural network (CNN) classification, and identification are some of the processes that are included in the techniques that have been proposed. Data mining (DM) is a process that makes it

possible to access methodologies that may extract significant relationships and patterns from massive databases. Brain malignancies may be recognized and thwarted in their earliest stages with the use of machine learning and data mining strategies.

Saba, Tanzila, and their other researchers [37] The most recent developments in cancer diagnosis in humans include the application of machine learning algorithms to different tumors that may occur in the human body. This research illustrates how supervised learning, unsupervised learning, and deep learning may all be used to help with the detection and treatment of cancer. Measures of accuracy, sensitivity, specificity, and false-positive outcomes are used with benchmark datasets in order to evaluate the results of a variety of innovative, cutting-edge methodologies. In conclusion, challenges are highlighted in order to provide suggestions for courses of future study.

Toktam Hatami, Mohammad Hamghalam, Omid Reyhani-Galangashi, and Sattar Mirzakuchaki are only a few of the individuals who have made contributions to this work. The Random Forest algorithm is used in order to provide recommendations on the segmentation of brain tumors. When the suggested approach is used to analyze MRI images of the brain, performance measures such the DSC and ACC are generated, and the findings are 99.64 and 98.32 percent accurate, respectively. According on the findings, the suggested model has the potential to outperform many alternative segmentation approaches. In the context of this investigation, the Random Forest method has also been theoretically modeled.

According to Sushma Megha Chadha and Jain's et al. [39], brain tumors are very dangerous and often result in the patient's death if they are identified at a later stage. Because the analytical processes now used in neurology are not entirely devoid of mistake, manual segmentation is not suggested. This research proposes a method based on machine learning that can segment brain pictures and identify tumors by utilizing the SVM classification methodology. The goals of this strategy are to increase performance, decrease complexity, and operate with real-time data.

Huseyin Kiraz and his fellow researchers. [40] Image processing with a focus on machine learning in order to diagnose brain tumors: design and implementation of the system An approach that uses MATLAB-generated models of brain MRI data is detailed in this article as a method for

detecting brain cancer at an earlier stage. The input data is prepared for feature extraction in the system by preprocessing techniques such as removing the skull, filtering the data, and using threshold segmentation. The Classification Learner App in MATLAB was used during the construction of the models. The weighted KNN technique was chosen from among these artificial models since it gives the highest accuracy (89.8%).

[41] Kshirsagar, Pravin R., Anil N. Rakhonde, Pranav Chippalkatti, and others. In MRI, the identification of tumors is accomplished by the use of algorithms that interpret imaging equipment. The proposed works of art may be broken down into the following categories: The preprocessing procedures are applied to the MRI photographs, and the focus on the grayscale is what gives the pictures their texturing capabilities. The matrix is finished off by providing instruction on how to master a tool.

Bhagyashri H. Asodekar, Sonal A. Gore, and others contributed to this work. The use of magnetic resonance imaging (MRI) allows for the detection and classification of brain tumors of all types, including those that are benign. In order to extract the MRI images, the MICCAI BRATS 2015 dataset was used. Image processing methods allow for the potential dissection of brain tumors into their component parts. The usage of shape-based attributes is made possible through feature extraction. Extracted shape-based features are put into machine learning algorithms such as the support vector machine and the random forest approach to determine whether brain tumors are benign or malignant. It achieved a level of accuracy for the random forest that was 86.66 percent.

Among the contributors of this book are authors such as Luca Brunese, Francesco Mercaldo, Alfonso Reginelli, and Antonella Santone. [43] It is argued that there is a mechanism for determining what constitutes an ensemble learner. The objective of the ensemble learner is to differentiate between the various stages of brain cancer using radiomic characteristics that do not need surgical intervention. First Order, Shape, Gray Level Co-occurrence Matrix, Gray Level Run Length Matrix, and Gray Level Size Zone Matrix are the five radiomic features that have been investigated. Through the use of hypothesis testing, decision boundaries, performance analysis, and calibration charts, they choose the best candidates for the classifier that are also practical for use by the

ensemble learner. They examined 111,205 brain MRIs taken from two different data sets that were made accessible to the public and evaluated the recommended technique. The study came to several encouraging conclusions, including a detection rate of 99 percent for all stages of brain cancer, ranging from benign to aggressive. The results of the experiments demonstrate that the ensemble learner provided as part of the approach may make more accurate predictions about the grade of brain cancer based on MRI data than the methods that are currently in use.

