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Brain Tumor Detection using Improved Binomial Thresholding Segmentation and Sparse Bayesian Extreme Learning Machine Classification

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ABSTRACT-People are dying these days from numerous deadliest diseases. One such illness is brain tumour, in which the unusual cells within the tumour quickly begin to damage the brain's healthy cells. Owing to this rapid growth, a person may pass away before the disease receives a correct diagnosis. Early disease detection is essential for any disease to help save the patient by providing them with better care. In a similar vein, a patient's life depends on early brain tumour detection. Brain tumour detection is an extremely challenging procedure that we would like to simplify in order to save time. The proposed model facilitates the quicker and more accurate identification of abnormal brain cells, leading to the early detection of brain tumours. In this work, an improved binomial thresholding-based segmentation (IBTBS) is introduced for segmentation purpose. From this segmented image, information theoretic based, wavelet transform (WT) based, and wavelet scattering transform (WST) based features are extracted. An optimization-based feature selection approach (OBFSA) is incorporated between feature selection and tumour classification in order to reduce the dimension of this retrieved feature. Finally, classification is performed using the Sparse Bayesian extreme learning machine (SBELM) classifier. The execution process of this proposed methodology takes an MRI image from the free accessible source. By computing and detecting four different parameters, the experimental analysis of the proposed approach displays the accuracy, specificity, and sensitivity values. This model can assist us in quickly diagnosing brain tumours, potentially saving the lives of patients.

Keywords: Segmentation, Feature Extraction, Feature Selection, Classifier.

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1. INTRODUCTION

Brain tumor stands out as one of the most devastating forms of cancer affecting both children and adults, leading to significant mortality. This condition arises from the abnormal proliferation of cells within the brain. Typically, medical professionals utilize MRI images used for the examination and identification of brain tumor. Predicting tumor progression quantitatively using patient data is crucial for tumors pose challenges in segmentation due to their variable shape, exterior, and position [1-2]. Segmentation method be able to be categorized as automatic or semi-automatic, with semi-automatic approaches requiring user interaction. Given the noisy nature of MRI data, constant filtering is necessary to remove high-frequency disturbances before processing.

Automatic segmentation employs conventional machine learning models, often incorporating handcrafted features. In current times, CNNs have gained prominence in brain tumor segmentation, extracting more sophisticated features from brain images. The proposed research aims to enhance tumor growth segmentation prediction through optimized modeling and deep learning algorithms, utilizing Modified Shuffled Frog Leaping Optimization (MSFO) for improved results.

The contributions of this work include:

1. An Improved Binomial Thresholding-Based Segmentation (IBTBS), is introduced for efficient segmentation.
2. The segmented image is then subjected to feature extraction scattering wavelet transform (SWT) based features.
3. To enhance the diagnostic process, a feature selection method with optimization is integrated before classification of tumour, reducing the dimensionality of the feature set.
4. Classification is accomplished through the application of the Sparse Bayesian Extreme Learning Machine (SBELM) classifier.
5. Experimental analysis, evaluating the proposed approach through the computation of four distinct parameters, reveals

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promising results.

The manuscript is planned as follows: *Section 2* briefly describes in recent times evolved tumor growth model-based segmentation technique. *Section 3* details the proposed methodology and their mathematical description. Section-4 presents segmentation results, discussions, and comparative analyses. Finally, *Section 5* summarizes the entire work.

2. RELATED WORK

Nowadays, the vast amount of image data generated by clinical laboratories poses challenges for efficient segmentation within acceptable time frames. Manual inspection of these images is laborious, prompting an increasing interest in computer-based methods for tumor segmentation and classification. The preprocessing step is crucial, as subsequent stages depend on its effectiveness. Magnetic Resonance (MR) images often contain artifacts impacting segmentation accuracy, such as noise and poor contrast.

