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Ensemble Deep Learning for Multi-Class Brain Tumour Classification: Integrating ResNet, Inception, and EfficientNet Architectures

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Abstract: ***Brain tumours represent critical medical conditions requiring accurate and timely diagnosis to improve patient outcomes and guide effective treatment strategies. Manual interpretation of magnetic resonance imaging (MRI) scans by radiologists remains time-consuming and subject to inter-observer variability. This study addresses these challenges by proposing an ensemble deep learning framework that integrates three complementary convolutional neural network architectures: ResNet101V2, InceptionV3, and EfficientNetB0. The methodology employs transfer learning from ImageNet pre-trained weights, leveraging global average pooling to extract discriminative features from brain MRI scans. The ensemble system classifies images into four categories: glioma tumours, meningioma tumours, pituitary adenomas, and normal brain tissue. Comprehensive experimental evaluation on a dataset of approximately 3,000 MRI images demonstrates an overall classification accuracy of 82%, with precision, recall, and F1 Score of 84%, 82%, and 80%, respectively. Class-specific analysis reveals exceptional performance for pituitary tumour detection, with 97% precision and 92% recall, while meningioma classification achieves 97% recall. The ensemble approach outperforms individual architectures by capturing complementary feature representations across multiple scales and hierarchies. These results demonstrate the clinical potential of ensemble deep learning for automated brain tumour diagnosis, offering a robust framework that balances computational efficiency with diagnostic accuracy. The proposed system provides a foundation for future development of clinical decision support tools in neuro-oncology.***

Index Terms: ***Brain Tumour Classification, Convolutional Neural Networks, Ensemble Learning, Medical Image Analysis, MRI, Transfer Learning***

Nomenclature:
CNN: Convolutional Neural Network
MRI: Magnetic Resonance Imaging
ResNet: Residual Network
GPU: Graphics Processing Unit
BraTS: Brain Tumour Segmentation
CRF: Conditional Random Field
GAP: Global Average Pooling

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I. INTRODUCTION

Brain tumours represent one of the most challenging medical conditions in modern healthcare. Timely and accurate diagnosis significantly impacts treatment planning and patient prognosis [1]. Currently, radiological assessment of magnetic resonance imaging (MRI) scans relies heavily on manual interpretation by experienced radiologists. This process is time-consuming, subject to inter-observer variability, and prone to human error [2]. Consequently, there is an urgent need for automated diagnostic systems that can assist clinicians in making accurate and consistent diagnoses.

Deep learning, particularly convolutional neural networks (CNNs), has revolutionised medical image analysis by enabling automatic feature extraction and classification [3]. However, individual CNN architectures exhibit varying strengths and limitations depending on the specific characteristics of the medical imaging task [4]. To address these limitations, we propose an ensemble learning framework that combines multiple complementary CNN architectures, leveraging their individual strengths while mitigating their weaknesses.

Our research introduces an integrated ensemble system that combines the ResNet101V2, InceptionV3, and EfficientNetB0 architectures. These architectures were strategically selected for their complementary feature extraction capabilities and diverse approaches to processing medical images [5]. The framework employs transfer learning from ImageNet pre-trained weights, followed by fine-tuning on brain tumour MRI data [11]. The final classification is obtained by weighted averaging of individual model predictions, thereby enhancing robustness and reducing overfitting.

The main contributions of this work are fourfold: (1) Development of a novel ensemble framework combining ResNet101V2, InceptionV3, and EfficientNetB0 specifically tailored for brain tumour classification; (2) Comprehensive experimental evaluation on a multi-class brain tumour dataset with detailed performance analysis; (3) Class-specific performance assessment identifying strengths and areas for improvement in tumour type detection; and (4)

Investigation of architectural synergies in ensemble learning for complex medical imaging tasks.

II. LITERATURE REVIEW

Significant advances have been made in applying deep learning to medical image analysis, particularly for brain tumour detection and classification [6]. Researchers have explored various ensemble strategies and architectural approaches to improve diagnostic accuracy and reliability.

A. Ensemble Learning Approaches

Multiple studies have demonstrated that ensemble methods combining diverse deep learning architectures consistently outperform single-model approaches [7]. Research has shown that heterogeneous ensemble combinations can improve classification accuracy by 5–8% compared to individual models [8]. This improvement stems from the ability of different architectures to capture complementary features and patterns in medical images.