T. Vijayakumar and the rest of the T. The most severe form of the disease is cancer of the brain, which strikes a disproportionately high number of young people. If doctors were able to discover brain tumors at an earlier stage and identify the kind of cancer that their patients had, they would be in a better position to choose the therapy that would be most effective for their patients. The research suggests using a machine learning method known as a capsule neural network to detect brain tumors at an early stage since it can be trained with less datasets than convolutional neural networks and is resistant to rotation and affine conversions.

This is one of the reasons why the method was chosen. In both the training and the testing environments, it was shown that the capsule neural network method of classifying the different subtypes of brain cancer was more accurate than the convolutional network method.

3. Proposed Method

To extract image uniqueness, the first stage includes the preprocessing to improve and bestow the interested image. The second stage is Discrete Wavelet Transform. The third stage includes is used to reduce the size of characteristics by Principal component analysis. The fourth stage includes with a collection of classification features was used as a Random Forest Classifier (RFC).

It includes:

- Preprocessing:
 - MR images resizing
 - Clustering by k-means
 - Segmentation
- DWT for Transformation and PCA for Reduction.
- Extraction of Feature.

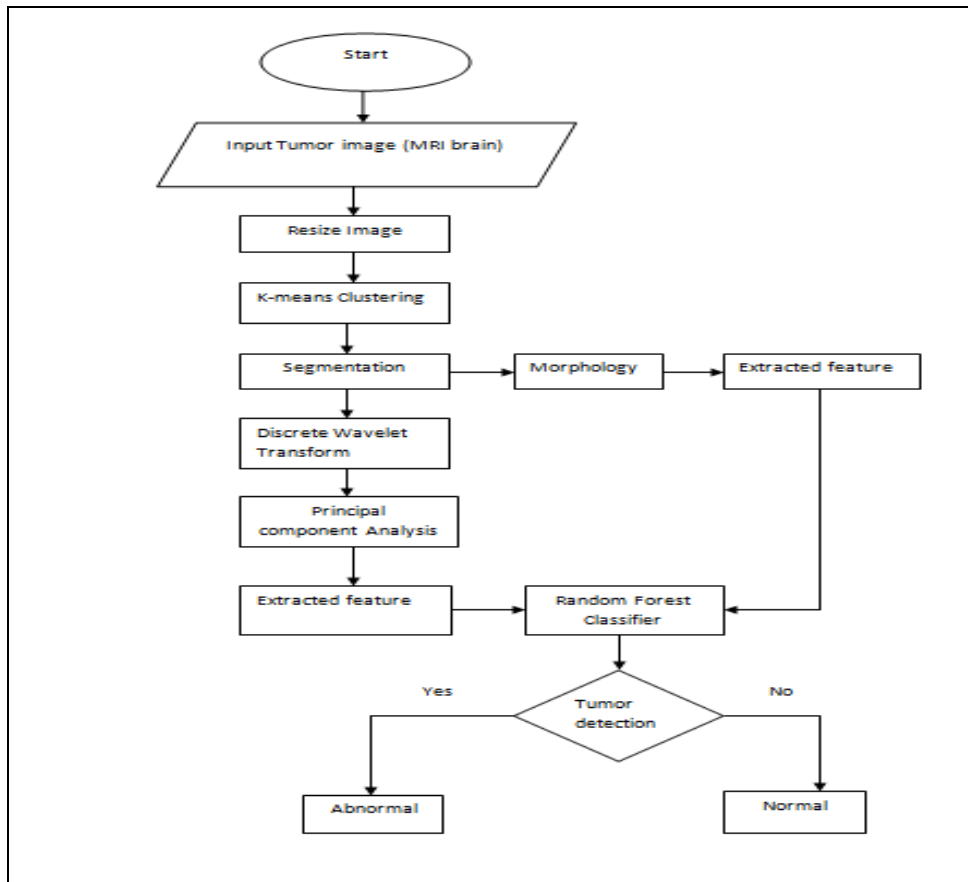


Fig 1. The proposed Algorithm Methodology

Preprocessing

MR images Resizing

Images of the brain were obtained using magnetic resonance imaging scanners of varying spatial resolutions. To allow for unbiased usage of the whole set, the MRI images' dimensions were adjusted using nearest neighbor interpolation such that the width or height doesn't exceed 256 pixels while retaining the images' aspect ratio.

