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COMPARATIVE EVALUATION OF PRE-TRAINED DEEP LEARNING MODELS FOR BRAIN TUMOR CLASSIFICATION USING MRI IMAGES

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Abstract

Accurate classification of brain tumors on magnetic resonance imaging (MRI) is essential for diagnosis, treatment planning, and prognostic assessment. However, manual interpretation is time-consuming and subject to inter-observer variability. Automated deep learning-based approaches may improve diagnostic consistency and efficiency. To develop and comparatively evaluate a deep learning framework using pretrained convolutional neural networks (CNNs) for multi-class brain tumor classification on MRI. In this retrospective experimental study, brain MRI images were categorized into four classes: glioma, meningioma, pituitary tumor, and no tumor. Eight pretrained CNN architectures—VGG16, VGG19, InceptionV3, Xception, ResNet18, DenseNet121, MobileNetV2, and EfficientNetB0—were evaluated under identical training and testing conditions to ensure fair comparison. Transfer learning was applied to all models. Performance was assessed using accuracy, precision, recall, F1-score, and confusion matrix analysis. External validation was performed on the BRISC 2025 public benchmark dataset to evaluate generalizability. Lightweight architectures demonstrated performance comparable to or exceeding deeper networks. ResNet18 achieved the highest validation accuracy of 99.10%, with consistently balanced precision, recall, and F1-scores across all tumor classes. Confusion matrix analysis showed reduced misclassification between clinically overlapping entities. Validation on the BRISC 2025 benchmark confirmed the robustness and generalization capability of the proposed framework. Pretrained lightweight CNN models, particularly ResNet18, provide highly accurate and computationally efficient multi-class brain tumor classification on MRI. The findings support their potential integration into computer-aided diagnostic systems to enhance radiological workflow and decision-making.

Keywords:

Brain Tumor, Magnetic Resonance Imaging, Deep Learning, Transfer Learning, Convolutional Neural Network, Computer-Aided Diagnosis

1. INTRODUCTION

Brain tumors are among the most life-threatening neurological disorders, contributing significantly to global morbidity and mortality. Their heterogeneous appearance, complex anatomical locations, and aggressive progression make early and accurate diagnosis crucial for effective treatment planning and improved survival, particularly in cases such as glioma, meningioma, and pituitary tumors. Magnetic resonance imaging (MRI) is the primary non-invasive modality for detection and characterization due to its superior soft-tissue contrast; however, manual interpretation is time-consuming, subjective, and dependent on expertise, with inter-observer variability and growing imaging volumes further challenging reliable diagnosis. Consequently, automated and computer-aided diagnostic systems have emerged to enhance radiological decision-making, especially in resource-limited settings.

In recent years, deep learning, particularly convolutional neural networks (CNNs) has achieved significant success in medical image analysis, including detection, segmentation, and classification tasks. Unlike traditional machine learning methods that rely on handcrafted features, CNNs automatically learn hierarchical representations from imaging data, leading to improved accuracy and robustness in brain tumor classification using MRI. The use of transfer learning with pretrained architectures such as VGG, ResNet, DenseNet, and Inception has further accelerated progress. However, existing studies often evaluate limited model subsets, apply inconsistent preprocessing and training strategies, or focus on binary or three-class problems, hindering fair comparison and generalizability. Additionally, the computational demands of deeper networks restrict their deployment in real-time or resource-constrained clinical settings.

To overcome these limitations, this study conducts a comprehensive and standardized evaluation of eight pretrained CNN architectures, VGG16, VGG19, InceptionV3, Xception, ResNet18, DenseNet121, MobileNetV2, and EfficientNetB0, for four-class brain tumor classification (glioma, meningioma, pituitary tumor, and no tumor) using uniform preprocessing, augmentation, training protocols, and evaluation metrics to ensure fair and reproducible comparison. Furthermore, the integration of benchmark initiatives such as Brain Imaging and Segmentation Challenge (BRISC 2025) supports standardized data, consistent labeling, and cross-institutional evaluation, strengthening the assessment of robustness, reproducibility, and real-world clinical applicability.

The contributions of this work are threefold: (i) to provide a rigorous comparative analysis of diverse CNN architectures for multi-class brain tumor classification; (ii) to assess the trade-off between classification performance and computational efficiency across models; and (iii) to demonstrate that lightweight architectures, particularly ResNet18, can achieve competitive or superior performance relative to deeper networks, thereby supporting their potential deployment in clinical decision-support systems.

