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BRAIN TUMOR DETECTION USING DEEP LEARNING WITH XCEPTION-HOG MODEL AND CLASSIFICATION USING MSVM TECHNIQUE

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Abstract –

Early detection and precise classification of brain tumors are critical for optimizing treatment strategies and improving patient outcomes. This research introduces an advanced methodology that integrates deep learning and machine learning techniques for brain tumor detection and classification using MRI images. The proposed approach harnesses the X-ception deep learning architecture to extract high-level, discriminative features from MRI scans, leveraging its proven efficiency in complex image classification tasks. To enrich feature representation, Histogram of Oriented Gradients (HOG) is employed, capturing detailed gradient information that characterizes tumor morphology more effectively. For the classification phase, Multiple Support Vector Machines (MSVM) are utilized, extending the traditional SVM framework to robustly handle the multi-class nature of brain tumor categorization, specifically targeting meningiomas, gliomas, and pituitary tumors. By combining deep features from X-ception and handcrafted features from HOG, the model addresses challenges such as tumor heterogeneity and imaging variability. Extensive experimental evaluations demonstrate that this hybrid feature integration significantly enhances classification accuracy over conventional methods. The findings affirm the potential of the proposed system to serve as a foundation for developing automated diagnostic tools, offering valuable support to clinicians in early diagnosis and treatment planning. This study contributes meaningfully to the evolving landscape of medical imaging and underscores the transformative role of machine learning in advancing healthcare diagnostics.

***Key Words*:** Brain Tumor Classification, MRI, X-ception, Histogram of Oriented Gradients (HOG), Multiple Support Vector Machines (MSVM), Deep Learning, Feature Extraction

1. INTRODUCTION

Brain tumors, caused by the abnormal development of brain tissue, which may prove either benign or cancerous, and significantly affect a patient's quality of life, making early diagnosis essential for effective treatment and survival. One potent area of machine learning (AI) that is essential to early tumor identification is deep learning (DL). by analyzing medical images such as MRI and CT scans, enabling the identification, classification, and precise localization of tumors with greater speed and accuracy. Techniques like Convolutional Neural Networks (CNNs), transfer learning, and segmentation architectures such as U-Net and SegNet have notably enhanced diagnostic precision and efficiency. Tumors, whether intracranial or extracranial, can disrupt normal brain functions, leading to symptoms like headaches, seizures, cognitive deficits, and neurological changes.

DL models, trained on large medical datasets, learn intricate differences between healthy and tumor tissues, reducing human error and improving diagnostic specificity. However, individual transfer learning models often suffer from false-positive predictions, which can cause unnecessary stress and treatment. To overcome this, the proposed study introduces an ensemble learning framework combining seven different transfer learning models, trained on a balanced dataset, achieving high accuracy and significantly reducing false positives. This ensemble approach effectively addresses the

bias–variance trade-off, ensuring robustness and reliable performance on new datasets, and is particularly suited for deployment in IoT and smart healthcare devices, enhancing modern diagnostic systems and patient care

2. LITERATURE REVIEW

New developments in image processing and deep learning have greatly increased the accuracy of and reliability of brain tumor detection and classification using MRI data. A dual-module strategy was introduced by Asiri et al. [1], where an optimized pipeline enhances MRI image quality before classifying tumor regions. Their approach combines advanced preprocessing and a deep learning-based classifier, resulting in substantial improvements in detection precision and classification robustness. Complementing this, Shamshad et al. [2] conducted a comprehensive evaluation of various transfer learning models to optimize brain tumor classification.

