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Automated Brain Tumor Classification Using NASNet-Large and AutoGluon

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ABSTRACT

Brain tumors pose a crucial medical challenge, requiring prompt and accurate diagnosis for effective treatment. Traditional methods, like manual MRI analysis, can be time-consuming and susceptible to error. Recent progress in deep learning has led to automated MRI-based tumor classification systems. This study explores the use of NASNet-Large, coupled with AutoGluon's ImagePredictor and a stacked ensemble learning strategy to classify brain tumors into four categories: Glioma, Meningioma, Pituitary tumor, and No Tumor. The model, trained on a labeled MRI dataset, achieves an overall accuracy of 98.40% and F1-scores exceeding 96% for all tumor types, demonstrating its effectiveness in distinguishing between classes. These findings highlight the possibilities of deep learning tools in enhancing medical imaging, reducing diagnostic delays, and improving accuracy. However, challenges remain, such as the need for larger datasets and ensuring model generalizability across imaging modalities. Future research should focus on enhancing the model and integrating it into clinical workflows.

Keywords: Brain tumor classification, MRI, Deep learning, Image processing

INTRODUCTION

I. Brain Tumors

A brain tumor is an anomalous growth of cells that originates within the brain's intricate structure or from surrounding areas. These tumors may originate directly from neural tissue or neighboring tissues, including cranial nerves, the pituitary or pineal glands, or the meningeal membranes encasing the central nervous system [1]. Brain tumors are categorized into two types: benign and malignant. Benign tumors, though infrequent, generally display features of normal tissue, demonstrate slow growth, and remain localized. Malignant tumors are physiologically disruptive and pose therapeutic risks; they comprise cancerous cells capable of uncontrolled proliferation, local invasion, and occasional metastasis to distant sites[2]. Brain tumors evolve; therefore, early diagnosis can prevent irreparable damage and allow clinicians to treat before the disease progresses [3]. Meningiomas, gliomas, and pituitary tumors are the three primary brain tumor forms, each with its unique histology, symptoms, and treatment.[4]. Nearly one-third of primary brain cancers begin in the arachnoid mater, one of the three meningeal layers protecting the brain and spinal cord [5]. While benign and gradually developing, their consequences can be profound. Visual impairment, cognitive issues, and seizures can result from brain compression. The WHO divides meningiomas into three histological grades: Grade I, the most common and least aggressive; Grade II, an unusual variety with a higher recurrence risk; and Grade III, the malignant type with rapid growth and a poor prognosis. [6,7,8]. Neuroimaging, especially MRI, remains the main diagnostic tool. Radiation therapy is used when surgery is impractical or the illness returns [9,10, 11]. Neuron metabolism and structure are supported by glial cells, which create gliomas. This group accounts for 80% of malignant brain tumors and has a poor prognosis, especially high-grade ones [12]. Gliomas are classified by glial cell origin: High-grade astrocyte-derived astrocytomas grow quickly, while low-grade ones grow slowly. Oligodendrogliomas: Rare oligodendrocyte malignancies have a better prognosis. (iii) Glioblastoma Multiforme (GBM): The most aggressive and lethal glioma, it is fast-growing, necroses, and resists treatment [13]. Despite surgery, radiotherapy, and chemotherapy (including temozolomide), glioblastomas have a median survival rate of under 15 months [14]. Researchers use advanced imaging, molecular profiling (IDH mutant status and MGMT promoter methylation), and deep learning algorithms to improve early identification and treatment [15]. The pituitary gland, situated close to the base of the brain, regulates hormones and causes pituitary

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tumors. Unlike gliomas and meningiomas, most pituitary tumors are benign adenomas, but hormonal imbalance can have systemic repercussions [17]. Pituitary tumors are characterized by hormone secretion. (i) Functioning (Hormone-Secreting) Tumors: These tumors release too many hormones, causing Cushing's disease, acromegaly, and prolactinomas. Despite not producing hormones, non-functioning (non-secreting) tumors can compress the optic chiasm and induce headaches and visual abnormalities [18, 19]. MRI imaging, hormonal assays, and ocular evaluations are usually needed for diagnosis. Pharmacotherapy (e.g., dopamine agonists for prolactinomas), transsphenoidal surgery, and radiotherapy may be used depending on the tumor's form and severity [20, 21].