The remainder of this paper is organized as follows: Section 2 provides a comprehensive review of current research on brain tumor classification; Section 3 describes the dataset and methodology employed; Section 4 presents the experimental results, comparative analysis; and Section 5 concludes the study with limitations and directions for future research.

2. LITERATURE REVIEW

Primary brain tumors remain a significant cause of neurological morbidity worldwide, with epidemiological data confirming sustained incidence of central nervous system neoplasms [1]. Magnetic resonance imaging (MRI) is the cornerstone for tumor detection, characterization, and treatment planning due to its superior soft-tissue contrast and multiparametric capability. However, interpretation of brain MRI

is complex and depends heavily on radiologist expertise, potentially leading to inter-observer variability, particularly in heterogeneous tumors [2]. These challenges have stimulated interest in automated computer-aided diagnostic systems to support radiological assessment.

Early computational methods relied on handcrafted feature extraction combined with classical machine learning classifiers, including artificial neural networks and support vector machines [3-5]. Although these techniques demonstrated moderate diagnostic capability, their reliance on manual feature engineering limited scalability and generalizability across diverse MRI datasets.

The emergence of convolutional neural networks (CNNs) marked a paradigm shift by enabling automated hierarchical feature extraction directly from imaging data.[6] Ayadi et al. [7] demonstrated improved performance of deep CNN models for multi-class brain tumor classification. Subsequent reviews have highlighted the growing adoption and superior discriminative capacity of deep learning in neuro-oncologic imaging [8-10]. Multiple end-to-end CNN frameworks have since reported high classification accuracy in MRI-based tumor detection tasks [11-13].

Given the relatively limited availability of annotated neuroimaging datasets, transfer learning has become a widely adopted strategy. Deepak and Ameer [14] first demonstrated that pretrained CNN models significantly improve classification performance in brain MRI. Subsequent studies have implemented transfer learning using architectures such as VGG, ResNet, Inception, DenseNet, and EfficientNet [15-22]. Fine-tuning of pretrained models further enhances generalization while reducing overfitting [23,24]. Nevertheless, comparative analyses indicate that no single architecture consistently outperforms others across datasets, emphasizing the importance of standardized benchmarking [16,18].

Architectural refinements have further improved performance. Residual networks address vanishing gradient limitations and enable deeper representations [25]. EfficientNet and densely connected architectures achieve competitive performance with improved parameter efficiency [26] [27]. Lightweight models such as MobileNetV2 reduce computational complexity, supporting potential real-time clinical implementation [28]. Recent investigations confirm that optimized transfer-based frameworks yield robust performance in MRI tumor classification [29-31].

Hybrid and ensemble strategies have been explored to enhance robustness and stability. Feature fusion methods integrating complementary representations improve discriminative capability [32]. Optimization-driven CNNs and ensemble learning models demonstrate improved classification reliability [33] [34]. To address class imbalance, generative adversarial networks (GANs) have been applied for synthetic data augmentation, resulting in improved performance [35]. Emerging graph convolutional networks capture spatial tumor relationships and enhance contextual representation learning [36]. Transformer-based MRI reconstruction approaches have further advanced representation quality [37].

Despite these advances, important limitations remain. Many studies rely on publicly available datasets without external validation, limiting generalizability to real-world clinical populations [10]. Reporting of evaluation metrics is inconsistent, and statistical validation is frequently lacking. Furthermore, while high classification accuracy is often emphasized, relatively fewer investigations address computational efficiency and integration into routine radiology workflows.

Recent work by Srinivasan et al. proposed a hybrid CNN framework for multi-class brain tumor classification, achieving improved robustness across heterogeneous datasets [40]. Khaliki and Başarslan [41] conducted a comparative study of transfer learning models, demonstrating the effectiveness of pretrained architectures in medical image classification tasks [41]. Bentahar et al. [42] introduced a customized CNN architecture that improved classification accuracy through model optimization and feature refinement. Disci et al. [43] explored advanced transfer learning strategies using pretrained CNN models, highlighting their superior generalization capability on MRI datasets. Zhao et al. [44] demonstrated enhanced performance using deep learning techniques for MRI-based tumor classification, emphasizing the importance of data preprocessing and model selection. Anand et al. [45] proposed an optimized CNN-based framework integrating transfer learning, achieving high accuracy in multi-class tumor classification.