For instance, Usman et al. [1] used structural knowledge to remove noise, and Amin et al. [2] employed morphological operations to eliminate artifacts. Raju et al. [3] leveraged local and non-local neighborhood spatial information to mitigate noise effects. Filters like high-pass filters, sharpening filters, histogram equalization, Gaussian high-pass filters, and edge detectors are also applied in medical image analysis. In brain tumor detection, skull region removal is critical, achieved through manual processes or morphological operations. It utilized LBP and HOG features, demonstrating improved performance on the BRAST 2013 dataset. They proposed an ABC and FCM approach for brain tumor detection, achieving enhanced results. Authors introduced a fusion method combining spatial FCM and K-means clustering, outperforming existing methods. These approaches showcase ongoing efforts to enhance tumor segmentation and classification accuracy in medical image processing. Dasari et al. [5] proposed stacking based approached for predictions and Dasari et al. [6,7] proposed majority voting and deep hybrid model for improved better prediction. Dasari et al. [8,9] reviewed feature selection approached with embedding techniques. Dasari et al [11] performance of cloud-based architecture and enhances the sound classification [12] using artificial neural networks.

3. PROPOSED METHODOLOGY

In this sector, the proposed methodology consists of various stages. The work flow of the proposed structural design is shown in below figure [1]. Each stage of the module explained detailed in the below *sections 3.1 to 3.6*.

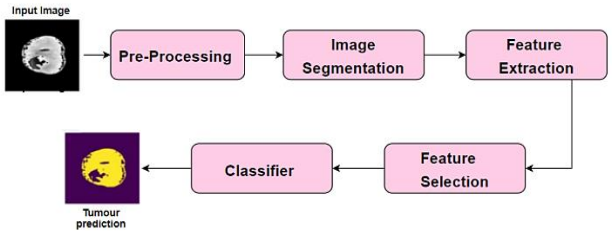

Figure 1. Work flow of the methodology

3.1. Pre-Processing

In Pre-processing preparing medical images, such as brain tumor images, for analysis and diagnosis. In this work, we use pre-processing techniques such as image rescaling and Normalization. These processes are ensured that images are on a consistent scale and have comparable intensity levels, which is often important in tumor classification. This equation scales pixel values based on the range of values in the original image, mapping them to a normalized range.

Image rescaling involves adjusting the size or resolution of an image. It is often performed to standardize the dimensions of images in a dataset. The process typically involves interpolation to estimate pixel values at the new resolution. The mathematical equation for rescaling an image can be expressed as shown in *equation (1).*

$$\mathrm{I}_{\mathrm{rescaled}}(\mathrm{x},\mathrm{y}) = \mathrm{I}\left(\frac{\mathrm{x}}{\mathrm{s}_{\mathrm{x}}},\frac{\mathrm{y}}{\mathrm{s}_{\mathrm{y}}}\right) \quad (1)$$

Where: $I_{rescaled}(x, y)$ is value at coordinates (x, y) in rescaled image.

I (x, y) am the original pixel value at coordinates $(\frac{x}{s_x}, \frac{y}{s_y})$.

s_x and s_y are scaling factors for the x and y dimensions, respectively.

Image normalization involves scaling pixel values to a standardized range, often between 0 and 1 or -1 and 1. The normalization equation is given by *equation (2).*

$$I_{normalized}(x,y) = \frac{I(x,y) - \min(I)}{\max(I) - \min(I)} \quad (2)$$

3.2. An improved binomial thresholding-based segmentation (IBTBS)

The original binomial thresholding method is a simple technique used for image segmentation. It involves comparing each pixel intensity with a threshold value. Pixels with intensities below the threshold are assigned to one class (background), and pixels with intensities above the threshold are assigned to another class (foreground). The segmented image shown at *figure (2).*