B. Spatial Feature Preservation

Recent research has emphasised the importance of preserving spatial information in medical image analysis [9]. Investigators have explored capsule networks and attention mechanisms to preserve spatial relationships among anatomical structures, though these approaches can be computationally intensive [10]. Attention-based mechanisms that automatically focus on diagnostically relevant regions have shown promise in both improving accuracy and providing interpretable visualisations.

C. Transfer Learning Applications

Transfer learning has become a cornerstone technique in medical imaging due to the often-limited availability of labelled training data [12]. Studies investigating the adaptation of pre-trained models from natural image domains to medical imaging have consistently demonstrated substantial improvements over training from scratch [13]. Various researchers have compared different deep learning frameworks designed explicitly for brain tumour analysis.

D. Comparative Architecture Studies

The consensus of contemporary research indicates that ensemble architectures consistently outperform individual models across diverse medical imaging applications [14]. Brain tumour segmentation benchmarks have established standardised evaluation protocols for comparing different approaches [15]. The Brain Tumour Segmentation (BraTS) challenge has advanced glioma analysis by providing large-scale annotated datasets and evaluation frameworks [16]. Additionally, integrated CNN approaches have shown enhanced robustness to data variability in multi-class classification problems [17].

Advanced network architectures combined with transfer learning have proven particularly effective in limited-dataset scenarios [21]. Deep neural networks with multi-scale processing capabilities have demonstrated superior performance in brain lesion segmentation tasks [18]. Recent developments in multi-scale 3D CNNs have improved brain lesion segmentation accuracy by incorporating fully connected conditional random fields [19]. Self-configuring deep learning methods have emerged as robust solutions for biomedical image segmentation across diverse imaging modalities [20].

Ensemble deep learning approaches designed explicitly for brain tumour classification have demonstrated significant improvements in diagnostic accuracy [24]. Hybrid ensemble architectures that combine multiple pre-trained networks have shown improved performance in distinguishing between tumour types [25]. Recent investigations into ensemble learning for medical image classification have established best practices for architecture selection and integration strategies [26].

Our work builds upon these foundations while introducing a novel contribution: the strategic combination of EfficientNetB0's parameter efficiency, ResNet101V2's deep residual learning capabilities, and InceptionV3's multi-scale processing. This integration creates a more comprehensive analytical framework than previously explored combinations.

III. DATASET DESCRIPTION AND PREPROCESSING

This study utilises a comprehensive Brain Tumour Classification MRI dataset containing approximately 3,000 magnetic resonance images distributed across four categories: glioma tumours, meningioma tumours, pituitary adenomas, and normal brain tissue. The dataset was partitioned into training and testing subsets, with a validation set extracted from the training partition for model optimisation and hyperparameter tuning.

A. Data Preprocessing Pipeline

Several preprocessing steps were implemented to optimise model training performance. First, all MRI scans were resized to a uniform 224 × 224-pixel resolution to match the input requirements of the pre-trained architectures. Second, pixel intensity values were normalised to the [0, 1] range by dividing by 255, improving convergence and numerical stability during training. Third, the dataset was partitioned using stratified sampling with an 80% training, 10% validation, and 10% testing split to ensure balanced class representation across all subsets. Fourth, categorical labels were converted to one-hot encoding to be compatible with multi-class classification.

The dataset exhibits balanced distribution across all four categories, providing sufficient samples per class for practical training and unbiased evaluation. Table I presents the detailed distribution of images across categories.

Table I: Dataset Distribution Across Tumour Categories (Authors' Own Compilation)

Category	Training	Validation	Testing	Total
Glioma	600	75	75	750
Meningioma	600	75	75	750
Pituitary	600	75	75	750
Normal	600	75	75	750

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IV. PROPOSED METHODOLOGY

A. Architectural Framework Overview

The proposed ensemble methodology integrates three complementary CNN architectures with distinct feature extraction characteristics. ResNet101V2 was selected for its residual learning framework, which enables training deep networks while mitigating vanishing-gradient problems [5]. InceptionV3 provides multi-scale feature extraction through parallel convolutional pathways with varying filter sizes [22]. EfficientNetB0 achieves parameter efficiency through a compound-scaling methodology [23].