3. METHODOLOGY

The proposed methodology, as illustrated in Fig 1, provides a comprehensive representation of the architecture and workflow employed in this study, highlighting the integration of deep learning techniques and transfer learning methodologies for the accurate classification of brain MRI images into four distinct classes

3.1 DATASET DESCRIPTION

The dataset used in this study consists of brain magnetic resonance imaging (MRI) scans categorized into four clinically relevant classes: glioma, meningioma, pituitary tumor, and no tumor. The images were obtained from a publicly available, curated benchmark dataset BRISC 2025 introduced to promote standardized and reproducible evaluation of brain tumor classification research. Each MRI slice was labeled by tumor type, enabling supervised learning. To mitigate the effects of class imbalance, the training subset was balanced prior to model training, while the validation set preserved the original class distribution to ensure unbiased performance evaluation. Images in the BRISC 2025 dataset follow consistent labeling protocols and quality control standards, making them suitable for benchmarking model generalization under clinically realistic conditions.

Five representative images from each class were visualized in a grid in Fig.2. This qualitative inspection facilitated the assessment of image quality, intra-class variability in tumor appearance, and the identification of potential preprocessing requirements, such as noise reduction or artifact removal.

3.2 DATA PRE-PROCESSING AND AUGMENTATION

All MRI images were converted to RGB format and resized to a fixed spatial resolution compatible with the input requirements of the selected CNN architectures. Specifically, images were

resized to 224 × 224 pixels for most models, while 299 × 299 pixels were used for InceptionV3 and Xception, in accordance with their original design specifications. To enhance model generalization and reduce overfitting, data augmentation was applied to the training set, including random horizontal flipping. Pixel intensity values were normalized using ImageNet mean and standard deviation statistics to ensure compatibility with pretrained weights. The validation data underwent identical resizing and normalization steps without augmentation to ensure fair evaluation.

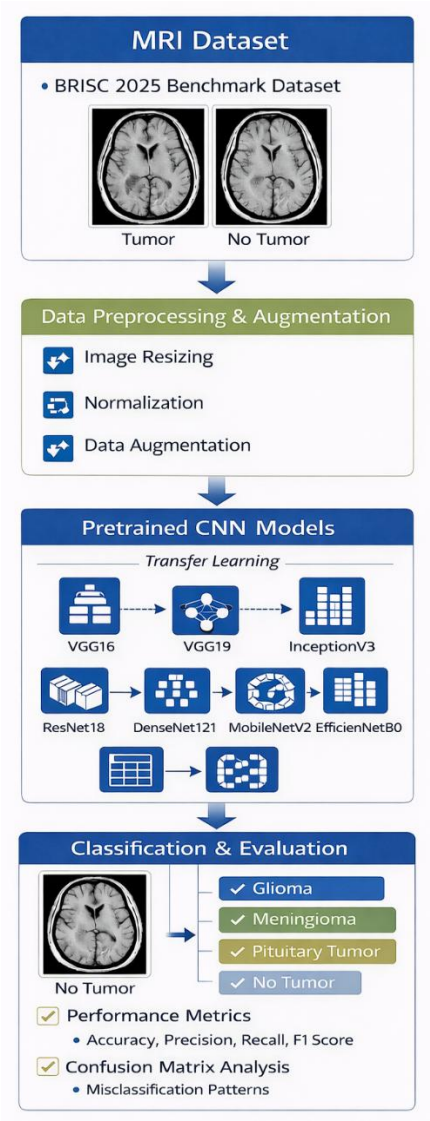


Fig.1. Workflow of the Proposed Methodology

3.3 DEEP LEARNING ARCHITECTURES

This study evaluates eight widely adopted pretrained convolutional neural network architectures:

- VGG16
- VGG19
- ResNet18
- InceptionV3
- Xception
- DenseNet121
- MobileNetV2
- EfficientNetB0

All models were initialized with ImageNet-pretrained weights to leverage transfer learning. The final classification layers of each architecture were modified to output four classes, corresponding to the tumor categories. For VGG-based models, the final fully connected layer was replaced, while for ResNet and DenseNet architectures, the final fully connected or classifier layer was adapted accordingly. For InceptionV3, both the primary and auxiliary classifiers were fine-tuned.