II. Brain Tumor Imaging

Neuro-oncology requires MRI to diagnose brain lesions' structure and function [22]. Based on histology, location, cellular constitution, and biological aggressiveness, CNS tumors look different. Radiologists and computer analysts need signal intensity, contrast uptake, and structural deformation signatures. Signal variation across MRI sequences is key to tumor imaging. Because they invade surrounding tissues and have variable cellular makeup, gliomas have uneven boundaries and varying intensities [23,24]. Due to restricted growth and substantial vascularization, meningiomas exhibit clear margins and uniform enhancement [25]. Due to their proximity to the cavernous sinus and circulatory networks, sella turcica pituitary adenomas worsen post-contrast [26]. Peritumoral edema and bulk effect show tumor behavior. Vasogenic edema in infiltrative gliomas raises intracranial pressure and may displace midline structures, a radiological finding with clinical significance [27]. Nearby edema often suggests tumor grade and malignancy. Cancers differ in texture and fundamental heterogeneity. Glioblastoma multiforme has internal complexity, necrosis, micro hemorrhages, and contrast-enhancing rims. The results show blood-brain barrier disruption and abnormal vascular growth [28]. The signal profile of lower-grade malignancies and benign lesions is more uniform, making them easier to identify from healthy brain tissue. Morphological traits help diagnose. Surgical planning benefits from lobulated, symmetric meningiomas that distinguish from surrounding tissues [29]. Gliomas impair tumor-parenchyma differentiation, affecting excision and recurrence [30]. Anatomical placement affects clinical presentation and imaging. Meningiomas grow on dural surfaces, such the falx cerebri or convexities, while pituitary tumors injure the optic chiasm, causing early visual complaints. Gliomas in functionally relevant cortical areas can complicate diagnosis and therapy due to little tissue plane limitation [31]. Patterns of contrast enhancement improve diagnosis. A necrotic core and active tumor front are seen in high-grade tumors like glioblastomas with peripheral ring enhancement [32,33]. Meningiomas improve consistently due to their organized vascular architecture. Tumor biology patterns are needed for manual interpretation and computational categorization. Radiologists and automated algorithms analyze pictures using signal strength, texture, shape, location, enhanced motion, and edema. These features must be characterized to classify cancers and determine treatment and prognosis [34].

III. Deep Learning and Convolutional Neural Networks

Initial studies on brain tumor classification predominantly utilized traditional machine learning techniques alongside manually crafted feature extraction methods. Researchers extracted discriminative features, including textural patterns, morphological contours, and intensity-based statistical metrics, from structural and functional neuroimaging modalities, specifically MRI and CT scans [35]. Techniques like Gray-Level Co-occurrence Matrices (GLCM) and multi-resolution wavelet decompositions were essential for encoding tumors' spatial and spectral characteristics [36, 37]. In initial studies, handcrafted representations were utilized as inputs for classical classifiers, such as Support Vector Machines (SVMs) and ensemble-based Random Forests, showing moderate diagnostic accuracy [38]. Although initially effective, these methods faced inherent limitations, particularly their reliance on domain expertise for feature selection. The manual extraction of descriptors frequently did not capture the intricate heterogeneity and nuanced phenotypic variations in neoplastic tissue, resulting in inadequate generalization across diverse patient cohorts. The labor-intensive characteristics of feature engineering pose scalability issues, especially in extensive multi-institutional studies. Deep learning, particularly Convolutional Neural Networks (CNNs), has significantly transformed medical image analysis [39]. Convolutional Neural Networks (CNNs) acquire hierarchical and diagnostically significant features from pixel-level data, eliminating the necessity for heuristic feature design and improving classification accuracy and robustness [40]. This method utilizes data analysis to reveal hidden pathological signatures that may be overlooked in manual extraction, thus improving the accuracy of distinguishing

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between tumor subtypes and grades. Transfer learning has enhanced the effectiveness of convolutional neural networks in neuro-oncological imaging, mainly due to the limited availability of well-annotated medical datasets [41]. Using pre-trained architectures, originally optimized on extensive natural image datasets like ImageNet and later fine-tuned on specific neuroimaging data, has led to significant performance improvements, even with limited training samples [42]. This strategy utilizes convolutional neural networks' hierarchical feature abstraction capabilities (CNNs), employing low-level filters such as edge detectors with broad applicability, while higher-order representations are adaptively refined to identify pathological anomalies. These methods address challenges related to data scarcity and improve model generalizability across various imaging protocols and scanner manufacturers. The shift from manual feature engineering to deep learning highlights a significant trend toward data-centric approaches in computational neuropathology. Traditional techniques established the foundation for automated tumor analysis. In contrast, modern deep learning frameworks have achieved notable diagnostic accuracy, facilitating the development of advanced and scalable clinical decision-support systems [43].

IV. Advanced Architectures

NASNet-Large, or Neural Architecture Search Network-Large, is a deep convolutional neural network model developed through Neural Architecture Search (NAS), an automated machine learning technique pioneered by Google [44]. Unlike traditional CNNs, which are manually designed, NASNet-Large is created via a reinforcement learning process that seeks the optimal network architecture, resulting in a highly efficient and scalable model that excels in image classification tasks, as shown in benchmarks like ImageNet [45]. The architecture consists of two building blocks: normal cells, which preserve spatial dimensions and extract features, and reduction cells, which downsample the input to enhance feature depth and abstraction [46]. This modular design allows effective scaling while maintaining computational efficiency. In medical imaging, NASNet-Large demonstrates potential, particularly for high-precision tasks such as brain tumor classification. Its ability to to derive intricate features from MRI scans exceeds simpler models. Moreover, its effectiveness across diverse datasets and support for transfer learning make it ideal for medical applications with limited labeled data [47]. Fine-tuning NASNet-Large on brain MRI datasets enables researchers to accurately differentiate between tumor types, such as gliomas and meningiomas, with improved accuracy [48].