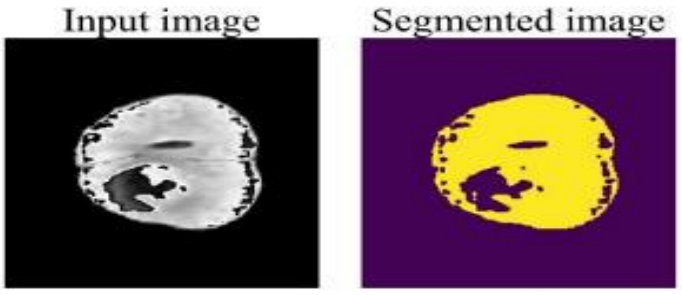

Figure 2. Input image and segmented image

Mathematically, the binomial thresholding decision can be expressed as shown in *equation (3).*

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$$\begin{matrix} 0 \text{ if } (I(x,y) < T \\ 1 \text{ if } (I(x,y) \geq T \end{matrix} \quad (3)$$

3.3 Feature Extraction

Feature extraction is a crucial step in brain tumour classification from medical images. It involves selecting relevant information from the images to represent them in a way that is suitable for machine learning models. We use feature extraction approaches such as scatter wavelet transform. Wavelet Scattering Transform (WST).

The Wavelet Scattering Transform, often referred to simply as the Scattering Transform, is a powerful signal processing technique [22] used for feature extraction, particularly in the context of image and signal analysis. The Scattering Transform is inspired by the scattering series introduced by mathematician Jean Morlet and has been extended and developed for various applications, including computer vision and pattern recognition. In this work we use.

Given an input image x (n1, n2), the Wavelet Scattering Transform can be expressed as follows:

Wavelet Transform: Apply a wavelet transform to the input image.

Let Wx denote the wavelet coefficients shown in *equation (4).*

$$W_x(t,a,\theta) = x(t) * \psi_{a,\theta}(t) \quad (4)$$

Where:
$Wx\ (t,\ a, \theta)$ is the wavelet coefficient at time t, scale a, and orientation θ.

Represents convolution.
$\psi a, \theta(t)$ is the wavelet function parameterized by scale a and orientation θ.

3.3.Optimization-Based Feature Selection Approach (OBFSA)

In this approach, its relevant subset of features. In the context of brain tumour classification, this can be crucial for enhancing model accuracy, reducing computational complexity, and avoiding overfitting. OBFSA objective function that combines classification accuracy and a penalty for the number of features. It is used to find the feature subset that maximizes or minimizes this function shown on below *equation (5).*

$$J(W) = \alpha \cdot \text{Accuracy(w)} - \beta \cdot \text{Penalty(w)} \quad (5)$$

w is a binary vector representing the feature subset (1 if the feature is selected, 0 otherwise).

α and β are weights to balance accuracy and the penalty term.
Accuracy (w) is the classification accuracy of the model using the selected features.

Penalty(w) is a penalty term for the number of selected features.

Penalty term to discourage the selection of too many features. This term could be a simple count of selected features or a more sophisticated measure. This penalty term sums up the selected features in the subset in *equation (6).*

$$\text{Penalty(w)} = \sum_{i=1}^{N} w_i \quad (6)$$

N is the total number of features.

wi is an element of the binary vector w.

The feature selection as an optimization problem, seeking the optimal binary vector w∗ that maximizes or minimizes the objective function shown in *equation (7).*

$$W^* = \text{argmax}_w J(w) \quad (7)$$

3.5. Traditional Machine learning based classifier

3.5.1. Decision Tree

In a decision tree algorithm for tweet classification, a tree-like structure is constructed. Each node within the tree corresponds to a decision-based on a particular feature, and each branch represents the potential outcomes resulting from that decision. The terminal nodes, or leaves, of the tree store the ultimate classification labels. The decision at each node is determined using a mathematical condition based on input data. The Gini impurity is employed as a metric to gauge how frequently a randomly selected element would be misclassified within a dataset. For a binary classification problem, the Gini impurity (IG) is defined as:

D: Dataset at a particular node.
C: Set of classes
Gini(D): Gini impurity of dataset D.

The GI for a dataset D is given by the formula as shown in equation (8):

$$\text{Gini(D)} = 1 - \sum_{i=1}^{n} (\text{Pi})^2 \quad (8)$$

where
n - number of classes.