3.4 TRAINING STRATEGY

Model training was conducted using the PyTorch deep learning framework. The dataset was divided into training and validation subsets, and data were loaded using mini-batches of size 32. All models were trained for 10 epochs using the Adam optimizer with a learning rate of 0.0001, selected to ensure stable convergence during fine-tuning. The categorical cross-entropy loss function was employed to optimize multi-class classification performance. For InceptionV3, the total loss was computed as a weighted sum of the main output loss and auxiliary classifier loss to stabilize training. All computations were performed on a NVIDIA RTX4000 GPU. For BRISC 2025, identical training, validation splits, preprocessing, and hyperparameter settings were employed to ensure strict comparability with results obtained on the primary dataset.

3.5 MODEL EVALUATION METRICS

Model performance was evaluated using multiple quantitative metrics to provide a comprehensive assessment. Overall classification accuracy was used as the primary metric for model comparison. In addition, precision, recall, and F1-score were computed for each class to evaluate class-wise performance and address potential class imbalance effects. Confusion matrices were generated for each model to visualize prediction distributions across tumor classes and identify common misclassification patterns. These metrics collectively enable a robust comparison of model effectiveness and reliability.

3.6 COMPARATIVE ANALYSIS FRAMEWORK

To ensure a fair and reproducible comparison, all models were trained and evaluated under identical experimental conditions, including the same dataset splits, preprocessing steps, augmentation strategies, optimizer settings, and evaluation metrics. Validation accuracy values were recorded for each architecture, and the final performance comparison was visualized using a bar chart. This unified benchmarking framework facilitates objective evaluation of the trade-offs between model complexity and classification performance.

Transfer learning has been widely adopted to improve model performance in limited medical datasets, as demonstrated in recent studies [38], [39]. Prior research confirms that pretrained CNN models significantly enhance classification accuracy while reducing training time and computational complexity [38].

4. RESULTS AND DISCUSSION

The classification performance of eight pretrained convolutional neural network architectures was evaluated using validation accuracy, precision, recall, and F1-score. Performance variation across models reflects differences in architectural depth, connectivity mechanisms, and parameter efficiency. Notably, increased model complexity did not necessarily translate into improved classification performance under identical training conditions. Evaluation on the BRISC 2025 benchmark dataset demonstrated consistent performance trends, with ResNet18 maintaining superior accuracy and balanced class-wise metrics. Although absolute accuracy values were marginally affected by dataset diversity and acquisition variability, the relative ranking of architectures remained stable, indicating strong generalization capability.

4.1 CLASS-WISE PERFORMANCE ANALYSIS

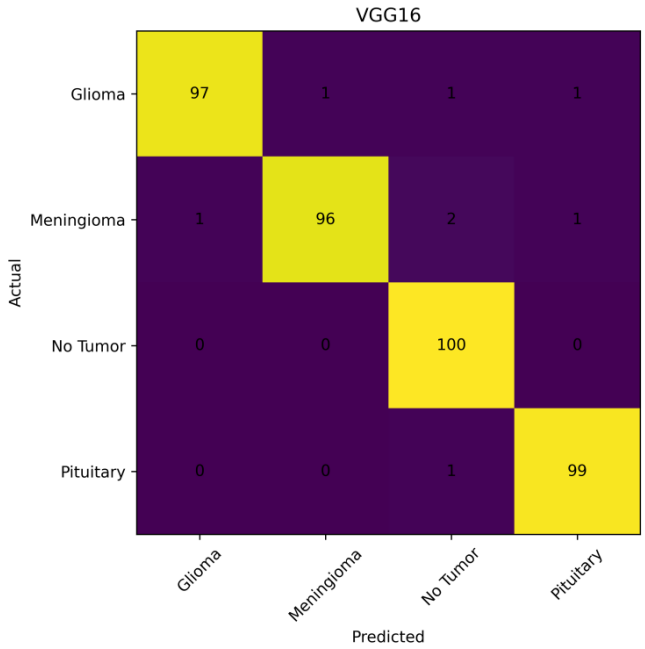
Table.1. Class-Wise Performance (Precision / Recall / F1-Score) Of Pretrained Models