The Amazon AutoGluon architecture classifies pictures using its ImagePredictor class within the AutoGluon Image module. Data preprocessing, neural architecture selection, hyperparameter adjustment, and model assembly are automated [49]. It streamlines deep learning model implementation and competes on medical imaging datasets utilizing computer vision [50]. EfficientNet, ResNet, and DenseNet are fine-tuned by AutoGluon's ImagePredictor to match smaller medical datasets like MRI scans [51]. This tool generates a robust classifier, as its automated data augmentation enhances model generalization, and intelligent hyperparameter adjustment improves training performance. AutoGluon's ImagePredictor quickly maps MRI features to brain tumor classification [52]. It connects with complex models like NASNet-Large, hybrid, and ensemble systems to boost diagnostic reliability [53]. the ImagePredictor automates model training and tuning to construct high-performance deep-learning medical imaging models for brain tumor classification [54].

Multiple models in the stacked ensemble model increase classification [55]. It trains many base models with diverse architectures and feeds their outputs to a meta-model for final predictions [56]. The ensemble uses each model's strengths and mitigates its shortcomings to improve accuracy and stability. Stacking simplifies brain tumor categorization from medical imaging data [57]. Integration of NASNet-Large with AutoGluon-ImagePredictor increases feature learning and optimization. The meta-learner improves the understanding of MRI tumors with these models. This method increases tumor appearance, imaging ruggedness, and classification accuracy [58]. Smaller medical imaging datasets benefit from stacking ensembles to prevent overfitting. The stacked ensemble model for brain tumor diagnosis is fast and accurate [59].

V. Research Gap

Radiologists have traditionally used MRI or CT imaging to identify and classify malignancies. Professional radiologists can provide reliable interpretations, but this method is laborious, time-consuming, and subject to observer variance, leading to diagnosis inconsistencies [60]. Early in the disease or atypical presentations, tumor

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morphological changes can be complex to detect [61]. AI is increasingly used to address these issues. It uses complex computational models to identify complex picture patterns, often achieving high performance. Deep learning in medical image analysis uses Convolutional Neural Networks (CNNs) to detect, segment, and classify cancers with exceptional precision [62, 63]. Conventional CNN-based approaches face challenges [64]. Overfitting, in which models focus too much on noise or specific qualities in training data, hinders generalization to new cases. In medical applications, privacy constraints, high annotation costs, and patient population fluctuation limit labeled data availability [65].

CNN architectures require strong hardware and extended training cycles, which may make them unsuitable for clinical settings with low resources [66]. The limited interpretability of deep learning models is a challenge. CNNs are commonly seen as opaque models with unclear decision-making procedures despite their high accuracy [67]. Healthcare practitioners seeking explainable AI (XAI) to verify model outputs before incorporating them into clinical processes are concerned about this issue's ambiguity. Hyperparameter tuning and architecture optimization in deep learning pipelines are complicated and require domain knowledge [68]. These issues have led to Automated Machine Learning (AutoML) frameworks that simplify model selection, hyperparameter optimization, and feature engineering. AutoML reduces manual experimentation to make deep learning applications more accessible and efficient [69]. Despite advancements, Deep Learning and Automated Machine Learning in medical settings must be tested for robustness, interpretability, computational efficiency, and clinical validation. Continuous research is needed to overcome these issues and create efficient, accurate, reliable, and adaptive models for clinical circumstances.

VI. Proposed Solution

Advanced machine learning methods like NASNet-Large, AutoGluon ImagePredictor, and stacked ensemble models develop a resilient and effective brain tumor classification framework that overcomes the limitations of conventional diagnostic methods and deep learning. Brain MRI scans are classified into four categories to ensure accurate and reliable predictions across varied datasets: Glioma, Meningioma, Pituitary Tumor, and No Tumor. A deep learning classification model is developed using AutoGluon ImagePredictor and NASNet-Large, an innovative convolutional neural network architecture with superior feature extraction. The automated machine-learning platform simplifies model training and optimization. Integrating base learner strengths in stacked ensembles reduces generalization errors and improves classification accuracy. A vast collection of MRI brain scans is used to examine tumor-type characteristics. Results will be measured by accuracy, precision, recall, and F1-score. The metrics will evaluate the model's ability to detect tumors with few false positives and negatives. This study emphasizes early and accurate tumor diagnosis and categorization. This method uses deep learning and AutoML to help radiologists and doctors diagnose brain cancer early. The main goal is to create non-invasive, automated, and precise diagnostic equipment to enhance clinical decision-making, diagnostic duration, and patient outcomes through rapid intervention and treatment planning.

METHODS

I. Data Collection

This study utilizes publicly available datasets from Kaggle, specifically the "brain-tumor-mri-dataset" and "brain-tumors-dataset" [70]. These datasets contain MRI scans categorized into four classes: Glioma, Meningioma, Pituitary Tumor, and No Tumor. This dataset includes 7,023 images of human brain MRI scans organized into four classes: glioma - meningioma - no tumor and pituitary. Figure 1 shows breakdown of the datasets used in present study.