3.5.1.2. Random Forest

A RF yields the classification mode or mean prediction (for regression) of the individual trees as the final output. It Combine the predictions of all the trees to obtain the final prediction. In classification tasks, this is often achieved through a majority vote, where the class with the most votes is selected. this typically involves a majority vote, while in regression, it may be computed as the average. Entropy serves as a metric for impurity within a set of labels. In the context of a set D containing C classes, the entropy H(D) is computed as follows in *equation (9).*

$$\text{H(D)} = -\sum_{i=1}^{c} (\text{Pi}) \left(\log_2^{\text{Pi}}\right) \quad (9)$$

Where
pi - proportion of samples in class i.

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3.5.1.3. GaussianNB

GNB is Compute the prior probability of each class P(yi), which represents the probability of a randomly selected tweet belonging to class i. For each feature xj in X, compute the mean (μij) and standard deviation (σij) of xj for each class i. This assumes that the distribution of xj within each class is Gaussian in *equation (10)* and *equation (11).*

$$\mu ij = \frac{1}{N_i}\sum_{k=1}^{Ni} x_{kj} \quad (10)$$

$$\sigma_{ij} = \sqrt{\frac{1}{N_i}\sum_{k=1}^{Ni}(x_{kj} - u_{ij})^2} \quad (11)$$

Where are you
Ni - number of samples in class i.

3.5.1.4. K-Nearest Neighbors

KNN stand as a straightforward and intuitive classification algorithm. It categorizes an input sample through considering the majority class between its k-nearest neighbors in feature space. While various distance metrics can be employed to gauge similarity between samples, Euclidean distance is a frequently chosen measure.

For a new input sample xnew, calculate the distance between xnew and all samples in X. Commonly used distance metrics include Euclidean distance is shown in *equation (12).*

$$\text{Euclidean Distance}(x, x_i^1) = \sqrt{\sum_{i=1}^{n}(x_i - x_i^1)^2} \quad (12)$$

3.5.1.5. Support Vector machines

SVM is another popular ML algorithm that able to apply to brain tumour classification. SVM is effective for both binary and multiclass classification tasks. It aims to identify optimal values for β that maximize the margin between the two classes. This objective is formulated as the minimization of the following objective function is shown in *equation (13).*

$$\min\beta, \beta 0 \frac{1}{2} || \beta || + C \sum_{i=1}^{m} \left[\max\left(0, 1 - y(i)\left(f\left(X(i)\right) + \beta 0\right)\right)\right] \quad (13)$$

Here:
||β|| is the Euclidean norm of the coefficient vector.

3.5.1.6. LightGBM

LightGBM is a gradient boosting framework that uses hierarchal learning-based algorithms. It's a powerful tool for various machine learning tasks, including classification problems like brain tumour detection. Describing LightGBM with mathematical equations involves understanding the principles of gradient boosting and the specifics of LightGBM.

In gradient boosting, the goal is to minimize the loss, which is a measure of the discrepancy between target values and forecast values. The loss function and a regularization term make up the desired function for LightGBM is shown in *equation (14).*

$$Objective(\phi) = \sum i \ = 1nLoss\left(yi, y^{i(\phi)}\right) + \sum k = 1K\Omega(fk) \quad (14)$$

Here,
n is the number of samples,
yi - i-th sample,
y^i(ϕ) is the predicted i-th sample,
K is the number of leaves in the tree,
fk represents a leaf,
Ω(fk) is a regularization term.

3.5.1.7. Multi-Layer Perceptron (MLP)

A MLP is a type of ANN commonly used for classification tasks, including brain tumor classification.

Given an input vector x, the forward propagation in an MLP involves computing the activations of each neuron in the network layer by layer.