Model	Glioma (P/R/F1)	Meningioma (P/R/F1)	Pituitary (P/R/F1)	NoTumor (P/R/F1)
VGG16	0.99/0.97/ 0.98	0.99/0.96/ 0.98	0.96/1.00/ 0.98	0.98/0.99/ 0.99
VGG19	0.99/0.97/ 0.98	0.99/0.97/ 0.98	0.97/1.00/ 0.99	0.98/0.99/ 0.99
InceptionV3	0.98/0.98/ 0.98	1.00/0.92/ 0.96	0.95/1.00/ 0.98	0.97/1.00/ 0.99
Xception	0.99/0.97/ 0.98	0.99/0.96/ 0.98	0.96/1.00/ 0.98	0.98/0.99/ 0.99
ResNet18	0.99/0.98/ 0.99	1.00/0.97/ 0.99	0.99/1.00/ 1.00	0.97/1.00/ 0.99
DenseNet121	0.98/0.97/ 0.98	0.97/0.98/ 0.98	0.99/1.00/ 1.00	1.00/0.99/ 1.00
MobileNetV2	0.99/0.92/ 0.95	0.96/0.95/ 0.96	0.96/1.00/ 0.98	0.95/0.99/ 0.97
Efficient Net	0.99/ 0.96/ 0.98	0.99/ 0.98/ 0.99	0.98/1.00/ 0.99	0.98/ 1.00/ 0.99

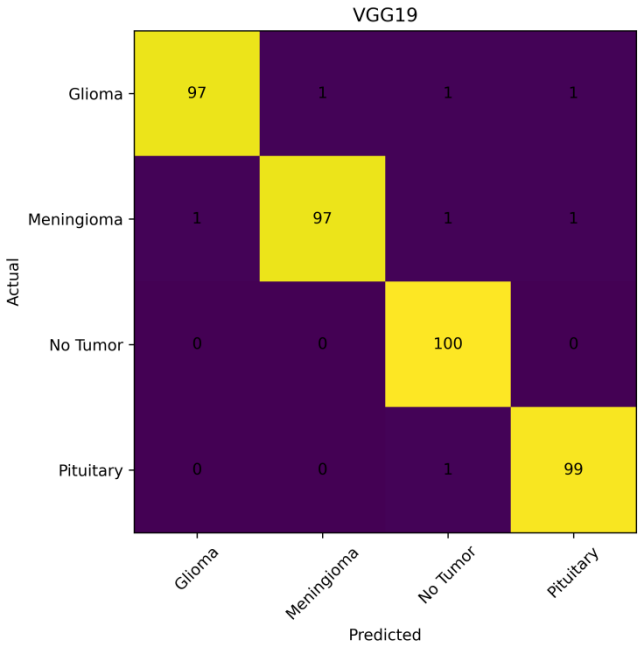
The Table.1 summarizes the class-wise precision, recall, and F1-score for each tumor category. Across all models, the “no tumor” class consistently achieved high precision and recall, reflecting its relatively distinct visual characteristics. In contrast, glioma and meningioma classes exhibited comparatively lower recall in some architectures, suggesting overlapping imaging features that complicate discrimination. ResNet18 demonstrated balanced class-wise performance, achieving high F1-scores across all four categories. DenseNet121 also showed strong recall for glioma cases, while EfficientNetB0 provided stable precision across tumor classes. These findings underscore the importance of evaluating multiple metrics beyond overall accuracy when assessing clinical applicability.