K means clustering

During the clustering process, a pattern is divided into multiple subgroups, or clusters, where other patterns with similar qualities will be placed. Analysis using clustering has almost eliminated the need for image segmentation. Among the many possibilities, the k-means clustering technique is particularly well-liked. K-means is an unsupervised clustering technique, and the area of interest extracted from the background is a common segment. [20].

Distinct region of interest (ROI)

The MRI is segmented into manageable pieces so that it may be read more easily. The value of ought to provide an idea of the whole dimensions of the picture. To put it another way, segmentation is the act of splitting a larger whole (A) into a number of increasingly smaller sections (A1, A2, A3, and so on). In order for this to be effective, every pixel has to be contained inside the region's boundaries, every point needs to be contained within the region's network, and no two regions may share a boundary. [21], [22]. Dilatation and erosion are the two ways that are likely to be most prominent in this situation. Dilation is the process of adding pixels to the border area of an object, as opposed to erosion, which removes pixels from that region. These operations were carried out based on the structuring components by comparing all of the pixel values in the region specified by the structuring element around the input picture. This area was surrounded by the image being processed. When all of the pixel values in the input picture area are compared, dilation chooses the pixel with the highest value, while erosion chooses the pixel with the lowest value. [23]. The section of an image that will be altered in some way throughout the editing process is referred to as a region of interest (ROI). You may construct a binary image that is the same size as the picture you wish to analyze by making use of a binary mask. This image is known as an area of interest (ROI), and it is the same size.

Transformation

When dealing with 2D visuals, the DWT was applied in an individual fashion to each dimension. As a consequence of this, there are four separate ranges within each scale. These ranges are denoted by the letters LL, LH, HH, and HL. After that, a DWT in two dimensions is carried out using the LL sub-band. It is common practice to regard the LL sub-band to be an approximation of the overall image, but the LH, HL, and HH sub-bands are the components that provide greater levels of detail. As a result of this, wavelets provide a simple hierarchical structure for making sense of the visual fine-grain. The Harr wavelet must be decomposed in a three-stage process in order for our suggested method to work.

Principal Component Analysis

Dimensionality reduction and feature extraction are two of the most common applications of principle component analysis (PCA), which is used often in the domains of data science and machine learning. It is used to translate data that has high dimensions into a space with reduced dimensions, while maintaining a high degree of unpredictability in the data. In order to accomplish this, principle component analysis (PCA) separates linear combinations of the initial characteristics. These linear combinations are referred to as principal components, and they are accountable for explaining the majority of the variation in the data. The primary actions involved in doing PCA are as follows:

Remove the mean from each attribute and divide it by the standard deviation to standardize the data.

At this point, the PCA algorithm is adjusted such that each characteristic is given the same weight.

Calculation of the Covariance Matrix: Determine the covariance matrix of the standardized data. The covariance matrix depicts the interactions between several characteristics and their variations.

Eigen decomposition: Determine the covariance matrix's eigenvalues and eigenvectors. The eigenvectors represent the principal components, and the related eigenvalues show how much variation each main captures. The eigenvectors are orthogonal to one another, implying that they are unrelated.

Principal Components Selection:

Sort the eigenvectors in descending order according to their eigen values. The top-k eigenvectors (primary components). Standardize the data by removing the mean from each characteristic and dividing it by the standard deviation. This stage guarantees that all traits of Principal Components are chosen by sorting the eigenvectors in descending order based on their associated eigen values. The top-k eigenvectors (principal components) with the highest eigen values are selected to build the new lower-dimensional feature space.

Projection: To acquire the converted dataset, project the original data onto the selected main components, which have lower dimensionality but keep the most significant information. Restore response

It is essential to lessen the amount of a data set that is composed of a large number of constant variables while also keeping the majority of the alternative PCA. In this step, the data set is reorganized into a brand-new collection of ordered variables that are connected with their respective variances or significance [24]. This approach has two different outcomes: first, it eliminates the components from the input vector that provide the least variance to the data collection; second, it makes the components of the input vector uncorrelated with one another so that they may be in the best position to appear first in terms of variance.