These three architectures were selected for their complementary feature-extraction mechanisms and proven effectiveness in medical imaging applications. Their integration creates a comprehensive analytical framework that captures diverse tumour characteristics across multiple scales and feature hierarchies.

B. Transfer Learning Implementation Strategy

Transfer learning from ImageNet pre-trained weights provides several advantages for this medical imaging task. First, pre-trained models encode general-purpose low-level feature extractors applicable across diverse image domains, including medical imaging. Second, transfer learning significantly reduces training time and computational requirements compared to training from scratch. Third, pre-trained weights serve as an effective regularisation mechanism, improving generalisation performance on unseen data.

In the proposed framework, the convolutional base layers of each pre-trained model were frozen, focusing training efforts on the final classification layers. This approach preserves learned representations while enabling adaptation to the specific brain tumour classification task.

The feature extraction process for each base model can be formulated mathematically as:

$$h_i(x) = g_i\left(f_i(x; \vartheta_{\text{frozen}_i}); \vartheta_{\text{trainable}_i}\right) \quad \ldots \quad (1)$$

Where $f_i(x; \vartheta_{\text{frozen}_i})$ represents the frozen convolutional feature extractor, and $g_i(\cdot; \vartheta_{\text{trainable}_i})$ represents the trainable classification head for model i. This formulation is adapted from standard transfer learning practices in deep learning [23].

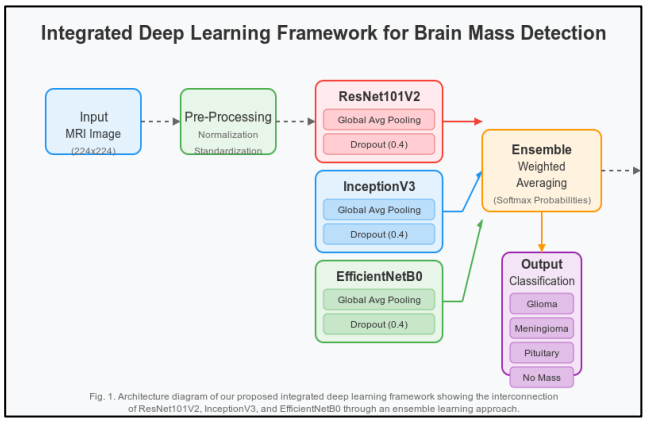
C. Individual Model Construction

Each model in the ensemble follows a consistent architectural pattern while preserving its unique feature extraction characteristics. The construction pipeline includes: (1) loading pre-trained weights from ImageNet; (2) freezing the convolutional base to preserve learned features; (3) adding global average pooling for dimensionality reduction; (4) incorporating dropout regularization (rate = 0.4) to prevent overfitting; and (5) appending a dense output layer with softmax activation for four-class classification.

The specific configurations for each model are as follows: ResNet101V2 utilises ImageNet pre-trained weights, global average pooling, 40% dropout, and softmax-activated dense output. InceptionV3 and EfficientNetB0 share identical configurations and specifications.

D. Ensemble Integration Methodology

Rather than relying on a single architecture, the proposed framework combines predictions from all three base models through an averaging ensemble strategy. Each base model generates class probability distributions independently, which are subsequently aggregated to produce the final classification decision. This approach reduces prediction variance and enhances generalization capability compared to individual models.



[Fig.1: Schematic Representation of the Proposed Ensemble Deep Learning Framework (Authors' Own Design)]

Mathematically, the ensemble prediction process can be formalised as follows: Let X represent an input MRI image, and let p1(X), p2(X), and p3(X) denote the softmax probability distributions produced by ResNet101V2, InceptionV3, and EfficientNetB0, respectively. The ensemble prediction $P_{\text{ensemble}}(X)$ is computed as:

$$P_{ensemble}(x) = P_1(x) + P_2(x) + P_3(x) \quad \ldots \quad (2)$$

The final predicted class corresponds to the category with maximum probability in $P_{\text{ensemble}}(X)$. This averaging approach follows ensemble learning principles established in machine learning literature [26].

E. Training Configuration and Implementation

The ensemble model was implemented using the TensorFlow and Keras frameworks with the following hyperparameters: an Adam optimiser with learning rate α = 1 × 10−4 and a categorical cross-entropy loss.