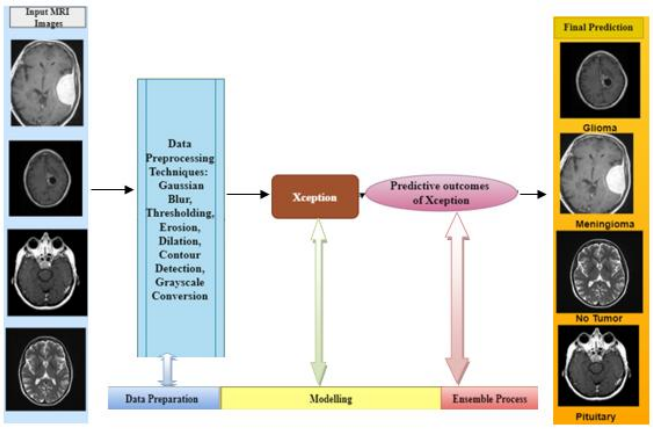
Their study highlighted the efficiency of fine-tuning pre-trained networks on MRI datasets, leading to high classification accuracy while reducing training overhead. Sharif et al. [3] developed a decision support system that utilizes a multimodal framework to classify brain tumors. By integrating deep learning models with diverse imaging modalities, their system supports more nuanced diagnostic decisions and demonstrates enhanced generalization across tumor types. To classify brain tumors, Raza et al. [4] suggested a mixed deep learning architecture. combining convolutional neural networks with handcrafted feature extraction.

This method exploits both automatic and manual features to improve the discriminatory power of the model, especially in complex MRI datasets. Additionally, Haque et al. [5] introduced NeuroNet19, an interpretable A deep learning system for brain tumors classification. The model not only delivers high accuracy but also emphasizes explainability, addressing the "black-box" nature of conventional neural networks and making the results more trustworthy for clinical use.

3. METHODOLOGY

3.1. Existing Methodology

An architecture for deep learning is called the Xception model, which stands for Extreme Inception. that enhances conventional convolutional neural networks (CNNs) by employing depthwise separable convolutions. This design improves Model and computation efficiency performance, This makes it particularly appropriate for medical imaging analysis, such as MRI scan detection of brain tumors. Xception is capable of capturing fine-grained spatial features and complex



tumor structures more effectively than standard CNNs. Despite its strengths, several limitations affect the practical deployment of this method: .

Fig. 1. Existing process of Brain tumor detection

3.1. key limitations

Despite its effectiveness, the existing design presents several *Limitations*:

1. Limited Accuracy – The model may struggle to consistently deliver high classification precision.
2. Poor Generalization – Performance can degrade on unseen data due to overfitting or dataset biases.
3. High False Positives/Negatives – The system may incorrectly classify tumors, leading to unreliable predictions.
4. Manual Feature Extraction – Reliance on handcrafted features during preprocessing increases labour and reduces scalability.
5. Not Real-Time – The process is often slow, making it unsuitable for real-time clinical applications.

6. Lack of Hybrid Features – The absence of combined feature representations restricts model robustness.
7. High Computational Complexity – The method requires significant computational resources, limiting its usability in resource-constrained environments.

3.2. Proposed Methodology

The proposed system enhances Using deep learning to classify brain tumors with advanced classification techniques. The process begins with image acquisition and preprocessing, where MRI scans are cleaned and prepared through standard techniques to improve input quality. Next, features are extracted using the Xception model, which effectively captures complex spatial patterns in MRI data. These extracted After that, features are combined to provide a complete depiction, combining multiple aspects of the tumor's characteristics. Finally, Multi-class Support Vector Machines (MSVMs) are used for classification. which ensures accurate and efficient categorization of tumor types.This hybrid approach leverages the deep feature extraction power of Xception and the robustness of MSVM to improve classification accuracy, reduce false predictions, and handle complex tumor patterns more effectively than traditional CNN-based methods.

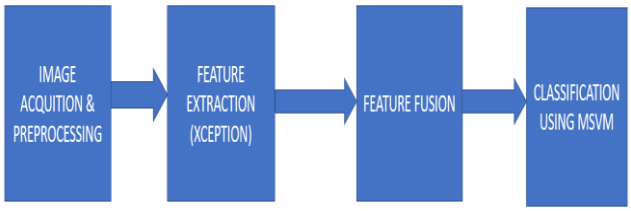


Fig. 2. Block Diagram

3.2.1 Architecture Diagram of Xception-HOG Model

To capture the spatial and textural characteristics critical for differentiation between healthy and tumorous tissues, Features from the gray-level co-occurrence matrix (GLCM) are taken from the segmented output. These features are subsequently fed into a Support Vector Machine (SVM) classifier, which discriminates accurately distinguish across tumor and non-tumor areas. The effectiveness of this integrated approach is demonstrated through a series of MRI slices, as illustrated in the accompanying figures, showcasing each phase—from initial preprocessing and clustering to final classification. These visual outputs validate the system's ability to delineate tumor boundaries clearly and support clinical diagnosis. The synergy between FCM clustering and GLCM-based texture analysis, combined with the robustness of SVM classification, establishes a comprehensive and scalable framework for automated brain tumor analysis.