Features Extraction

Texture study is quite good in differentiating normal tissues from irregular tissues, both for human sight and for machine sight. provides a means for distinguishing cancerous tissues from healthy ones in a patient's body. It does this by selecting quantitative traits that are useful for early diagnosis, which results in an efficiency improvement. In this experiment, the intensities of the segmented pictures were used to obtain the statistical textural analysis features of cross-correlation coefficient, Pearson correlation, and tumour area. PCA components were produced from the LL subbands of the first three-level wavelet decomposition, and those components were used to extract textural information from the data.

Radom Forest Classifier

The Random Forest classifier is a well-known and

strong machine-learning algorithm that may be used to categorize brain cancers. It is possible that this method might be used to diagnose brain tumors. It belongs to the family of methods known as ensemble methods, which aggregate the results of several different independent decision trees to provide more reliable and precise forecasts. The Random Forest method is extensively used in a range of sectors, including medical imaging and healthcare, due to its efficiency in processing intricate data and its ability to reduce overfitting. These two benefits contribute to the algorithm's widespread adoption. The following is a high-level summary of the many steps involved in the diagnosis of brain cancers using a Random Forest classifier:

Obtain a tagged collection of images or descriptions of brain tumors, with each sample being categorized as benign (meaning it does not cause cancer) or malignant (meaning it causes cancer). The dataset has to be broken up into two distinct sections: the input data (features), and the output data (class labels).

Image processing comes to a close with the categorization of the many elements included inside a picture into their respective subcategories. We provide the results of random forest classifiers and compare them with other models. The suggested system's dependability was put through its paces using five rounds of cross-validation, during which the training samples were selected at random.

The random forest method is one of the supervised learning approaches. On the other hand, it is never used outside of circumstances connected to categorization. We are all aware that trees are what make up a forest, and a forest that has a greater number of trees is in better condition. In a similar manner, the random forest approach uses data samples to construct decision trees, then gathers estimates from each tree, and finally chooses the vote option that received the most positive feedback. The most effective plan is one that is integrated.

4. Results

Data Set

These databases include T2-weighted magnetic resonance (MR) brain images acquired from the OASIS dataset and the Harvard Medical School's websites (<http://med.harvard.edu/AANLIB/> and <https://www.oasis-brains.org/>). Because of the

superior contrast and clarity of T2 images over those of the T1 and PET modalities, we opted for the T2 model. Out of the 181 images selected, 81 showed healthy brains and 100 showed abnormal ones.

K-fold stratified cross-validation

The suggested strategy makes use of cross-validation in order to mitigate the negative effects of overfitting. Cross-validation will not improve the accuracy of classification over the long run, but it will provide a robust classifier that can be used on new data sets. There are three different

processes that fall under the category of cross-validation: k-fold cross-validation, random subsampling, and leave-one-out validation. Each and every piece of data is put to use throughout the training process as well as the validation phase, and K-fold cross-validation is performed. The dataset is partitioned into K-folds using the technique, K-1 folds are used for training, and the remaining fold is used for validation. The operation is carried out K times, and the error rates from each of those K trials are then averaged together.

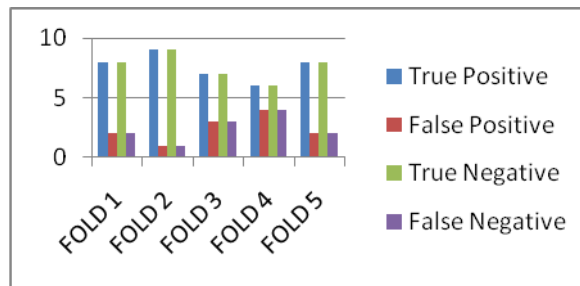


Fig 3. 5-fold cross-validation

The details regarding the validation process for training with both abnormal and normal images can

be found in Table 1, where the images are presented.