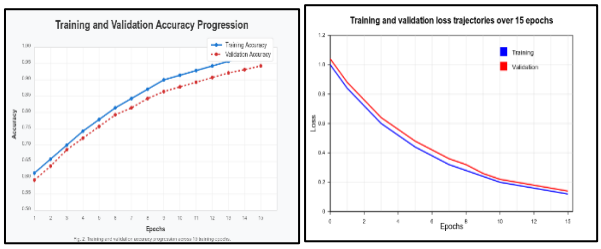
Cross-entropy loss function, batch size of 32 samples, and training duration of 15 epochs. Additionally, early stopping with patience of 5 epochs was implemented based on validation loss monitoring, and model checkpointing was configured to save the best-performing weights based on validation accuracy.

All experiments were conducted on an NVIDIA GeForce RTX 3080 GPU with 10GB of memory. Callback mechanisms for early stopping and model checkpointing were employed to prevent overfitting and preserve optimal model configurations during training.

V. EXPERIMENTAL RESULTS AND PERFORMANCE ANALYSIS

A. Training Performance Progression

Figure 2 presents the evolution of training and validation metrics across 15 training epochs. The model demonstrates consistent improvement in both accuracy and loss metrics, achieving training accuracy of 94.7% and validation accuracy of 92.0%. The convergence patterns indicate effective learning without significant overfitting issues.



[Fig.2: Model Training Performance Showing Accuracy and Loss Metrics Throughout Training (Authors' Experimental Results)]

B. Overall Performance Metrics

The integrated ensemble framework was evaluated using standard classification metrics on independent test data. Table II summarises the overall performance achieved by the proposed system.

Table II. Comprehensive Performance Evaluation Metrics (Authors' Experimental Results)

Performance Metric	Achieved Value
Classification Accuracy	82.0%
Precision	84.0%
Recall (Sensitivity)	82.0%
F1-Score	80.0%

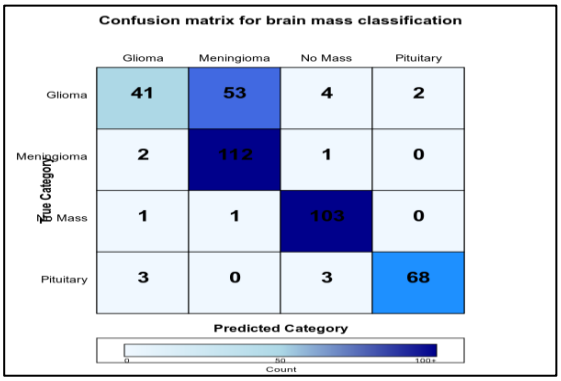
C. Class-Specific Performance Analysis

Table III provides detailed class-wise performance metrics, offering insights into the model's effectiveness for different tumour types and standard tissue classification.

Table III. Detailed Class-Specific Performance Metrics (Authors' Experimental Results)

Tumor Category	Precision	Recall	F1-Score
Glioma	87%	41%	56%
Meningioma	78%	97%	86%
Pituitary	97%	92%	94%
Normal Tissue	74%	98%	84%

Analysis of the confusion matrix (Figure 3) reveals several noteworthy patterns. The model achieves exceptional performance for pituitary adenomas, with 97% precision and 92% recall, indicating high accuracy in identifying this tumour type. For gliomas, the model exhibits relatively low recall (41%), suggesting challenges in detecting all glioma cases, while maintaining high precision (87%) when glioma predictions are made. Both normal tissue and meningiomas demonstrate very high recall rates (98% and 97%, respectively) but moderate precision, indicating some false positive classifications.



[Fig.3: Confusion Matrix Showing Classification Performance Across all Four Tumour Categories (Authors' Experimental Results)]

These performance patterns highlight specific areas where the framework excels and identify opportunities for future improvement, particularly in enhancing the sensitivity of glioma detection.

VI. DISCUSSION AND CLINICAL IMPLICATIONS

The experimental results demonstrate that the proposed ensemble approach achieves promising performance in automated brain tumour classification. The overall accuracy of 82.0% represents substantial progress for this challenging four-class classification task, particularly given the inherent complexity of differentiating brain tumour types in medical imaging.

