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Improved Brain Tumor Diagnosis and Classification Using VMS Integ-Net

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Abstract: Brain tumors pose a significant challenge in medical imaging due to their variability and the need for precise classification. Our study aims to address this problem by developing a new method for detecting and classifying brain tumors. The key goal of this research is to improve brain tumor classification accuracy in medical imaging. This research is motivated by the need for accurate brain tumor diagnosis and treatment planning. The BRATS dataset, which contains 1000 images of four different types of brain tumors: glioma, meningioma, metastasis, and astrocytoma, was used in our study. In this research, we use the advanced VMS Integ-Net model to address the critical challenge of brain tumor detection and classification. The VMS Integ-Net model is unique in that it combines the HoG-based Feature extraction stage with the VGG-19's feature extraction, as well as its capability with Multi-Class Support Vector Machine (SVM) for robust and efficient classification. With an astounding accuracy rate of 99.57%, our method was an enormous accomplishment. It had a high sensitivity of 99.3405% and a high specificity of 99.3523%. These findings outperform previously published methods, emphasizing the significance of our work in advancing brain tumor diagnosis and classification. This major study advances medical decision-making and opens the door to automated diagnostic solutions in neurology and oncology.

Keywords: *brain tumors, Glioma, Meningioma, Metastasis, Astrocytoma, early detection, accurate classification, VMS Integ-Net model, deep learning, machine learning, accuracy, specificity, sensitivity, diagnosis, healthcare*

1. Introduction

Brain tumors are a serious health issue that affects the lives of countless people all over the world [1]. These pernicious anomalies can strike anyone, at any age, and their consequences are often disastrous [2]. They can cause a wide range of symptoms, from cognitive impairment to physically debilitating conditions. Furthermore, the severity of the situation is exacerbated by the wide range of brain tumor types, each of which necessitates specialized treatment and care [3]. Glioma, Meningioma, Metastasis, and Astrocytoma are examples of these types, each with distinct characteristics that necessitate precise identification. The range of brain tumors is broad, and they are classified into several types. Glioma, a common malignant tumor, has an infiltrative nature that makes surgical removal difficult [4]. Meningioma, which starts in the meninges, and Metastasis, which occurs when cancerous cells spread from other organs, both present unique challenges [5]. Astrocytoma, which is most commonly found in the brain or spinal cord, has distinct characteristics that necessitate customized medical treatment. Brain tumor risk factors include genetic predisposition, radiation exposure, and environmental influences [6]. Prompt diagnosis enables timely medical intervention, which can save a person's life [7]. Furthermore, tumor types must be classified in order to determine the most effective treatment strategies [8-10]. It can have serious consequences for a patient's prognosis, treatment options, and overall quality of life. The unpredictability of the occurrence of these tumors emphasizes the importance of early detection and accurate classification [11]. Because early intervention can save lives and have a significant impact on treatment decisions, classification is critical for patients' prognoses and overall well-being [12].

By introducing the VMS Integ-Net model, a novel approach to brain tumor detection and classification, we contribute to address these critical concerns. This cutting-edge system expertly combines deep learning with traditional machine learning techniques, resulting in remarkable accuracy. This work is an important step towards closing the gap between cutting-edge technology and urgent healthcare needs, ultimately improving the lives of brain tumor patients and providing hope for a brighter future.

The following is how the research paper is organized: We provide an overview of the critical issue of brain tumors in the first section, "Introduction," discussing their prevalence and impact. We investigate the risk factors for these tumors and highlight the various types, including Glioma, Meningioma, Metastasis, and Astrocytoma, emphasizing the critical need for early detection and accurate classification. The second section, "Related Works," is a thorough literature review that provides insights into

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existing methods and approaches in the field. In the third section, "Proposed System," we present the novel VMS Integ-Net Model, which combines deep learning and machine learning techniques. We discuss the architecture of the model, its integration, and provide an overview of the methodology. The fourth section, "Results and Analysis," includes a description of the dataset, its partitioning, and a detailed performance evaluation using accuracy, specificity, and sensitivity metrics. We present a discussion of the findings and their implications. The fifth section, "Conclusion," summarizes the key findings of the study and their significance in the context of medical imaging. We discuss potential future research directions. Finally, the sixth section of the paper, "References," provides citations and sources used throughout the paper.