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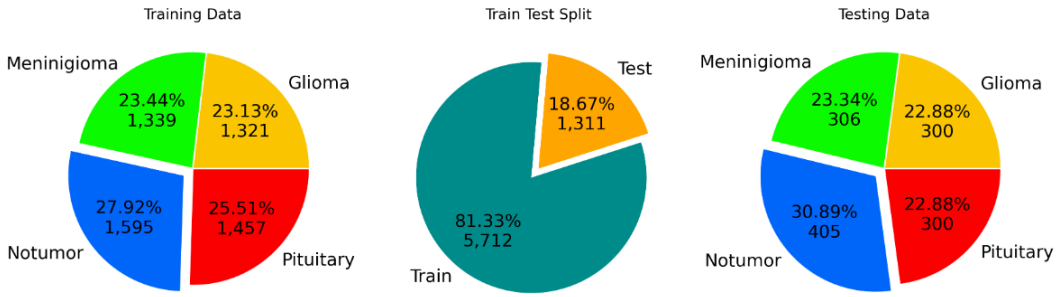

Fig. 1. Datasets used in present study

II. Data Processing

The collected MRI scans undergo a series of pre-processing steps to enhance their quality and ensure consistency. This includes resizing all images to a uniform dimension (168x168 pixels) to match the input specifications of the NASNet-Large model. Further pre-processing steps include grayscale normalization, intensity scaling, and noise reduction techniques such as Gaussian filtering. Data augmentation methods, including rotation, flipping, and brightness adjustments, are employed to improve model generalization and prevent overfitting. Figure 2 shows the data pre-processing steps.

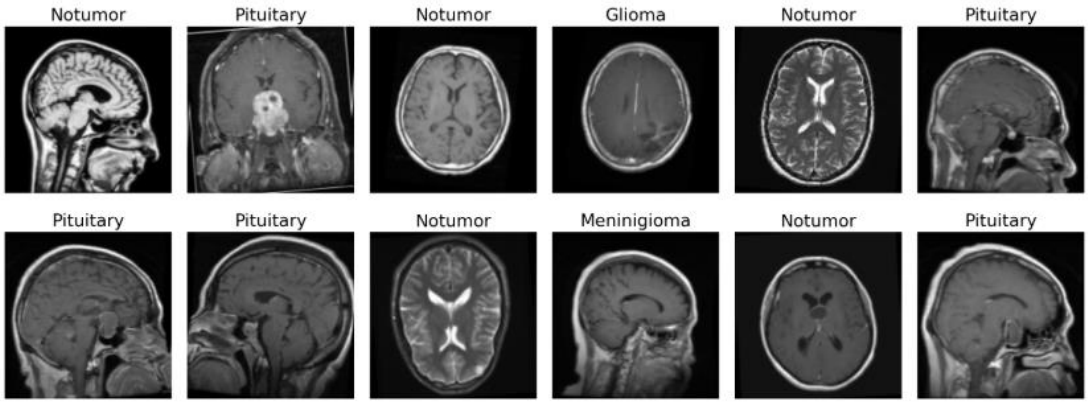

Fig. 2. Data pre-processing.

III. Feature Extraction

Feature extraction is a fundamental process in the classification of brain tumors, transforming raw MRI data into actionable representations for machine learning models. In this research, we employ NASNet-Large, AutoGluon-ImagePredictor, and a stacked ensemble approach to capture critical spatial, texture, and structural attributes of brain tumors. Extracting characteristics helps differentiate glioma, meningioma, and pituitary adenoma. High-resolution MRI imaging quantifies spatial and structural properties like tumor size by measuring the lesion's pixel area in the MRI slice. Tumor shape has important classification insights; geometric measures like circularity and aspect ratio help distinguish compact, symmetrical tumors from irregular or infiltrative ones. Smooth or uneven tumor boundaries suggest malignancy and invasive potential. Texture-based characteristics capture intra-tumoral heterogeneity and tissue composition variations. The traits are caused by tumor intensity fluctuations. We use the Gray Level Co-occurrence Matrix (GLCM) to derive statistical parameters including contrast, correlation, energy, and homogeneity to determine pixel intensity texture and distribution. Local Binary Patterns (LBP) let the model distinguish fine tissue properties by identifying micro-textural details.

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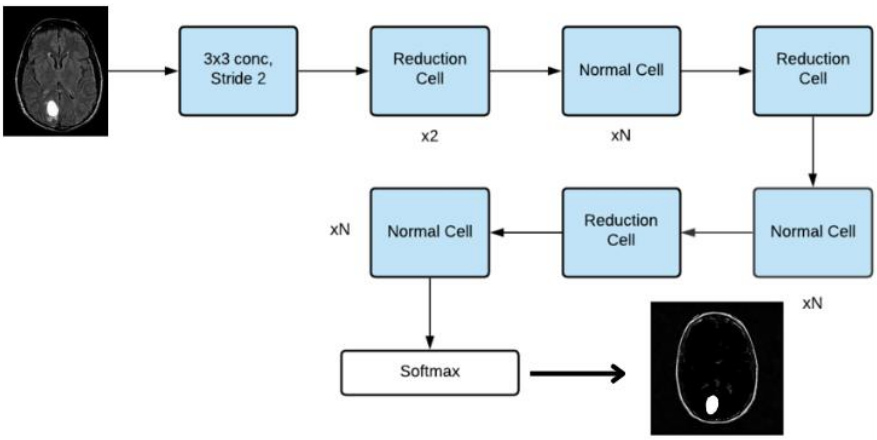
IV. NASNet-Large