Input Layer a (0) =x;

Hidden Layers: For each hidden layer l, compute the weighted sum (z(l)) and the activated output (a(l)) shown in *equation (15).*

$$Z^{(l)} = W^{(l)}.a^{(l-1)} + b^{(l)}$$
$$a^{(l)} = \sigma(z^l) \quad (15)$$

Here,
W(l) is the weight matrix for layer l,
b(l) is the bias vector for layer l,
σ (·) is the activation function (commonly sigmoid, tanh, or ReLU), a(l−1) is the output from the previous layer.

3.6. Proposed Classifier-Sparse Bayesian extreme learning machine (SBELM)

It is an extension of the traditional Extreme Learning Machine (ELM) algorithm that incorporates sparsity and Bayesian techniques for improved model interpretability and generalization performance. The goal of SBELM is to enhance the ELM algorithm by selecting a subset of important features and improving the generalization capability of the model.

Consider the standard ELM objective function with a regularization term for sparsity is shown in *equation (16).*

$$J(w, \beta) = \frac{1}{2}||H_w - y||^2 + \frac{\lambda}{2}||w||^2 + \beta\sum_{i=1}^{N} g_i \quad (16)$$

w is the output weights.
H - hidden layer
y is the target output.
λ is a regularization parameter.
β is a sparsity-inducing parameter.
gi is a binary variable (0 or 1) indicating whether the weight wi is relevant or not.
N is the number of features.

SBELM introduces sparsity by incorporating a sparsity-inducing prior in the Bayesian framework. This encourages the learning algorithm to select only a subset of relevant features, leading to a sparse representation of the input data. SBELM integrates Bayesian principles, specifically Bayesian inference, into the ELM model. Bayesian methods allow for the incorporation of prior beliefs about the model parameters and provide a probabilistic interpretation of the model.

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Sparse Bayesian learning techniques, such as relevance vector machines or sparse Bayesian ELM, involve placing a sparsity-inducing prior on the weights. This encourages the model to automatically select a small subset of relevant features during the training process.

Bayesian prior on the output weights is shown in *equation (17)*.

$$p(W|\alpha) = N(W|0, \alpha^{-1}I) \quad (17)$$

where
α is a precision parameter.
During the training of SBELM, the algorithm iteratively updates the model parameters using Bayesian inference. The sparse nature of the solution is achieved by encouraging many weights to be close to zero.

spike-and-slab prior to encourage sparsity is shown in *equation (18).*

$$P(w|\alpha, g) = \prod_{i-1}^{N} \left(\frac{\beta}{2}\exp\left(-\frac{\beta}{2}w_i^2\right)\right)^{gi} * \left(\frac{1}{2}\exp\left(-\frac{1}{2}w_i^2\right)\right)^{1-g_i} \quad (18)$$

The optimization involves finding the posterior distribution is shown in *equation (19).*

$$p(w|y, \alpha, \beta) \propto p(y \mid H, w) \cdot p(w \mid \alpha, g) \quad (19)$$

4. PROPOSED MODEL

The proposed model facilitates the quicker and more accurate identification of abnormal brain cells, leading to the early detection of brain tumour.

In this work, IBTBS is introduced for segmentation purpose. From this segmented image, information theoretic based, wavelet transform (WT) based, and wavelet scattering transform (WST) based features are extracted. OBFSA is incorporated between feature selection and tumour classification in order to reduce the dimension of this retrieved feature. Finally, classification is performed using the SBELM classifier. The proposed method work flow is shown in figure [3].