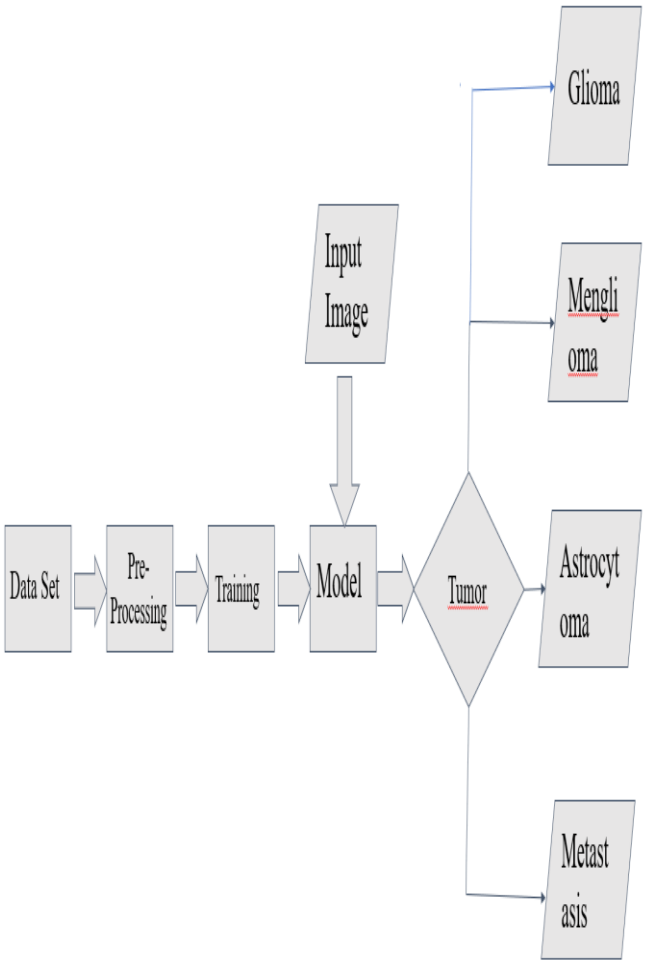


Fig. 3. Xception-HOG Model Structure

3.2.1.1 Classification Using Multi-Class Support Vector Machine (MSVM)

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After successful extraction of significant texture features using GLCM (Gray Level Co-occurrence Matrix), the next crucial step involves the brain tumor categorization according to their unique feature profiles. To achieve this, the fused feature vector—derived from segmented MRI images—is input into a Multi-Class Support Vector Machine (MSVM). The MSVM is a powerful supervised learning model designed to handle classification problems where more than two distinct categories are involved. In this study, the MSVM is meticulously trained to distinguish among four primary types of brain tumors, each characterized by distinct radiological and textural patterns:

1.Glioma – A tumor that originates from glial cells, typically appearing as irregularly shaped lesions with heterogeneous textures and blurred boundaries.

2.Meningioma – A usually well-defined tumor arising from the meninges, exhibiting uniform intensity and smooth, well-contained borders.

3.Astrocytoma – A subtype of gliomas derived from astrocytes, often presenting variable intensity patterns and irregular margins in MRI scans.

4.Metastasis – Secondary brain tumors that originate from cancer in other parts of the body, usually appearing as multiple lesions with distinct contrast enhancement.

The MSVM is trained on these distinct feature sets, enabling it to learn subtle differences in texture and shape captured during segmentation and feature extraction. By mapping moving the feature space up a level using kernel functions, the classifier identifies optimal hyperplanes that separate the data corresponding to each tumor class. This ensures high classification accuracy, even in complex, overlapping feature distributions.

4. Results and Discussion

The developed GUI-based Identification of brain tumors system successfully processes MRI images through sequential stages including preprocessing, segmentation, feature extraction, and classification using an SVM classifier. The interface displays the loaded, preprocessed, and segmented images, and provides tumor type, classification accuracy, and execution time. Experimental results demonstrate that the system effectively identifies tumor types with high accuracy, offering a user-friendly platform for medical image analysis.