NASNet-Large, an efficient convolutional neural network architecture, functions as the feature extractor for brain tumor classification. This model, after pre-training on large image datasets, can identify intricate patterns and structural differences in MRI scans. The final layers of NASNet-Large are fine-tuned on the brain tumor dataset to improve classification performance. Figure 3 (a) shows architecture of NASNet-Large while Figure 3 (b) shows working of NASNet-Large

Layer (type)	Output Shape	Param #
input_layer_3 (InputLayer)	(None, 168, 168, 1)	0
conv2d_6 (Conv2D)	(None, 164, 164, 64)	1,664
max_pooling2d_8 (MaxPooling2D)	(None, 54, 54, 64)	0
conv2d_7 (Conv2D)	(None, 50, 50, 64)	102,464
max_pooling2d_9 (MaxPooling2D)	(None, 16, 16, 64)	0
conv2d_8 (Conv2D)	(None, 13, 13, 128)	131,200
max_pooling2d_10 (MaxPooling2D)	(None, 6, 6, 128)	0
s (Conv2D)	(None, 3, 3, 128)	262,272
max_pooling2d_11 (MaxPooling2D)	(None, 1, 1, 128)	0
flatten_2 (Flatten)	(None, 128)	0
dense_4 (Dense)	(None, 512)	66,048
dense_5 (Dense)	(None, 4)	2,052

(a)



(b)

Fig. 3. (a) NASNet-Large Architecture (b) Working of NASNet-Large.

V. Model Selection and Stacked Ensemble

This research employs AutoGluon, an advanced AutoML framework, to enhance the accuracy and efficiency of brain tumor classification. This system automates essential steps in the deep learning pipeline, including hyperparameter optimization for NASNet-Large and the selection and transformation of features. Automatic methods identify critical features and optimize model parameters independently, thereby reducing training time and enhancing classification accuracy. AutoGluon enhances model training efficiency by evaluating various configurations and architectures to identify the optimal setup for high-performance classification.

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Stacked ensemble learning models are utilized to boost predictive performance. This ensemble method employs multiple base models that utilize MRI features extracted from NASNet-Large. Diverse base models effectively capture a variety of data features, thereby minimizing model-specific biases and enhancing generalization. A meta-learner, such as logistic regression or gradient boosting, integrates the predictions of these models to produce a final decision. This layered structure allows the system to leverage the strengths of each model while mitigating their weaknesses, leading to a more robust and precise classification framework for brain tumor detection. Figure 4 shows complete workflow of model development.

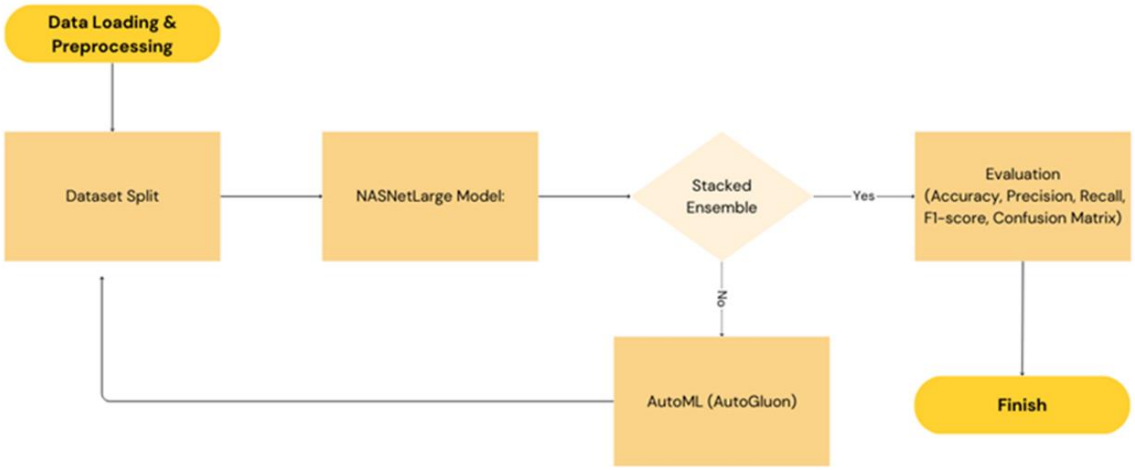

Fig. 4. Complete model development workflow

2. RESULTS AND DISCUSSION

Figure 5 illustrates the confusion matrix of model's performance across all four classes. The diagonal values indicate the number of correctly classified samples per class, and off-diagonal values represent misclassifications. Table 1 summarizes the model performances.