Class-specific performance analysis reveals essential insights into the framework's diagnostic capabilities. The exceptional performance in pituitary adenoma detection, with both high precision and recall, suggests that pituitary tumours exhibit distinctive imaging characteristics that facilitate automated identification compared with other tumour types.

The lower recall observed for glioma classification indicates that these tumours exhibit more heterogeneous imaging patterns that occasionally lead to misclassification. This reflects the inherent complexity of gliomas on MRI scans, which can vary significantly by tumour grade, location, and infiltration patterns. This challenge aligns with previously reported difficulties in automated glioma classification.

The high recall but moderate precision for normal tissue and meningiomas suggests occasional misclassification of other tumour types into these categories. This indicates opportunities to refine feature extraction and discrimination for these classes, potentially through enhanced techniques for discriminative feature learning.

From a clinical perspective, the high precision for glioma classification (87%) is particularly valuable, as false positive glioma diagnoses could lead to unnecessary patient anxiety and potentially inappropriate treatment decisions. Conversely, the high recall rates for the meningioma and standard tissue categories ensure that most cases in these categories are correctly identified, reducing the risk of missed diagnoses.

The integration of multiple architectures has proven beneficial in capturing diverse

tumour characteristics that individual models might overlook. ResNet101V2's depth enables complex feature learning, InceptionV3's multi-scale processing captures tumours of varying sizes, and EfficientNetB0's efficiency makes the system practical for clinical deployment.

VII. LIMITATIONS AND FUTURE DIRECTIONS

While the proposed ensemble approach demonstrates promising results, several limitations should be acknowledged. The relatively lower recall for glioma classification indicates room for improvement in detecting all instances of this tumour type. Additionally, while the dataset is substantial, it could benefit from increased diversity in tumour presentations and imaging protocols.

Future research should focus on several directions. First, incorporating attention mechanisms could enhance the model's ability to concentrate on tumour-specific regions. Second, exploring additional architectural combinations might further improve ensemble diversity. Third, implementing advanced data augmentation techniques could improve generalisation capabilities. Fourth, investigating three-dimensional convolutional approaches for volumetric tumour analysis could provide valuable spatial context. Fifth, developing explainable AI components would enhance clinical interpretability and trust.

VIII. CONCLUSION

This research presents a novel ensemble deep learning framework that effectively integrates ResNet-101V2, InceptionV3, and EfficientNetB0 for automated brain tumour classification. The proposed approach demonstrates promising diagnostic performance across four distinct tumour categories, achieving 82% overall accuracy, with powerful results for identifying pituitary adenomas.

The ensemble integration strategy effectively leverages complementary feature-extraction capabilities, improving diagnostic reliability compared to individual models. While challenges remain in glioma classification, the overall framework shows significant potential for clinical application. The successful implementation of this integrated framework suggests substantial promise for similar ensemble approaches in other complex medical image analysis applications. Future developments addressing current limitations could further enhance classification accuracy across all tumour categories, potentially advancing automated medical diagnosis and supporting clinical decision-making processes.

These findings contribute to the growing body of evidence supporting ensemble methodologies in medical AI applications, demonstrating that strategic architectural combinations can yield superior diagnostic performance compared to single-model approaches. This work provides a foundation for future investigations into multi-architecture fusion techniques for medical imaging applications.

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DECLARATION STATEMENT

Historical References Justification: This manuscript includes references older than 10 years that represent foundational work in brain tumour segmentation benchmarks (BraTS challenge) and deep learning in medical imaging. These seminal works established evaluation protocols and methodologies that remain relevant and are still cited in contemporary research.

As the article's author, I must verify the accuracy of the following information after aggregating input from all authors.

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Chinthamaani Ajay is pursuing a Bachelor of Technology in Computer Science and Engineering at KL University, Guntur, India. His academic and research interests primarily focus on deep learning and its applications in medical image analysis, particularly in developing automated diagnostic systems for pneumonia detection and brain tumour classification. He has gained practical experience in designing and training convolutional neural networks, performing advanced image preprocessing, and analysing clinical datasets using machine learning techniques. He has actively contributed to research projects involving model evaluation, performance analysis, and result interpretation. His work aims to design reliable, efficient, and accessible AI-based diagnostic solutions that can support clinicians and improve healthcare delivery in resource-constrained environments.

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