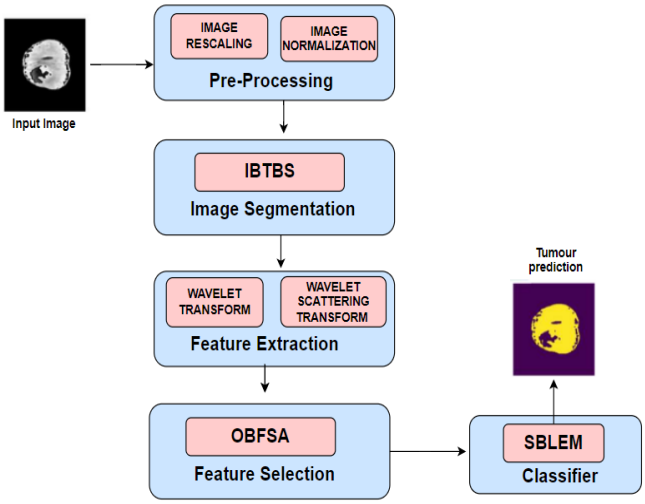

Figure 3. Proposed architecture

5. EXPERIMENTAL ANALYSIS

In this section, we investigating the proposed feature extraction and feature selection-based methods such as WST and OBFSA with SBELM classifier for the tumour prediction with their presence and absence. The proposed model was compared with the different machine learning approaches with their performance.

Notations as follows:
DT-Decision tree, RF-Random Forest, GNB-Gaussian Naive Bayes, K-Nearest Neighbors, Linear SVM-Support Vector machines, LightGBM (Light Gradient Boosting Machine), MLP-Multi-Layer Perceptron, FE-Feature Extraction, FS-Feature Selection. TP- True Positives, TN-True Negatives, FP-False Positives, FN-False Negatives.

5.1 Dataset Description

In this work, we use BRATS2018, BRATS 2019 and BRATS 2020 datasets are used for tumor classification. The BRATS 2018 consists of 240 HGG features and 70 LGG features, the BRATS 2019 consists of 280 HGG features and 80 LGG features where as in BRATS 2020 consists of 151 HGG features and 70 LGG features. We combine all the three datasets into a single unit of dataset for analysis of the performance. The combine BRATS 2018, 2019,2020 dataset consists of 671 HGG features and 220 LGG features. We split the dataset into 80:20 ration for training as well as for testing.

5.2 Evaluation Metrics

In the context of brain tumour classification, the performance metrics such as Accuracy, Precision, Recall (Sensitivity), and F1-Score are commonly used to assess the effectiveness of a classification model.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (20)$$

$$Precsion = \frac{TP}{TP + FP} \quad (21)$$

$$Recall = \frac{TP}{TP + FN} \quad (22)$$

$$F1 - Score = \frac{2.Precision.Recall}{Precision + Recall} \quad (23)$$

These equations help evaluate the classification performance of a model in the context of brain tumour classification. It's important to consider these metrics together to gain model's effectiveness, especially in scenarios where imbalances exist between the classes.

5.3 Performance Analysis

The results of the implementation of the aforementioned techniques are examined in four cases.

5.3.1 Performance analysis without FE and without FS

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Table1. Performance analysis Without FE and without FS

Algorithm	Accuracy	Precision	Recall	F1-Score
DT	76.27	66.67	67.86	80.00
RF	77.75	71.79	85.86	78.25
GNB	61.02	64.71	39.29	48.89
KNN	72.88	73.08	67.86	70.37
Linear-SVC	76.27	70.59	85.71	77.42
LightGBM	75.14	75.00	70.00	83.89
MLP	55.93	62.50	17.86	27.78
Proposed model	**79.75**	**73.79**	**87.86**	**80.25**

Evaluation 1: The proposed model outshines others with an accuracy of 79.75%, precision of 73.79%, recall of 87.86%, and an F1-Score of 80.25%. RF and Linear-SVC also perform well, balancing precision and recall. GNB and MLP face challenges, showing lower recall values.

5.3.2 Performance analysis with FE and without FS

Table 2. Performance of machine learning algorithms

Algorithm	Accuracy	Precision	Recall	F1-Score
DT	83.05	73.68	83.33	84.85
RF	**86.83**	**82.35**	**88.32**	**90.32**
GNB	62.71	62.50	53.57	57.69
KNN	66.10	65.38	60.71	62.96
Linear-SVC	47.46	47.46	53.57	64.37
LightGBM	83.05	78.13	89.29	83.33
MLP	72.88	83.33	53.57	65.22
Proposed model	**92.20**	**90.48**	**90.48**	**90.48**

Evaluation 2: The proposed model emerges as the top performer with outstanding accuracy (92.20%), precision (90.48%), recall (90.48%), and F1-Score (90.48%). Random Forest and DT also exhibit strong overall performance, achieving high precision, recall, and accuracy. GNB, KNN, and LightGBM deliver balanced results, while Linear-SVC struggles with lower accuracy and precision. MLP performs well in precision but struggles with recall.