Table 1. Training and test images are cross-validated

Total No. of images	Training (143)		Validation (35)	
	Normal	Abnormal	Normal	Abnormal
178	58	85	13	22

Classification Accuracy

Overfitting is eliminated in the proposed system through cross-validation. Even while cross-validation won't improve overall accuracy, it will improve the classifier's accuracy and make it usable on new datasets. K-fold cross-validation is used since it makes full use of all data for both training and validation, and for other reasons as well. As shown in Figure 3, the approach is used to split the whole dataset into K subsets, train each subset using K repetitions, and then average the error rates over K experiments. The 5-fold parameters for both the training photographs and the validation shots are shown in Table 1.

Sensitivity:

Sensitivity is a statistical parameter that reveals how effectively a diagnostic test or classification model can properly identify the existence of a brain tumor in patients who have the

tumor. Sensitivity is evaluated as the ratio of true positive predictions to the total number of people who have the brain tumor.

Specificity:

Specificity is one of the performance indicators used to assess the model's capacity to properly identify malignant brain tumors in the context of brain tumor classification using machine learning algorithms. By improving sensitivity, healthcare workers can improve early discovery and treatment possibilities, resulting in improved patient outcomes.

Accuracy:

Accuracy is a statistical metric that indicates a diagnostic test's or classification model's overall accuracy in properly recognizing both positive and negative instances.

Table 2 compares the proposed algorithm's experimental findings to those of previous studies. The outcome of the suggested approach is that it

enables medical professionals to determine and diagnose.

Table 2. Evaluation of Feature Methods

Features methods	Classifier	Accuracy	Reference
Searching about the pathological area by symmetry checking	SVM	91.15%	Dvořák <i>et al.</i> [36]
First-order statistical, GLCM, GLRL, HOG, LBP	SVM	97.40%	Nabizadeh <i>et al.</i> [35]
MGLCM	MLP	97.80%	Hasan <i>et al.</i> [29]
Hybrid DWT-PCA-GLCM	RF	98% Accuracy 99.2% Sensitivity 97.8% Specificity	Proposed System

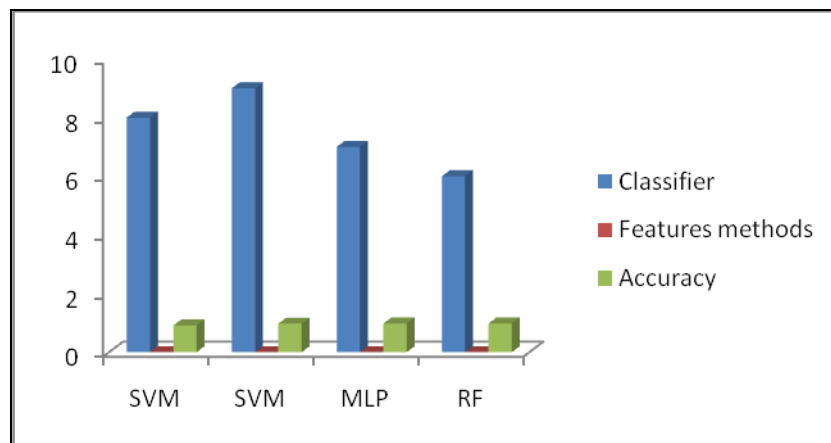


Fig 3. Featured algorithm contrasted with prior research

The suggested approach is intended to categories and distinguishes between normal and pathological tumors in MR images of the brain. For the tested dataset, the system's accuracy is 98%. LL subbands' 3-level wavelet decomposition's PCA component allowed statistical textural information to be recovered.

Based on the obtained data, it was determined that the suggested method performed better and clearly distinguishes between normal and abnormal tumors, allowing clinical specialists to make reliable diagnosis choice

5. Advantages of the Proposed System

Enhanced Feature Extraction: The discrete wavelet transform allows the extraction of both frequency and spatial information from brain tumor images. This can enhance the representation of subtle and intricate patterns present in the images,

potentially leading to improved tumor detection accuracy.

Multiresolution Analysis: The discrete wavelet transform enables analysis of different frequency components of the images at various scales. This can be particularly advantageous for detecting tumors of varying sizes and characteristics, as it captures both fine and coarse details effectively.

Dimensionality Reduction: Principal Component Analysis (PCA) aids in reducing the dimensionality of the feature space while retaining the most relevant information. This can mitigate the "curse of dimensionality" and enhance the efficiency of subsequent classification algorithms.