2. Related Works

Deep learning approaches for detecting and classifying anomalies in CT images have received a lot of consideration in current ages [13]. Deep learning models' ability to automatically learn intricate patterns and representations from large-scale datasets has yielded promising results in the medical imaging domain, especially in detecting and classifying anomalies in CT images [14-16]. These approaches have outperformed traditional machine learning algorithms and have the potential to help radiologists make more accurate diagnoses [17]. Deep learning models have achieved cutting-edge performance in a variety of benchmarks, and they have the potential to help radiologists make more accurate diagnoses, reduce false positives/negatives, and improve patient outcomes [18-20]. The purpose of this literature analysis is to investigate the significance of deep learning approaches in this field and to summarise key findings from relevant studies.

Sharma AK et al. (2022) [21] develops a model using recurrent networks and CNN (ConvNets) that have been demonstrated to be suitable. Different regions of the input image are treated equally and independently by ConvNets. They cannot explicitly model spatial relationships and dependencies between far-flung pixels or regions. This limitation can be problematic for tasks requiring reasoning about global context or long-distance dependencies. The accuracy obtained here is 98.3%.

Recently, Hasanah et al. (2021) predicted a process based on Machine Learning [22]. A support vector machine model was used to classify distinct types of tumors with an average accuracy of 95.83 percent. In medical applications such as brain tumor classification, imbalanced datasets are common, with one class (e.g., tumor) vastly outnumbering the other (e.g., healthy tissue). SVMs are susceptible to imbalanced data, which may result in classification results that favour the majority class. Handling class imbalance with SVMs necessitates careful consideration of sampling techniques or the application of cost-sensitive learning strategies.

Hossain T., et al. (2020) [23] propose a system to differentiate between normal and abnormal pixels. Texture-based and statistical features typically concentrate on the image's local characteristics while ignoring the spatial context. The convolutional layers of CNNs, on the other hand, are exceptional at capturing spatial dependencies. Combining texture-based and statistical features with CNNs may not fully exploit CNNs' ability to learn high-level spatial representations, potentially limiting their ability to recognize complex patterns and structures. CNN achieved an accuracy rate of 97.87%, which is quite impressive.

Khalil et al. (2020) proposed a modified two-step dragonfly mechanism system for segmenting 3D MR images of brain tumors [24]. If the images contain artefacts, noise, or low resolution, the accuracy and dependability of the segmentation results may be compromised. The effectiveness of the system may be limited when dealing with heterogeneous or irregularly shaped tumors. The system's segmentation algorithms may struggle to precisely capture and delineate complex tumor boundaries, resulting in under- or over segmentation. Inappropriate parameter selection may produce suboptimal segmentation results. Lastly, the computational requirements and processing time of the system can be considerable, especially when dealing with large 3D MR image volumes. This limitation may restrict its use in real-time or resource-constrained environments. The accuracy achieved with this system is 98.20%.

Avsar E (2019) [25] used faster Region-based CNN for diagnosing human brain tumors. It has limitations and drawbacks in diagnosing human brain tumors. It is observed that acquiring and annotating huge datasets for brain tumor diagnosis can be time-consuming and expensive, as well as subject to inter-observer variability. Limited or skewed training data can result in overfitting or biased model predictions, potentially affecting the system's accuracy and generalizability. Second, the interpretability of DL models is still an issue. While region-based CNNs can achieve impressive diagnostic performance, it is difficult to understand the model's underlying features and decision-making process [26-28]. This lack of interpretability can undermine system trust and acceptance, particularly in critical medical decision-making scenarios. This system has a higher accuracy of 91.66 percent than other systems using the same dataset.

In addition to the works mentioned above, a few others have been written in Literature and are listed below. The Whale Harris Hawks optimization-based method in combination with Deep Neural Networks was introduced in 2020 by Rammurthy D and Mahesh PK [33]. Because of deep learning techniques, this approach demonstrated advantages

in terms of the potential for accurate classification. However, one potential limitation is the method of optimisation chosen and its adaptability to various types of brain tumors.

In 2023, Aggarwal et al. [34] presented a deep neural network-based method for early detection and segmentation of brain tumors. The strength of this approach is its potential for early diagnosis, which can lead to more timely medical interventions. However, in cases with heterogeneous or atypical tumor presentations, it may encounter difficulties, potentially affecting segmentation accuracy.

In 2023, Geetha et al. [35] published Conditional Random Field-Recurrent Neural Network (CRF-RNN) segmentation. The advantage of this technique is that it focuses on segmentation accuracy, which improves understanding of tumor boundaries. The computational intensity of CRF-RNN in large datasets could be a potential limitation.

In 2022, Sivapathi Arunachalam and Gopalakrishnan Sethumathavan [36] proposed i-YOLOV5, a tumor detection method based on deep CNN. This approach has the advantage of being efficient, as YOLOV5 has demonstrated speed and accuracy in object detection. However, due to the nature of the detection algorithm, it may encounter difficulties in classifying tumors with intricate or irregular shapes.