5.3.3 Performance analysis without FE and with FS

Table3. Performance of machine learning algorithms

Algorithm	Accuracy	Precision	Recall	F1-Score
DT	76.27	66.67	66.67	80.00
RF	**86.44**	**77.78**	**71.43**	**87.50**
GNB	62.71	66.67	42.86	52.17
KNN	72.88	71.43	71.43	71.43
Linear-SVC	67.80	84.62	39.29	53.66
LightGBM	86.14	78.00	87.29	86.89
MLP	49.15	48.08	89.29	62.50
Proposed model	**88.14**	**80.00**	89.29	**88.89**

Evaluation 3: The proposed model stands out as the highest performer, an impressive accuracy 88.14%, precision 80.00%, recall of 89.29%, and an F1-Score of 88.89%. RF also exhibits strong performance, excelling in accuracy and F1-Score. Linear-SVC struggles with recall despite high precision. GNB and MLP face challenges.

5.3.4 Performance analysis with FE and with FS

Table 4. Performance of machine learning algorithms

Algorithm	Accuracy	Precision	Recall	F1-Score
DT	88.14	83.87	92.86	88.14
RF	**91.53**	**89.66**	**92.86**	**91.23**
GNB	62.71	66.67	42.86	52.17
KNN	77.97	82.61	67.86	74.51
Linear-SVC	79.66	80.77	75.00	77.78
LightGBM	88.14	88.89	85.71	87.27
MLP	75.14	75.00	70.00	83.89
Proposed model	**94.55**	**92.86**	**82.86**	**92.86**

Evaluation 4: The proposed model stands out as the top performer, achieving exceptional accuracy (94.55%), precision (92.86%), recall (82.86%), and F1-Score (92.86%). Random Forest (RF) also demonstrates strong Linear-SVC and showcase well-balanced results across metrics. DT and LightGBM exhibit robust performance, particularly in recall.

5.4 Performance Comparison

In this Section, the proposed model was tested with feature extraction and feature selection approaches with their present and absence. The detailed investigation with different machine learning approaches and proposed classifier is shown in table [1-4] and the below investigation showcases the proposed model significantly improved with WST feature extraction approach with OBFSA feature selection approach. The features are feed to the SBELM classifier for the best tumour prediction.

M1- Without FE and Without FS approaches
M2- With FE and Without FS approaches
M3- Without FE and With FS approaches
M4- Proposed method (It consists of WST with OBFSA and SBELM classifier)

Table 5. Performance of the proposed model

Metrics	M1	M2	M3	M4
Accuracy	79.75	92.20	88.14	**94.55**
Precision	73.79	90.48	80.00	**92.86**
Recall	87.86	90.48	89.29	**82.86**
F1-Score	80.25	90.48	88.89	**92.86**

5. CONCLUSION

In the face of the rising threat of deadly diseases, the urgency to enhance early detection mechanisms is underscored,

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particularly in the case of brain tumors. This study addresses the critical need for swift and accurate identification of abnormal brain cells to expedite the early detection of brain tumors. The proposed model introduces the Improved Binomial Thresholding-Based Segmentation (IBTBS) for efficient segmentation, followed by the extraction of features using information theoretic, wavelet transform, and wavelet scattering transform methods. The inclusion of an Optimization-Based Feature Selection Approach (OBFSA) aims to streamline the feature dimensionality, enhancing the subsequent tumor classification using SBELM classifier. The model, evaluated on MRI images, demonstrates promising accuracy, specificity, and sensitivity values. This streamlined methodology holds the potential to revolutionize brain tumor diagnosis, offering a timely and life-saving intervention for patients.

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