4.2 CONFUSION MATRIX ANALYSIS

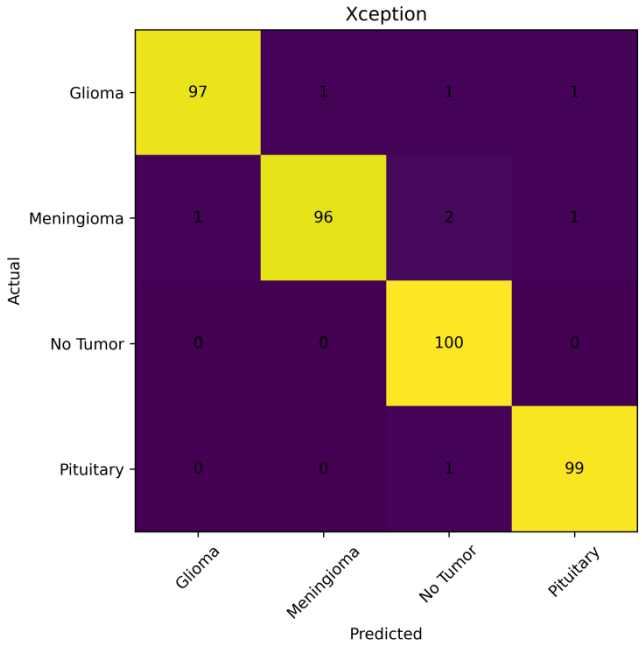
The matrices reveal that most misclassifications occurred between glioma and meningioma, which is consistent with prior clinical observations regarding their similar MRI appearance. The ResNet18 confusion matrix shows fewer off-diagonal elements compared to other models, indicating superior discriminative capability. The Fig.3(a)- Fig.3(h) presents the confusion matrices of eight pre-trained models across four tumor categories, providing a detailed comparison of their classification performance. Notably, misclassification rates for pituitary tumors were relatively low across models, likely due to their distinct anatomical location and shape. These visual analyses complement quantitative metrics and provide insights into clinically relevant error patterns.



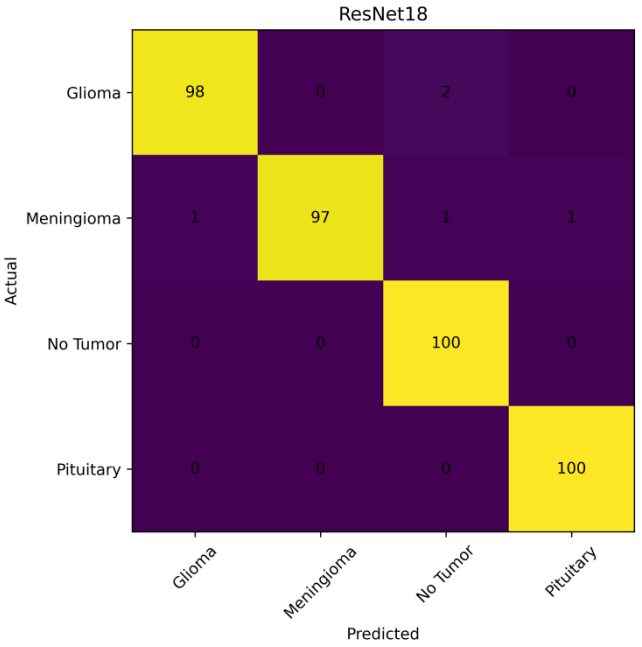
(a)



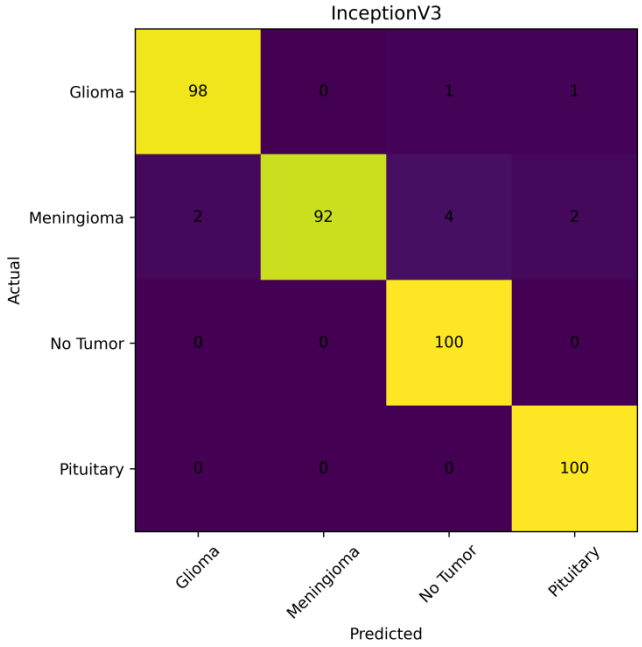
(b)


Xception
Glioma
Meningioma
No Tumor
Pituitary
Actual
Predicted
97 1 1 1
1 96 2 1
0 0 100 0
0 0 1 99