3. Proposed System

The proposed methodology for brain tumor classification, as shown in Fig.1, is a comprehensive approach that includes multiple key stages, with the goal of accurately classifying brain images into different tumor categories. The procedure starts with the acquisition of brain images from the BRATS dataset [18], and the quality and consistency of these initial scans are critical for successful classification. The first major step is preprocessing, which involves resizing the images to a standardised 256x256-pixel format using bilinear interpolation and converting them to grayscale. These transformations ensure that the data is consistent and that the images are ready for further analysis.

Following the preprocessing stage, a critical filtering step is performed, in which a median filtering technique is used. The median filter operation improves image quality significantly, paving the way for further investigation.

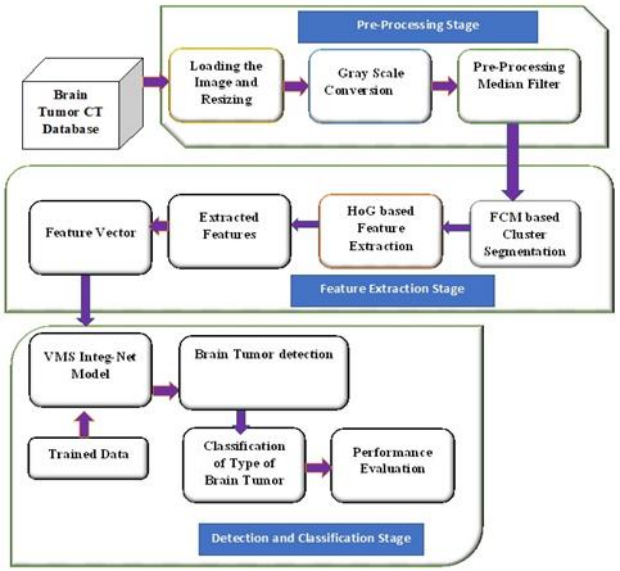


Fig 1. Proposed Brain Tumor detection and Classification System

The use of the Fuzzy C-Means (FCM) clustering method to segment the images, effectively partitioning them into different clusters based on pixel values, is one of this methodology's distinguishing features. Although FCM clustering is not a traditional segmentation technique, it is useful in identifying different tissue types or regions, including potential tumor areas.

The Histogram of Oriented Gradients (HOG) method is used in the following feature extraction stage to capture local texture features and gradients within the images. These characteristics, which include mean, standard deviation, entropy, variance, smoothness, contrast, correlation, and energy, provide a thorough understanding of image patterns and structures. The HOG-based features are critical input for the classification stage, which employs a sophisticated model known as VMS Integ-Net. This model combines VGG-19, a deep convolutional neural network, and multiclass Support Vector Machines (SVM) to classify brain images into tumor categories such as 'Glioma,' 'Meningioma,' 'Metastasis,' and 'Astrocytoma.'

The final results, which include segmented images, selected features, classification results, and performance metrics, are presented in order to provide a clear understanding of the methodology's capabilities and potential for improving brain tumor classification. This methodology combines preprocessing, feature extraction, and classification, making it a powerful and promising approach in medical image analysis, and it is discussed in detail below with mathematical discussions

In the beginning stage of our approach, we load the acquired brain images from the BRATS dataset [18]. Let us say I(x,y) represents the original pixel value at coordinates (x,y) in the input image.

Following image loading, preprocessing plays an important role in standardizing image dimensions, typically resizing them to a standardised 256x256-pixel format.

To resize the image, I to a new width W and height H, we can use bilinear interpolation, which smoothly scales the pixel values:

I'(x',y')=∑i=01∑j=01I(x+i,y+j)·w(i)·w(j)…………………..(1)

Bilinear interpolation ensures a smooth transition of pixel values in the resized image, resulting in a visually pleasing and artifact-free image. Next, we use colour mapping to convert the image into a Grayscale image, which is the appropriate format.

Conversion to grayscale is commonly done using the luminance formula:

Y=0.299·R+0.587·G+0.114·B……………………………(2)

This formula ensures that the luminance information in the grayscale image is captured, which is required for subsequent processing.

Preprocessing ensures data consistency. We've arrived at the filtering stage, which is crucial for improving the quality of the input images. This Pre-Processing step involves the use of a median filtering technique. This technique reduces image noise and smoothes out small variations in pixel values.