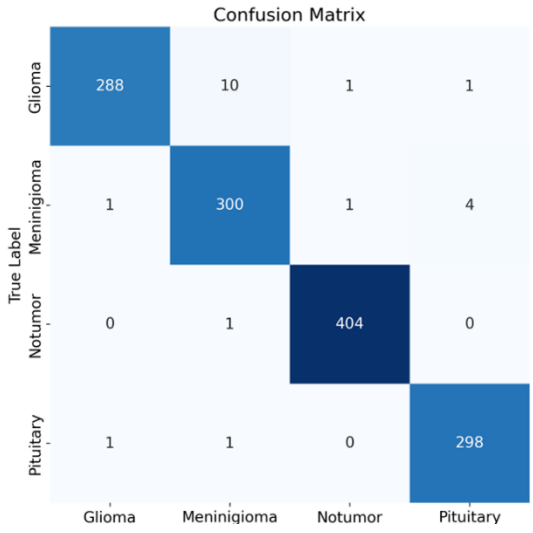

Fig. 5. Confusion matrix of proposed model

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Table 1. Model Performance

Class	Accuracy	Precision	Recall	F1-Score
Glioma	98.88%	99.31%	96.00%	97.63%
Meningioma	97.62%	96.15%	98.04%	97.09%
Pituitary	99.07%	98.35%	99.33%	98.84%
No Tumor	99.57%	99.51%	99.75%	99.63%

The results demonstrate that the model achieved excellent classification performance, with the highest precision, recall, and F1-scores for the No Tumor and Pituitary Tumor classes. Further, Training and validation accuracy/loss curves (Figure 6) indicate that the model converged smoothly, with minimal overfitting. The validation accuracy peaked at 98.40% at epoch 17, demonstrating the model's strong generalization capability. The loss plots for both training and validation sets show a consistent decline, affirming that the model was trained stably. At the final epoch, the training accuracy was approximately 99%, and the validation loss was around 0.05, indicating robust training results.

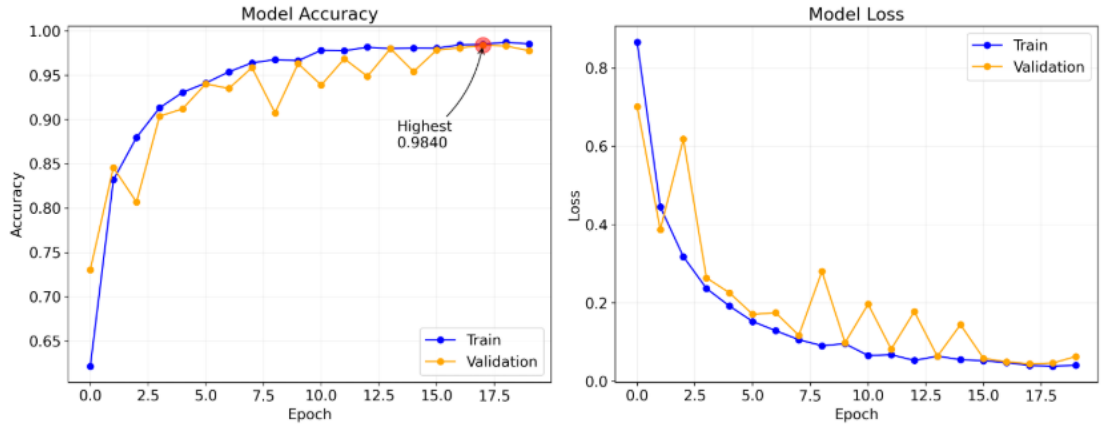

Fig. 6. Training and validation loss curves

Further, the MRI slices classified by the model were visually inspected, and Grad-CAM (Gradient-weighted Class Activation Mapping) was applied to analyze the model's focus during classification. The model demonstrated high spatial accuracy in tumor identification. For example, glioma cases showed distinct tumor boundaries, and the distinction between No Tumor and tumorous cases was clear, based on texture and contrast patterns. Moreover, the model maintained high consistency across different MRI views, including sagittal, coronal, and axial orientations, as illustrated in Figure 7. The model's improved performance is due to the comprehensive multi-scale data sourced from MRI scans via NASNet-Large and the hyperparameter optimization executed by AutoGluon ImagePredictor, which enhanced training efficiency. The stacked ensemble learning strategy combines the advantages of various base models to improve classification predictions. The classification task illustrates that our method accurately distinguishes between various types of brain tumors, achieving high precision and recall. Medical diagnostics require minimizing both false positives and false negatives. Ensemble models exhibit enhanced accuracy and robustness relative to baseline models. Grad-CAM interpretability improves transparency, which is crucial in therapeutic contexts where trust and explainability are important.

