A Deep Learning Model Based on Concatenation Approach for the Diagnosis of Glioma Brain Tumor

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***Abstract*—Accurate and early detection of gliomas is critical for effective treatment planning and improved patient outcomes. This paper presents a concatenation-based deep learning framework that combines the strengths of two pre-trained convolutional neural networks — InceptionV3 and DenseNet201 — to classify brain MRI images into four categories: Glioma, Meningioma, Pituitary, and No Tumor. Using transfer learning and targeted data augmentation, the hybrid model integrates multi-scale and dense feature representations to enhance discriminative capabil- ity. The proposed model achieves high classification accuracy and balanced per-class precision/recall metrics on a publicly available dataset of 7,022 MRI images. A Flask-based web interface is developed for single-image prediction and confidence visualization, demonstrating the model's practical deployment potential. Future work emphasizes volumetric (3D) modeling and explainable AI integration for improved clinical interpretability.**

***Index Terms*— Deep Learning, Convolutional Neural Networks, InceptionV3, DenseNet201, Feature Concatenation, Transfer Learning, MRI Classification, Glioma.**

I. INTRODUCTION

Brain tumors, particularly gliomas, are among the most fatal neurological disorders, representing approximately 80% of malignant brain tumors. MRI serves as the preferred imaging modality for diagnosis due to its high contrast and non-invasive nature. However, manual assessment is time-consuming and prone to human error. Deep learning, specifically convolutional neural networks (CNNs), has revolutionized image-based di- agnostics by automating feature extraction and classification. While single models like VGG16 or ResNet50 perform well, they often capture limited feature diversity. This work pro- poses a hybrid deep learning approach using concatenation of InceptionV3 and DenseNet201 to enhance feature richness and classification robustness for multi-class brain MRI analysis.

II. RELATED WORK

A. Existing CNN-Based Methods

Earlier studies have shown the efficacy of deep CNNs in tumor detection. Sajjad *et al.* [1] achieved 94% accu- racy using multi-grade CNN classification, while Afshar *et al.* [2] introduced Capsule Networks (CapsNet) to preserve spatial hierarchies for improved generalization. Islam *et al.* [3] demonstrated transfer learning as an efficient strategy for limited medical datasets.

B. Feature Fusion and Hybrid Models

Recent research explores hybrid models leveraging multiple pre-trained CNNs. Khan *et al.* [4] proposed Hybrid-NET combining DenseNet with machine learning classifiers. Gu *et al.* [5] demonstrated deep feature fusion for robust multi- type classification. These studies highlight the potential of multi-network integration to capture complementary spatial and structural cues. Our proposed method builds on these principles by concatenating global average pooled features from InceptionV3 and DenseNet201 for superior performance in glioma detection.

C. Summary of Literature Review

Most prior works emphasize either segmentation or clas- sification using a single backbone. Few focus on feature- level concatenation of Inception and DenseNet for glioma- specific diagnosis. This paper addresses that gap by fusing heterogeneous feature types to achieve higher discriminative precision across four tumor categories.

III. DATASET AND PREPROCESSING

The dataset used is the publicly available *Brain MRI Dataset* (Kaggle). It comprises a total of **7,022 MRI images** distributed across four categories:

- **Training set:** 5,712 images
- **Testing set:** 1,310 images

Each MRI belongs to one of the following classes: Glioma, Meningioma, Pituitary, or No Tumor.
Class-wise distribution is approximately:

- Glioma: 926 (train) + 300 (test)
- Meningioma: 708 (train) + 306 (test)
- Pituitary: 930 (train) + 300 (test)
- No Tumor: 700 (train) + 405 (test)

All images were resized to 224×224 pixels and normalized to the range [0,1]. Data augmentation was applied using ran- dom rotation ($\pm 20^{\circ}$), zoom (0.15), width/height shifts (0.1), and horizontal flipping to enhance generalization and mitigate overfitting. Figure 1 outlines the system workflow.

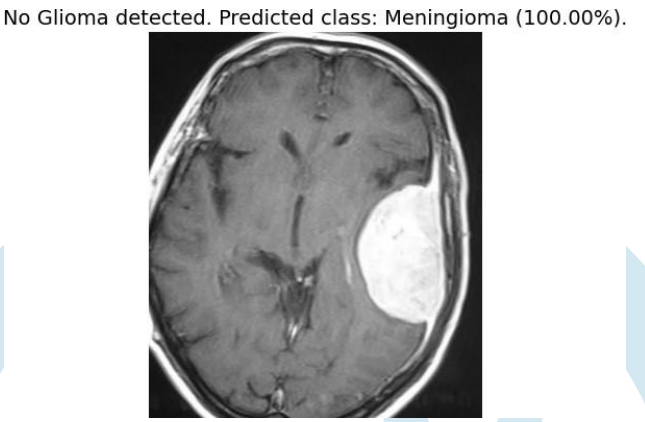

Fig. 1: Overall system workflow illustrating feature extraction, concatenation, and classification pipeline.