Median filtering is a non-linear image processing technique that improves image quality by reducing noise. By replacing each pixel value with the median value within a local neighbourhood, it smoothes out small variations in pixel values. To reduce noise and improve image quality, we apply it to each pixel location in the resized image. The median filtering operation is mathematically represented as follows:

I''(x',y')=median(I'(x'-1,y'-1),I'(x'-1,y'),I'(x'-1,y'+1), I'(x',y'-1),I'(x',y'),I'(x',y'+1),I'(x'+1,y'-1), I'(x'+1,y'),I'(x'+1,y'+1))….(3)

This operation is applied to each pixel in the resized image to smooth out transitions and improve image quality, preparing it for the next stages of our brain tumour classification methodology.

We use FCM method here, with the goal of partitioning the image into different clusters based on pixel values [37].

However, FCM clustering is not traditionally regarded as segmentation in this context. It is more of a clustering method that can be used to identify different tissue types or regions within a medical image, which is frequently an important step in tumour classification [38].

The input data 'X' represents the pre-processed image, with each pixel representing a data point with multiple features such as grayscale intensity. The letter 'C' represents the desired number of clusters, which could correspond to various tissue types or regions of interest, including tumour areas [39].

The FCM algorithm seeks to minimise an objective function that quantifies the difference in membership between each pixel and the cluster centroids. The objective function 'J' is frequently defined as:

J = ∑(∑(w_ij)^m * |(|X_i- V_j |)|^2) ………………….(4)

The FCM algorithm updates the membership degrees and cluster centroids iteratively.

Update on Membership by 'w_ij' should be calculated for each data point based on its similarity to cluster centroids.

by Centroid Update Using the updated membership degrees, recalculate the cluster centroids 'V_j'.

The algorithm will repeat these steps until a convergence criterion is met. The maximum number of iterations between iterations is used in this criterion.

Each pixel in the pre-processed image will have membership degrees for each cluster at the end of the segmentation, indicating how strongly it belongs to different regions, such as tumour and non-tumor regions.

The FCM segmentation output can provide segmented regions that are more likely to contain tumours [40]. The incorporation of FCM into the methodology improves the ability to identify and isolate potential tumour regions, which contributes to the overall success of the brain tumour classification method [41-44].

Following that, we will look at feature extraction, which is an important step in our methodology. To extract local texture features, we use the Histogram of Oriented Gradients (HOG) method [29-30].

The HOG method is used to extract local texture features that accurately characterise the distribution of intensity gradients within an image, thereby capturing important image patterns [31]. Below are the mathematical equations and formulas for the HOG-based feature extraction.

The gradients of the image are calculated as the first step in HOG feature extraction. The gradients represent the rate at which pixel intensities change [32]. The gradient magnitude (M) and gradient orientation (θ) are typically calculated using the formulas:

$$M(x,y) = \sqrt{\left(I_x(x,y)\right)^2 + \left(I_y(x,y)\right)^2} \quad \ldots\ldots\ldots\ldots\ldots(5)$$

$$\theta(x,y) = arctan\frac{I_y(x,y)}{I_x(x,y)} \quad \text{.....(6)}$$

3.1 Proposed VMS Integ-Net Model

VMS Integ-Net, which stands for Visual Geometry Group and Multi-Class Support Vector Machine Integration Network, is a novel approach to the difficult task of brain tumour classification in medical imaging. Because of the wide variety of tumour types and the need for accurate differentiation, brain tumour classification in this context is complex, making traditional methods less effective. Furthermore, because brain tumour images vary in size, quality, and appearance, robust preprocessing, feature extraction, and classification techniques are required to analyse the images for diagnosis and treatment planning.

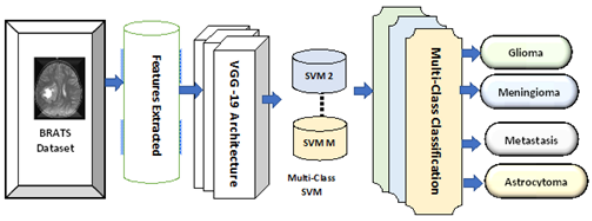


Fig. 2 Architecture of the Proposed VMS Integ-Net Model

The VMS Integ-Net architecture shown in Fig. 2 is justified by the need to address the inherent complexities in brain tumor classification. It makes use of deep learning, specifically VGG-19, a deep convolutional neural network capable of learning high-level features from raw image data. These characteristics capture intricate patterns and textures, which are critical for accurate tumor characterization. Furthermore, the incorporation of Histogram of Oriented Gradients (HOG) features enhances this approach by providing useful information about image texture and intensity gradients.

Another strong justification for this approach is the use of Multi-Class (SVM). It is well-suited to the complexities of this multi-class problem due to its ability to handle multiple classes and determine appropriate decision boundaries.