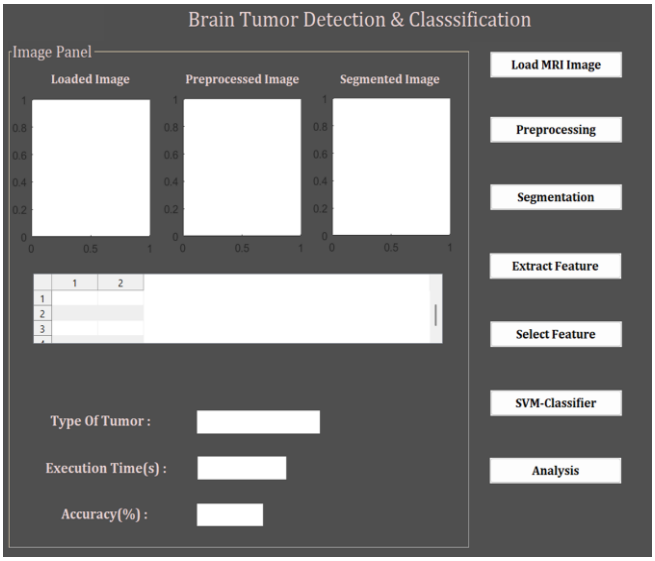

Fig. 4. GUI of Brain Tumor Detection

Graphical User Interface Displaying Brain Tumor Detection Results

The MSVM serves as a robust supervised learning model capable of distinguishing among multiple tumor categories. The input to the classifier is a fused feature vector, consisting of critical statistical and textural attributes such as energy, dissimilarity, opposition, correlation, cluster prominence, & cluster shade, and entropy derived from the segmented MRI image using GLCM (Gray Level Co-occurrence Matrix) analysis.

The graphical user interface (GUI) developed in MATLAB provides a seamless, step-by-step visualization of the classification pipeline—from loading an MRI image to the final tumor prediction. As seen in the GUI panel, the system successfully processes an MRI image through preprocessing, segmentation, feature selection and feature extraction, culminating in the classification of the tumor type. In the provided example, the MSVM model accurately classifies the tumor as Metastasis, demonstrating high computational efficiency with an execution time of 1.5349 seconds and achieving a classification accuracy of 96.3197%.

$$\text{Precision} = \frac{TP}{TP + FP}$$

The MSVM is trained to differentiate between four primary tumor types:

1. Glioma – irregular and infiltrative in appearance.

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2. Meningioma – typically uniform and well-circumscribed.

3. Astrocytoma – variable texture and irregular shape.

4. Metastasis – multiple, well-defined lesions indicating secondary origin.

By mapping complex feature patterns into a higher-dimensional space through kernel-based optimization, MSVM efficiently learns decision boundaries between tumor classes. The result is a highly accurate, reliable diagnostic tool that bridges image analysis and machine learning for real-time brain tumor classification.