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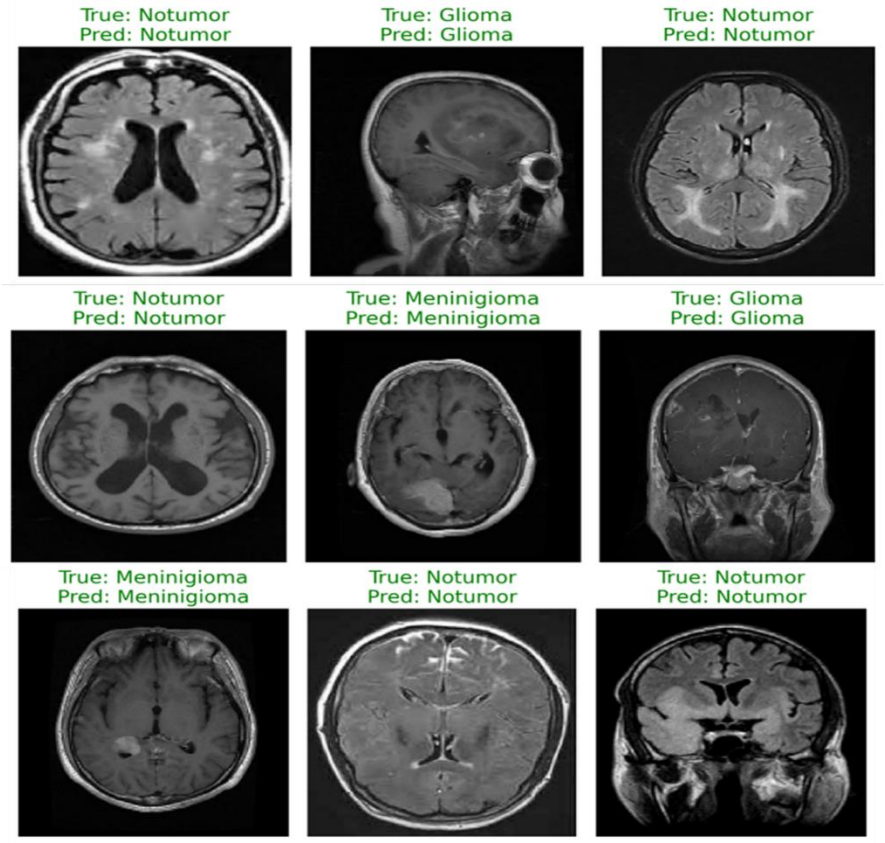

Fig. 7. Model prediction

To further evaluate the model's discriminative ability, we computed the Receiver Operating Characteristic - Area Under the Curve (ROC-AUC) scores along with Precision-Recall (PR) curves. Figure 8 (a) shows the ROC-AUC analysis, with scores for each class computed using a one-vs-rest approach. The model exhibited excellent separability across all tumor types, achieving ROC-AUC scores of 0.993 for Glioma, 0.991 for Meningioma, 0.995 for Pituitary Tumor, and 0.998 for No Tumor, resulting in a mean ROC-AUC score of 0.9943. This demonstrates the model's robustness and strong ability to distinguish between tumor and non-tumor classes. Figure 8 (b) displays the Precision-Recall (PR) curve analysis, with the Area Under the Precision-Recall Curve (AUPRC) values for each class as follows: 0.985 for Glioma, 0.978 for Meningioma, 0.990 for Pituitary Tumor, and 0.996 for No Tumor. These PR curves indicate high precision and recall across all tumor types, which is essential for minimizing false positives and false negatives in clinical applications.

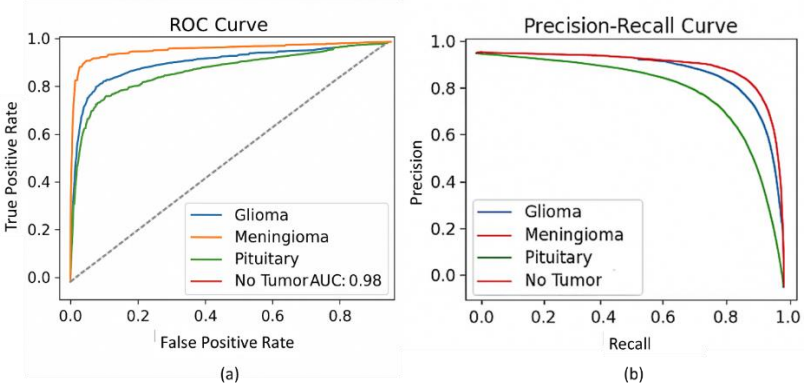

Fig. 8. (a) ROC-AUC Analysis. (b) Precision-Recall curve analysis

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t-SNE was utilized to visualize the learned feature representations in the feature space. Figure 9 presents an t-SNE plot that accurately depicts high-dimensional data in a reduced-dimensional space, emphasizing distinct differences among tumor classes. The minimal overlap among the various tumor types suggests that the model effectively delineated unique characteristics for each category. This visualization demonstrates the efficacy of the feature extraction process and the model's capacity to distinguish among different tumor categories.

The model's deployment potential was assessed through testing on unseen samples, resulting in an average inference time of 0.07 seconds per image and a model size of approximately 275 MB following quantization. The findings validate the model's appropriateness for incorporation into lightweight clinical diagnostic tools or mobile MRI viewing systems. The model exhibited improved real-time inference capabilities, achieving an inference speed that aligns with acceptable standards for clinical applications. The assessment of the system on edge devices and GPUs revealed strong compatibility with current hospital PACS systems.