This fusion produces a classification system that is both accurate and robust. The VMS Integ-Net outperforms standalone methods by combining VGG-19's ability to extract rich features with SVM's efficient classification capabilities.

Furthermore, the adaptability of this integrated approach extends beyond the classification of brain tumors. It can be used for a variety of medical imaging tasks, providing a versatile solution for a variety of diagnostic challenges. Furthermore, it has the potential for automation, which could reduce reliance on manual interpretation and speed up the diagnosis and treatment decision-making process.

3.2 Algorithm of VMS Integ-Net Model

This algorithm describes the steps involved in VMS Integ-Net, emphasizing its adaptability and robustness in multi-class classification tasks by integrating the advanced features of VGG-19 with the robustness of multiclass Support Vector Machines (SVM).

Algorithm: VMS Integ-Net Model

Step 1: Load and Preprocess Data

// Load the medical imaging dataset

// Preprocess the images:

For each image in the dataset:

- Resize the image
- Enhance contrast
- Normalize pixel values

Step 2: Data Splitting

// Split the dataset into a training set and a testing set

For each image in the dataset:

If a random number is less than the desired training/test split ratio:

Add the image to the training set

Else:

Add the image to the testing set

Step 3: VGG-19 Model Setup

// Initialize the VGG-19 model

// Load pre-trained weights for VGG-19

Step 4: Feature Extraction

// Initialize empty lists for training and testing set features

// For each image in the training set:

- Extract features using the VGG-19 model
- Append the features to the training set features list

// For each image in the testing set:

- Extract features using the VGG-19 model
- Append the features to the testing set features list

Step 5: Histogram of Oriented Gradients (HOG) Features

// Initialize empty lists for training and testing set HOG features

// For each image in the training set:

- Compute HOG features
- Append the HOG features to the training set HOG features list

// For each image in the testing set:

- Compute HOG features
- Append the HOG features to the testing set HOG features list

Step 6: Feature Fusion

// Initialize empty lists for training and testing set fused features

// For each image in the training set:

- Combine VGG-19 features and HOG features

- Append the fused features to the training set fused features list

// For each image in the testing set:

- Combine VGG-19 features and HOG features

- Append the fused features to the testing set fused features list

Step 7: Support Vector Machine (SVM) Classifier

// Train a Multi-Class Support Vector Machine (SVM) classifier

- Use the fused features from Step 6 as input

- Choose an appropriate SVM kernel and regularization parameters

Step 8: Model Evaluation

// Initialize variables to store evaluation metrics

// For each image in the testing set:

- Use the trained SVM classifier to predict the tumor type

- Compare the predicted label with the true label and update evaluation metrics

Step 9: Making Predictions

// Pre-process a new brain tumor image

// Extract features using the VGG-19 model

// Compute HOG features for the new image

// Combine VGG-19 features and HOG features

// Use the trained SVM classifier to predict the tumor type

End of the Algorithm

4. Results and Analysis

The brain scan obtained from the BRATS dataset is depicted in Figure 3 of our methodology. This figure is critical because it represents the raw data from which we start. The accuracy and reliability of the entire process are heavily influenced by the quality and consistency of the initial data. Understanding the distinct features and complexities of brain scans is critical for accurate diagnosis and classification. This graph serves as the starting point for the rest of our analysis.

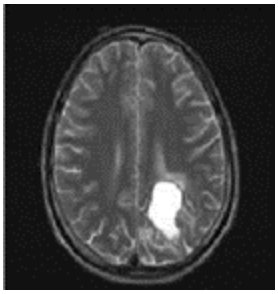


Fig. 3 Input Brain Scan

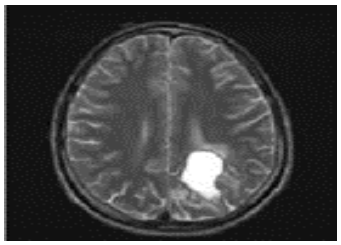


Fig. 4 Resized Image

Figure.4 shows the resized image, which is an important intermediate step in our method. The resizing process, as previously described, uses bilinear interpolation to standardize the image dimensions to a 256x256-pixel format. This diagram shows how the original brain scan is converted into a consistent and manageable format. This resized image shows a smooth transition of pixel values and the absence of artefacts. It demonstrates how the resizing technique was successfully implemented, preparing the data for further processing.

Figure.5 depicts the grayscale conversion stage. This transformation is critical because it reduces the image's color information to grayscale. Grayscale images are ideal for medical image analysis because they highlight variations in intensity, which can indicate underlying structures or anomalies.