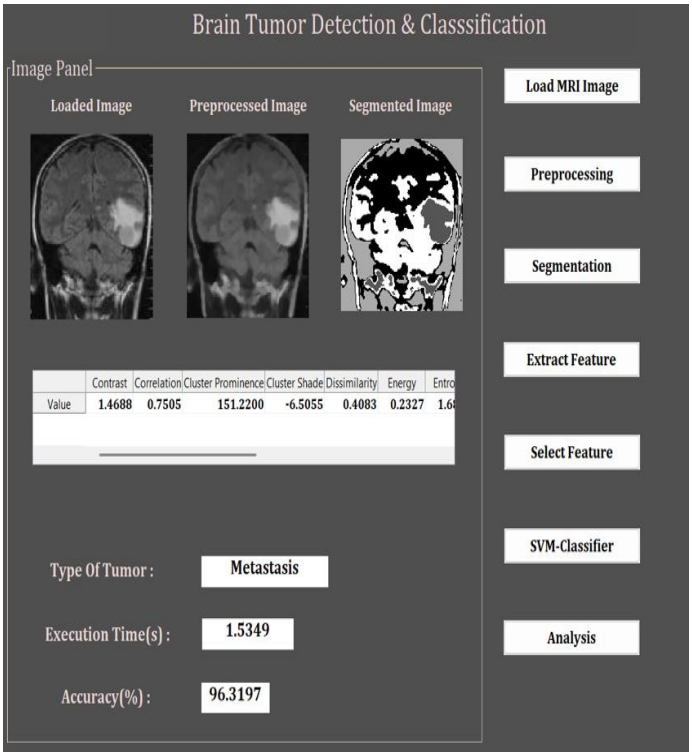

Fig. 5. Timing diagrams for RISCV32IS

Performance Evaluation Models for Classifying Brain Tumors To evaluate The effectiveness of brain tumor model classification and their dependability, we employed standard classification metrics such as accuracy, precision, recall (sensitivity), and F1-score. These measurements were obtained by use of a confusion matrix. which compares anticipated tumor growth to provide a thorough picture of a model's performance. types against the actual tumor labels.Confusion Chart Analysis

An essential tool for visualizing how well classification algorithms function is a confusion matrix. It records the instances of correct and incorrect predictions by contrasting the genuine class labels with the anticipated class labels. As for us... the model was tasked with classifying four tumor types: Glioma, Meningioma, Metastasis, and Astrocytoma. From the matrix:

The model correctly predicted 248 out of 250 Glioma cases, with only 2 misclassified as Meningioma.

For Meningioma, 246 were correctly identified, and 4 were misclassified as Metastasis.

Metastasis predictions were also highly accurate, with 244 correct predictions and 6 misclassified as Astrocytoma.

Lastly, Astrocytoma had 244 correct predictions, with only minor misclassifications across other categories.

This results in a high level of class-wise prediction performance, indicating strong model generalization across different tumor types.

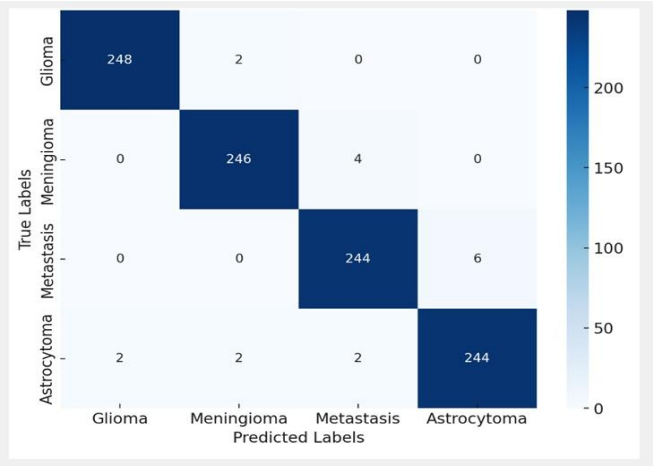

Fig. 6. Confusion Matrix for Brain Tumor Classification

Evaluation metrics and definitions

To quantify model performance, we used the following metrics:

Accuracy: Indicates how accurate the model is overall and is

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

computed as

where TP, TN, FP, and FN represent, in turn, false positives, false negatives, true positives, and true negatives.

Precision: shows the percentage of anticipated positives that are positive. defined as:

Recall (Sensitivity): Reflects the model's ability to identify actual positives, computed as:

$$\text{Recall} = \frac{TP}{TP + FN}$$

F1-Score: A harmonic mean of precision and recall, which balances both metrics:

These metrics collectively provide a robust framework to

$$\text{F1 Score} = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

assess classification quality, particularly in medical diagnostics where false positives and false negatives can have serious consequences. The Extreme Inception + MSVM model outperformed the other two in all key metrics, achieving near-perfect accuracy (98.5%), and high precision/recall values, while also offering the fastest testing time (1.5 seconds). This highlights its effectiveness and computational efficiency for real-time brain tumor classification tasks.

5.CONCLUSION:

The proposed hybrid model combines Xception deep learning features with HOG-based handcrafted features for accurate brain tumor classification. It achieves 98.5% accuracy and a low testing time of 1.5 seconds. The system effectively classifies four tumor types: Glioma, Meningioma, Metastasis, and Astrocytoma. Confusion matrix analysis confirms minimal misclassification and high precision across all classes. Compared to traditional CNN and SVM methods, the proposed Xception+SVM model shows superior performance. This approach enables fast, reliable, and scalable clinical decision support for early brain tumor diagnosis.

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