Noise Reduction: The discrete wavelet transform can help suppress noise and artifacts present in brain tumor images, resulting in cleaner and more reliable feature representations. This, in turn, can contribute to the accuracy and robustness of tumor

identification.

Improved Classification: By combining the strengths of discrete wavelet transform and PCA, the overall classification performance can potentially be boosted. The enhanced features obtained from both techniques can lead to better discrimination between healthy brain tissue and tumor regions.

Adaptability: The combined approach is adaptable to different types of brain tumor images and imaging modalities. It can be applied to various imaging techniques such as MRI, CT scans, and others, making it versatile in clinical applications.

Interpretability: The transformed features obtained through this combined approach could be more interpretable for medical professionals. This can aid in better understanding the nature and characteristics of detected brain tumors.

Robustness to Variability: Brain tumor images often exhibit variability due to factors such as patient positioning, imaging settings, and tumor heterogeneity. The combined approach can potentially handle such variability by capturing relevant features across different cases.

Potential for Early Detection: The high sensitivity of the combined approach might enable the detection of tumors at early stages when they are less conspicuous. This can significantly impact patient outcomes by facilitating timely interventions.

Contribution to Research: The combination of discrete wavelet transform and PCA showcases innovation and contributes to the ongoing research in medical image analysis. It opens avenues for further exploration and improvement in brain tumor identification methods.

6. Social Welfare of the Proposed System

Social welfare implications of using a combined approach of discrete wavelet transform and principal component analysis for brain tumor detection. While the primary focus of such an approach is on medical and technical aspects, there can be indirect social welfare benefits as well:

Improved Healthcare Access: Accurate and efficient brain tumor detection can lead to early diagnosis and intervention. This can enhance overall healthcare access and reduce the burden on healthcare systems by addressing medical issues in their earlier stages.

Enhanced Patient Outcomes: Early detection and accurate classification of brain tumors can significantly impact patient outcomes. Timely treatment and appropriate medical decisions can lead to better prognoses, lower mortality rates, and improved quality of life for patients.

Reduced Treatment Costs: Early detection and precise localization of brain tumors can result in more targeted treatment plans. This can potentially reduce the need for extensive or aggressive treatments, leading to cost savings for both patients and healthcare systems.

Minimized Side Effects: Targeted treatment strategies based on accurate tumor identification can help minimize unnecessary interventions and associated side effects. This can improve patients' overall well-being and quality of life during and after treatment.

Resource Allocation: Accurate brain tumor identification can assist in effective resource allocation within healthcare facilities. Hospitals can better manage staff, equipment, and facilities by focusing on cases that require immediate attention.

Research Advancement: The adoption of advanced techniques like the combined approach of wavelet transform and principal component analysis contributes to medical research. This progress may lead to further innovations, benefiting the broader field of medical imaging and diagnosis.

Public Awareness: The successful implementation of innovative techniques can raise public awareness about the importance of early disease detection and the advancements in medical technology. This increased awareness may encourage people to undergo regular screenings and seek medical advice promptly.

Reduced Psychological Impact: Early detection and accurate diagnosis can alleviate the emotional and psychological stress experienced by patients and their families. A clear understanding of the condition and potential treatment paths can provide reassurance and reduce anxiety.

Healthcare Equity: Implementing advanced detection methods can contribute to more equitable healthcare services by ensuring that cutting-edge diagnostic technologies are accessible to diverse populations.

Economic Productivity: Effective medical interventions driven by accurate detection methods can help patients return to productive activities sooner. This contributes to economic productivity at both individual and societal levels.

7. Conclusion

This study presents a hybrid graphical linear clustering method (GLCM), discrete wavelet transform (DWT), and principal component analysis (PCA) identification system in order to categorize normal and sick brain MRIs. The primary takeaway from this research is the authors' suggestion to combine MR with GLCM in order to consistently differentiate between normal and pathological brain MR. This is the study's key contribution. It is possible that medical practitioners will be able to make more precise diagnoses using this method. Using T2 weighted MR images, it has been established that the statistical textural characteristics created by GLCM are acceptable in distinguishing sick patients from non-pathological patients. These findings were reached by using the GLCM. The majority of brain tumors show out more clearly than the surrounding brain tissue in these photos, which explains why this is the case.

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