Figure 6 depicts the median filtering pre-processing step. This diagram depicts the application of a median filter to a grayscale image. The visual representation of noise reduction and smoothing of small intensity variations within the image. This technique's success is critical because it prepares the data for subsequent stages such as segmentation. Each pixel location receives the mathematically represented median filter operation (equation 3), which contributes to improved image quality.

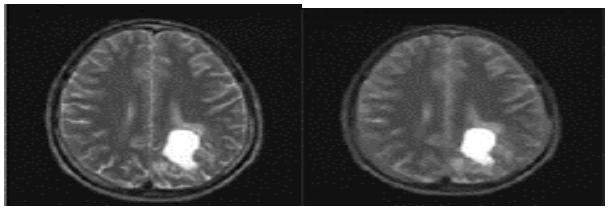


Fig.5 Grayscale Conversion **Fig.6** Median Filtered Image

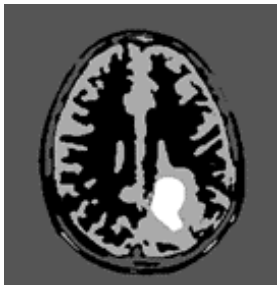


Fig. 7 Segmented Image Using FCM

Figure.7 shows the segmented image which is partitioned into different clusters based on pixel values in this step. The

diagram shows how FCM assigns pixels to different clusters, highlighting potential areas of interest such as suspected tumor areas. This is a critical step in our methodology because it establishes the foundation for future feature extraction.

Now these results are subjected to feature extraction stage and it is clearly explained in the next sub-section.

4.1 Feature Extraction

The features recovered using the Histogram of Oriented Gradients (HoG) feature extraction technique are organized in Table 1. These characteristics are extracted from a set of four samples, each from a different type of brain tumor, from a total of 1000 samples that were subjected to the proposed system. This table enables a thorough examination of the extracted features, demonstrating how the HoG technique was applied to these specific samples. In the context of medical imaging, feature extraction techniques such as HoG are critical in identifying distinct characteristics and patterns in images that can be used for diagnostic purposes. The tabulation of these features in Table 1 provides a clear overview of how the HoG method captures specific information from images associated with various types of brain tumors.

Table 1. Features extracted for Samples of Types of Brain Tumor Images

	Sample Brain Tumor Images			
Features Extracted	**Glioma**	**Meningioma**	**Metastasis**	**Astrocytoma**
Mean	0.0097	0.0063	0.0072	0.00571
Standard Deviation	0.0947	0.087	0.067	0.0632
Entropy	0.00921	0.0077	0.00886	0.0058
Variance	3.453	2.445	2.01	1.49
Smoothness	0.734	0.634	0.825	0.529
Contrast	0.44	0.358	0.266	0.208
Correlation	0.1067	0.1093	0.1083	0.1123
Energy	0.7155	0.6166	0.905	0.597

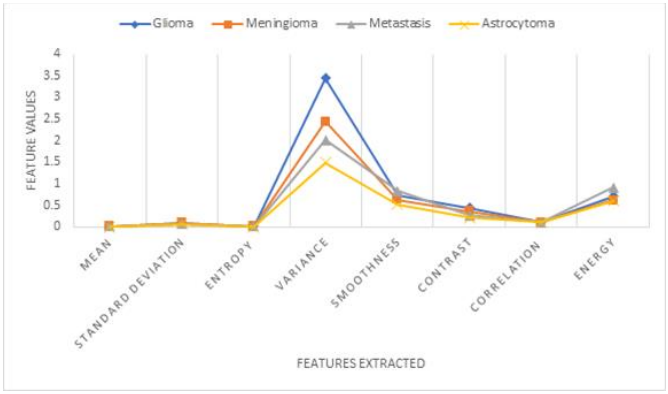


Fig. 8 Plot of Features extracted for each Type of Brain Tumor

Figure.8 illustrates the extracted features for each type of brain tumor, supplementing the information presented in Table 1. The x-axis of the plot represents the extracted individual features, while the y-axis shows the corresponding values of these features. This graph aids in understanding the distribution and variation of features across tumor types.

Figure 8 also provides a useful visual representation of the data, making it easier to compare and contrast the features across tumor types. This type of visualization can be extremely helpful for medical professionals and researchers in identifying patterns and differences in data that may be indicative of specific tumor characteristics.

4.2 Data Splitting and Classification

The BRATS dataset has been meticulously partitioned into specific subsets to facilitate comprehensive evaluation, as detailed in reference [18]. These subsets include training, validation, and testing, each of which is designed to serve a specific purpose. The percentage allocation of the dataset is as follows:

Glioma has 195 images for training, accounting for approximately 31.77% of the dataset. The validation subset contains 22 images, accounting for approximately 2.84% of the dataset, while the testing subset contains 121 images, accounting for approximately 19.06% of the dataset.