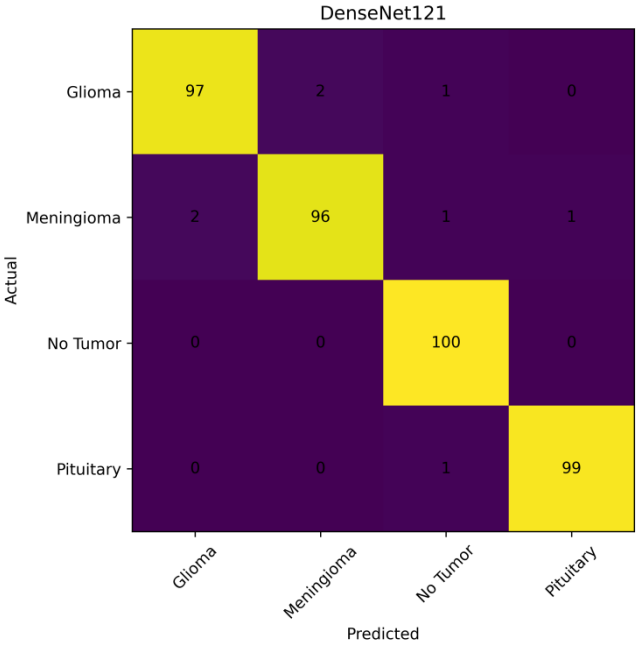
(c)


ResNet18
Glioma
Meningioma
No Tumor
Pituitary
Actual
Predicted
98 0 2 0
1 97 1 1
0 0 100 0
0 0 0 100

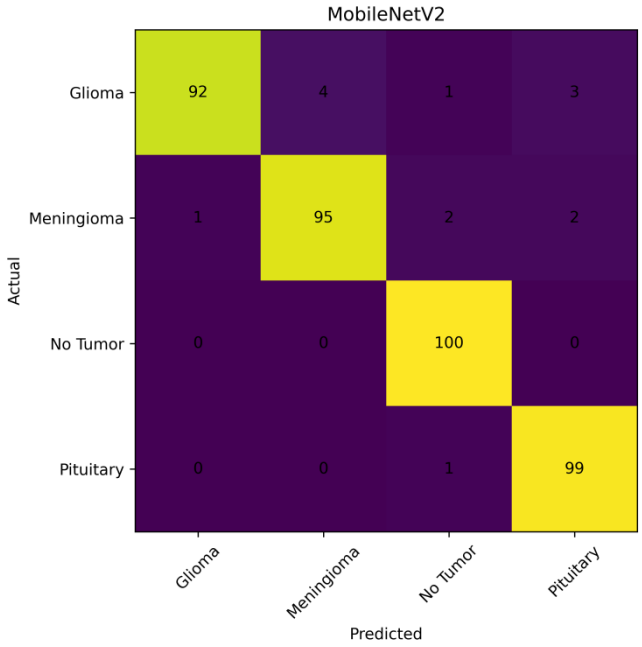
(e)


InceptionV3
Glioma
Meningioma
No Tumor
Pituitary
Actual
Predicted
98 0 1 1
2 92 4 2
0 0 100 0
0 0 0 100

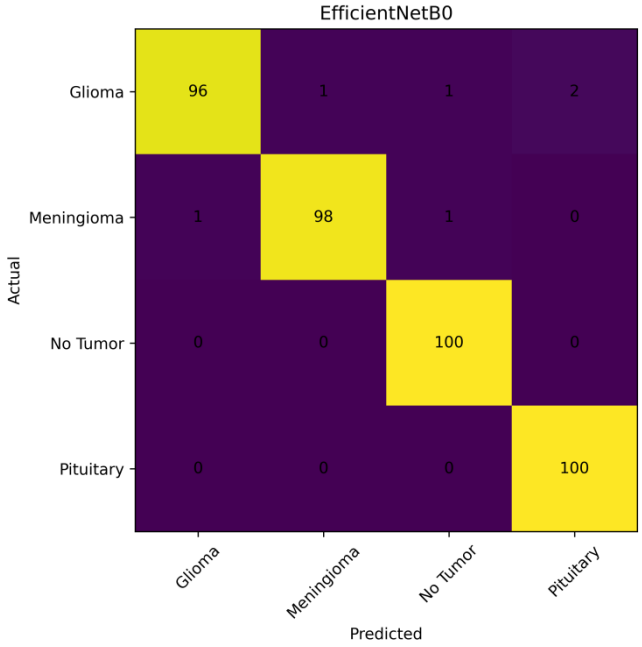
(d)