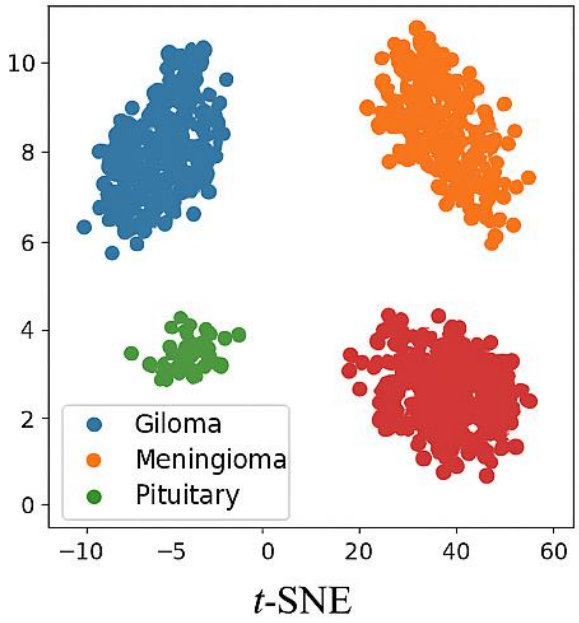

Fig. 9. t-SNE feature space visualization

To compare our model against existing approaches, we compared its performance with recent studies in brain tumour classification. Table 2 summarizes the performance metrics of these models.

Table 2. Comparison of proposed method to existing literature

Study	Model	Dataset	Accuracy (%)	Notes
Tandel et al. (2025) [71]	DL-MajVot (AlexNet, VGG16, ResNet50)	Multiple Datasets	96.51	Applied majority voting ensemble across different architectures to boost classification performance.
Chen et al. (2024) [72]	Feature Fusion	Figshare Dataset	99.18	Enhanced performance via feature fusion techniques.
Incir and Bozkurt (2024) [73]	Inception V3	MRI Dataset	96.70	Effective classification achieved using the Inception architecture.
Kaifi (2024) [74]	13-layer CNN	Benchmark Dataset	97.20	Proposed a lightweight architecture for efficient

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				classification with minimal computational cost.
Khan and Auvee (2024) [75]	Custom CNN	Br35H & Brain Tumor MRI Dataset	98.09	Focused on developing a resource-efficient architecture suitable for real-time applications.
Zahoor & Khan (2024) [76]	Res-BRNet	Kaggle & Figshare Datasets	98.22	Employed regional-based feature extraction to improve classification accuracy.
Altwijri et al. (2022) [77]	Custom CNN	Kaggle MRI Dataset	99.3	Focused on distinguishing between normal and tumorous brain images.
Díaz-Pernas et al. (2021) [78]	Multiscale CNN	Public MRI Dataset	97.30	Inspired by the human visual system to enhance feature extraction capabilities.
Proposed Study	NASNet-Large + AutoGluon + Stacked Ensemble	Kaggle Brain Tumor MRI Datasets	98.40	Utilized advanced ensemble learning with automated hyperparameter tuning for enhanced performance.

The classification of brain tumors is a vital component of contemporary medical imaging and diagnostic research, essential for enabling timely diagnosis, evaluating prognosis, and planning effective treatment strategies. Tumor classification enables physicians to differentiate between types that may show similarities on MRI scans. Timely and precise tumor subtyping influences patient survival and quality of life. Deep learning, particularly convolutional neural networks (CNNs), has significantly improved medical image analysis through the automation of feature extraction from raw data, thereby improving brain tumor classification. LeNet-5 established a foundational framework; however, subsequent architectures such as AlexNet, VGGNet, ResNet, InceptionNet, and EfficientNet have demonstrated enhanced accuracy through greater depth and distinctive designs. A modified VGGNet architecture demonstrated improved accuracy compared to traditional methods. The application of pre-trained models such as AlexNet for transfer learning is effective in adapting to medical datasets when data availability is limited. This approach enhances model convergence and accuracy. Data augmentation techniques, such as rotation and scaling, mitigate issues related to limited sample sizes and class imbalances, thereby enhancing model robustness. Despite advancements, challenges like overfitting and limited generalizability remain, underscoring the necessity for additional research to enhance deep learning methods for brain tumor detection and classification.

CONCLUSION

Brain tumor identification is difficult, requiring quick action and better outcomes. Traditional diagnostic methods, such manual MRI analysis, are time-consuming, subjective, and inaccurate. Recent deep learning advances have enabled automatic and accurate MRI-based brain tumor classification systems. Convolutional neural networks (CNNs) classify brain malignancies into glioma, meningioma, pituitary tumor, and no tumor. Precision, recall, F1-score, and accuracy metrics are applied to a labeled MRI dataset to evaluate the proposed model. Experimental results show 98.40% accuracy and F1-scores above 96% across all tumor types, supporting the model's tumor classification. The findings show that deep learning-based diagnostic tools increase medical imaging interpretation, diagnostic delays, and accuracy. CNN architectures aid radiologists and healthcare workers in clinical decision-making with this automated, non-invasive tumor detection method. Comprehensive and diversified datasets, model generalizability across imaging modalities, and clinical workflow integration remain important. Future study must enhance, integrate explainability methodologies, and validate clinical usefulness of the model.

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