Meningioma, on the other hand, is made up of 115 training images and accounts for approximately 18.75% of the dataset. There are 22 images in the validation subset, representing approximately 2.84% of the dataset, and 50 images in the testing subset, representing approximately 7.98% of the dataset.

Metastasis consists of 155 training images, accounting for approximately 25.25 percent of the dataset. There are 16 images in the validation subset, accounting for approximately 2.08% of the dataset, and 89 images in the testing subset, accounting for approximately 14.13% of the dataset. Astrocytoma contains 148 training images, which account for approximately 24.11% of the dataset. The

validation subset contains 14 images, accounting for approximately 1.81% of the dataset, and the testing subset contains 53 images, accounting for approximately 8.43% of the dataset. The BRATS dataset combines a significant number of images across these subsets, with approximately 613 training images (about 100% collectively), 74 validation images (about 100% collectively), and 313 testing images (about 100% collectively) distributed. This meticulous categorization and allocation of images across these subsets is critical for effectively training, validating, and testing.

After successfully extracting the features from the previous subsection and training the model with the split dataset, the next critical step is to test the proposed VMS Integ-Net model. Images of brain tumours are chosen and fed into the model for testing. This phase of the model evaluation process is critical because it determines how well the model can classify different types of brain tumours. The model's testing process yields the identification of the specific type of brain tumour detected in each image. This type of classification is critical for medical diagnosis and treatment planning because different tumour types may necessitate different approaches. As shown in Figure 9, the classification results are presented in the form of a Performance Matrix. This plot is a three-dimensional representation of the model's accuracy in classifying various types of brain tumours. It is essentially a "report card" for the accuracy of the model, a summary that aids in assessing its diagnostic capabilities.

The Performance Matrix, which functions similarly to a confusion matrix, shows how many tumours the model correctly identifies and how many it misclassifies for each type of brain tumour, such as glioma or metastasis. Each cell in the matrix represents a distinct combination of model predictions and ground truth labels. Each bar in the 3D bar chart generated from this matrix corresponds to the number of tumours correctly classified by the model and those incorrectly classified by the model for a specific tumour type. The labels on the chart's axes indicate which type of tumour is being considered, making it easier to evaluate the model's performance visually.

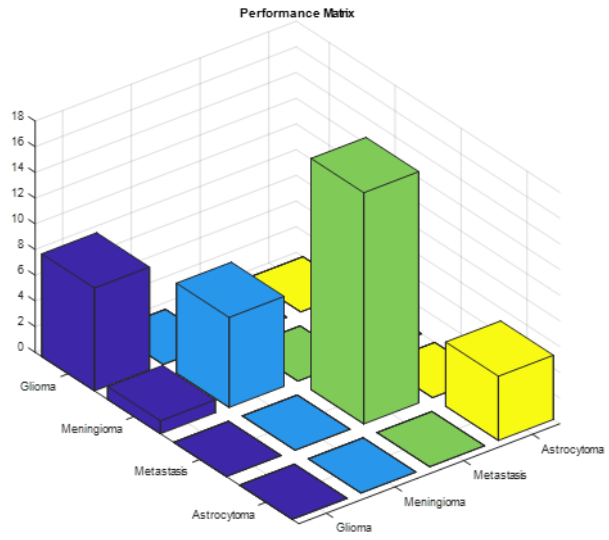


Fig. 9 Performance Matrix plot for types of Tumors

4.3 Accuracy

The accuracy metric during the brain tumor detection and classification can be computed using the following formula:

$$\text{Accuracy} = ((TP + TN))/((TP + TN + FP + FN)) \quad \ldots\ldots\ldots\ldots\ldots (7)$$

In Table 2, the proposed VMS Integ-Net Model is compared in terms of accuracy values to existing methods such as recurrent networks and CNN (ConvNets) [21], Machine Learning [22], Texture-based and statistical features [23], modified two-step dragonfly mechanism system [24], and faster Region-based CNN [25].