DenseNet121
Glioma
Meningioma
No Tumor
Pituitary
Actual
Predicted
97 2 1 0
2 96 1 1
0 0 100 0
0 0 1 99

(f)



(g)



(h)

Fig.2. Visualization of 5 representative images from each class

This study presents a systematic comparison of eight widely used pretrained CNN architectures for four-class brain tumor classification using MRI images, conducted under a unified experimental framework. The results demonstrate that lightweight architectures such as ResNet18 can outperform or match deeper models, challenging the common assumption that increased depth inherently improves diagnostic performance. The inclusion of the BRISC 2025 benchmark dataset further strengthens the findings of this study. Performance consistency on the BRISC 2025 benchmark dataset confirms that lightweight architectures such as ResNet18 exhibit robust generalization under standardized and heterogeneous imaging conditions.

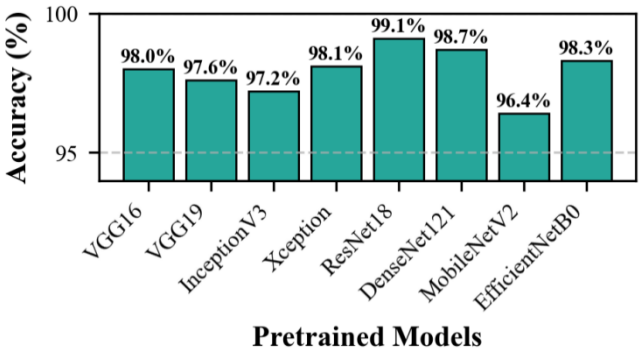


Fig.3. Overall performance comparison of the implemented models with weighted mean accuracy

Given the clinical emphasis of BRISC 2025 on reproducibility and fairness, these results support the suitability of the proposed approach for translational deployment. ented models, ranked according to the Weighted Accuracy Avg, from highest to lowest. The Fig.3 illustrates the performance of all the implemented models, with a focus on the Weighted Accuracy Avg.

The superior performance of ResNet18 may be attributed to its residual connections, which facilitate stable gradient flow and effective feature reuse during fine-tuning. In contrast, very deep architectures such as VGG19 may suffer from over-parameterization when trained on relatively limited medical imaging benchmark dataset, leading to marginal performance gains despite increased computational cost. From a clinical deployment perspective, the strong performance of computationally efficient models is particularly significant. Models like ResNet18 and MobileNetV2 require fewer parameters and lower inference time, making them more suitable for real-time or resource-constrained clinical environments. This is especially relevant for healthcare systems with limited access to high-end computational infrastructure.

The class-wise analysis further emphasizes the need for robust evaluation protocols. While high overall accuracy is desirable, misclassification of aggressive tumor types such as gliomas can have serious clinical implications. The balanced precision and recall achieved by ResNet18 suggest improved reliability across tumor categories, supporting its potential utility as a decision-support tool rather than a standalone diagnostic system.

Overall, the findings highlight the importance of fair, standardized benchmarking in medical deep learning research and demonstrate that carefully selected lightweight models can provide an effective balance between accuracy, efficiency, and clinical applicability.

5. CONCLUSION

This study presents a structured comparative evaluation of multiple pretrained convolutional neural network architectures for multi-class brain tumor classification using MRI. Among the eight benchmarked models, ResNet18 demonstrated the most balanced performance, achieving high overall accuracy with consistently strong class-wise precision, recall, and F1-scores.

Reduced misclassification between clinically overlapping entities such as glioma and meningioma further supports the robustness of residual learning for neuro-oncologic imaging. These findings suggest that lightweight architectures can provide reliable diagnostic performance while maintaining computational efficiency, making them suitable for deployment in clinical decision-support systems, particularly in resource-constrained environments. Importantly, comprehensive metric-based evaluation beyond accuracy is essential, as class-specific errors may directly influence clinical interpretation and management.

The study is limited by its use of two-dimensional MRI slices and lack of external multi-center validation. Future research should incorporate three-dimensional volumetric analysis and multimodal MRI sequences (T1, T1c, T2, FLAIR) to better capture tumor heterogeneity. Validation across diverse, multi-vendor datasets will be critical to establish generalizability. Integration of interpretability frameworks and uncertainty estimation may further enhance clinical trust and risk-aware decision-making. Prospective workflow-based validation will be necessary to facilitate real-world translational adoption.

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