Table 2. Accuracy Performance evaluation

Year	Techniques used	Accuracy (%)
2022	recurrent networks and CNN (ConvNets) [21]	98.3
2021	Machine Learning [22]	95.83
2020	Texture-based and statistical features [23]	97.87
2020	modified two-step dragonfly mechanism system [24]	98.20
2019	faster Region-based CNN [25]	91.66
2023	Proposed Method (Improved Enhanced Deep Learning)	99.57

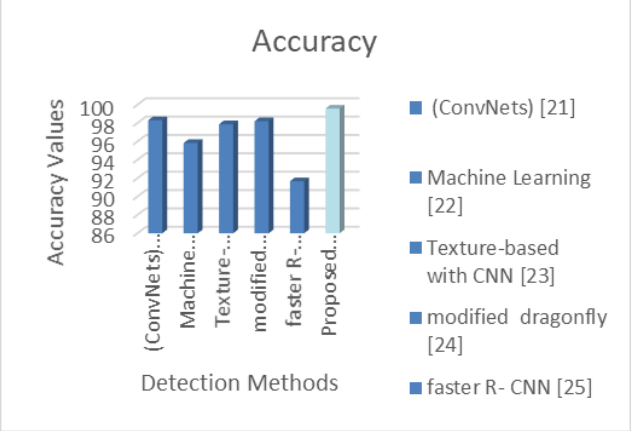


Fig. 10 Comparative Plot for Accuracy in Brain Tumor Detection

4.4 Specificity and Sensitivity

Specificity measures a diagnostic test's ability to correctly identify whether or not a person has a tumor, which is often referred to as "true negatives.". It indicates the model's ability to correctly classify non-tumor or non-cancer cases.

$$\text{Specificity} = TN/((TN + FP)) \quad \ldots\ldots\ldots\ldots\ldots\ldots (8)$$

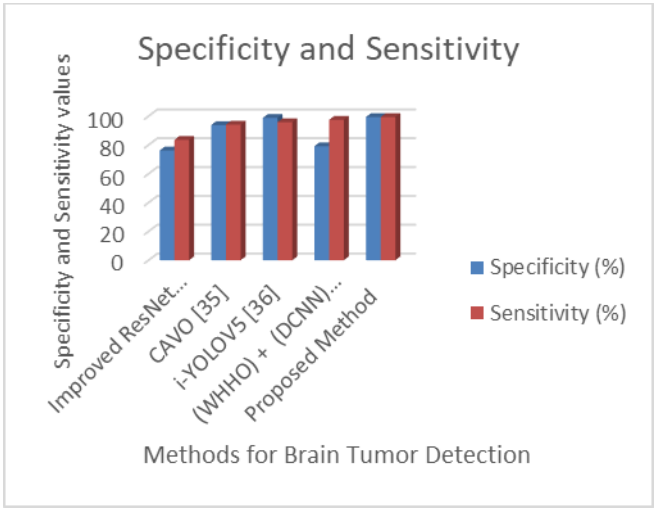
Sensitivity indicates the model's ability to correctly classify tumor or cancer cases.

$$\text{Sensitivity} = TP/(TP + FN) \quad \ldots\ldots\ldots\ldots\ldots\ldots (9)$$

Table 3. Performance evaluation for Specificity and Sensitivity in brain Tumor detection

Year	Techniques used	Specificity (%)	Sensitivity (%)
2023	Improved Residual Network [34]	76.13	83.5
2023	Chronological Artificial Vultures Optimization (CAVO) [35]	93.8	94.1
2022	*i*-YOLOV5 [36]	98.78	95.77
2020	Whale Harris Hawks optimization (WHHO) + deep convolution neural network (DCNN) [33]	79.1	97.4
2023	Proposed Method	99.3523	99.3405

A comparative plot for specificity and sensitivity in brain tumor detection is shown in Fig. 11. The plot visualizes the methods' performance across these metrics, allowing for direct comparison. The proposed method is evaluated and found to be superior to existing methods in terms of both specificity and sensitivity.



5. Conclusion

In a nutshell, our research focuses on the complex field of brain tumor detection and classification. We began our journey by emphasizing the importance of early detection and precise classification, especially given the wide range of brain tumor types, such as Glioma, Meningioma, Metastasis, and Astrocytoma. Our ground-breaking VMS Integ-Net model takes the spotlight, seamlessly combining deep learning and traditional machine learning techniques. Our model achieved an exceptional 99.57% accuracy rate, an impressive 99.3523% specificity, a remarkable 99.3405% sensitivity and a PSNR of more than 50 dB. These findings outperform existing methods, promising not only more accurate and timely diagnoses, but also a link between cutting-edge technology and pressing healthcare needs in neurology and oncology. Finally, our research provides a ray of hope, poised to improve patient care and improve the prospects for those suffering from brain tumors.

Author contributions

O.Homa Kesav: Conceptualization, Data curation Formal analysis, Methodology, Software Writing, original draft, investigation, resources.

G.K.Rajini: Writing—review and editing, visualization, supervision, project administration.

Conflicts of Interest

The authors affirm that they are aware of no personal or financial conflicts of interest that might have affected the research described in this paper

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