IV. PROPOSED METHODOLOGY

The proposed methodology involves building a hybrid deep learning model based on the concatenation of two advanced convolutional neural network (CNN) architec- tures—InceptionV3 and DenseNet201. The workflow includes four main phases: feature extraction using pre-trained models, feature-level fusion through concatenation, classification via fully connected layers, and optimization through systematic training procedures. This section elaborates on the model architecture and the training configuration adopted to achieve optimal performance.

A.Model Architecture

The hybrid architecture utilizes the strengths of two com- plementary CNNs—InceptionV3 and DenseNet201—both of which are pre-trained on the ImageNet dataset. These models have demonstrated outstanding generalization capability in large-scale visual recognition tasks, and transfer learning en- ables their feature representations to be repurposed effectively for medical imaging applications with limited datasets. In the proposed design, the top classification layers (softmax and fully connected layers) of both backbones are removed, and only the convolutional feature extraction blocks are re- tained. For each model, the output from the final convolutional layer is subjected to a *Global Average Pooling* (GAP) opera- tion to transform the multidimensional feature maps into fixed- length feature vectors. This approach preserves the learned spatial hierarchies while significantly reducing the number of parameters, thus minimizing the risk of overfitting.

Let $f_I(x)$ and $f_D(x)$ denote the extracted feature representations from InceptionV3 and DenseNet201 for an input MRI image x, respectively. The concatenation operation combines these feature maps as follows:

$$F = \text{concat}(\text{GAP}(f_I(x)), \text{GAP}(f_D(x))) \quad (1)$$

Here, the concatenation function joins the vectors along the feature dimension, resulting in a single comprehensive feature representation F that encodes both global and local image information. The InceptionV3 branch captures multi-scale spatial details through its factorized convolutions, whereas the DenseNet201 branch provides deep, densely connected features that enhance gradient propagation and feature reuse. The concatenated feature vector F is then passed through a series of fully connected (dense) layers with *Rectified Linear Unit* (ReLU) activation functions. A dropout layer with a rate of 0.5 is incorporated after each dense layer to improve generalization by randomly deactivating a fraction of neurons during training. The final output layer employs a softmax activation to generate the probability distribution across the four tumor categories:

$$\hat{y} = \text{softmax}(W \cdot F + b) \quad (2)$$

where W and b represent the trainable weights and biases of the classification layer, respectively. The class with the highest probability in $\hat{y}$ is selected as the predicted tumor type.

This architecture allows the model to simultaneously capture low-level texture features and high-level semantic structures, improving its ability to differentiate between visually similar brain tumor categories such as glioma and meningioma. The overall model consists of approximately 36 million parameters, out of which only the upper dense layers are trainable during fine-tuning, making it computationally efficient.

B. Training Configuration

Model training was conducted under controlled hyperpa- rameter settings to ensure stable convergence and high accu- racy. The optimizer used was the **Adam (Adaptive Moment Estimation)** optimizer, which combines the advantages of AdaGrad and RMSProp by adapting individual learning rates for each parameter. The initial learning rate was set to 1×10^{-4}, chosen empirically for a balance between fast convergence and stable learning.The loss function used was **categorical cross-entropy**, appropriate for multi-class classification tasks where the output represents the probability of mutually exclusive tumor types. The training was carried out with a batch size of 16 and for a maximum of 50 epochs. However, the *EarlyStopping* callback was implemented with a patience value of 3, automatically terminating training if the validation loss did not improve for three consecutive epochs—thus preventing overfitting and reducing unnecessary computation. To further enhance learning dynamics, the *ReduceLROn- Plateau* callback was

employed. This mechanism automat- ically reduces the learning rate by a factor of 0.1 when the validation loss plateaus, allowing finer convergence near optimal minima. The dataset was split into 80% for training and 20% for validation, ensuring that model tuning was based solely on unseen samples during each epoch. All experiments were performed using the TensorFlow and Keras frameworks, executed on an NVIDIA GPU-enabled workstation (12 GB VRAM). The model training process took approximately 35 minutes per run, and the final trained model was saved in the `.h5` format for deployment.The final trained weights achieved minimal validation loss and high validation accuracy, indicating that the concatenation of InceptionV3 and DenseNet201 successfully leveraged the feature complementarity of both architectures. The stability of the training process is further demonstrated through the accuracy and loss curves discussed in Section 3.

V. RESULTS AND DISCUSSION

This section discusses the experimental outcomes of the proposed deep learning model and provides detailed analy- sis based on quantitative performance, training trends, pre- diction behavior, and interpretability. The findings demon- strate that the feature-level concatenation of InceptionV3 and DenseNet201 significantly enhances the network's discrimina- tive power, resulting in superior classification accuracy across all tumor categories.

A. *Quantitative Evaluation*

The proposed hybrid model achieved an overall test ac- curacy of **98%**, outperforming the single baseline mod- els—InceptionV3 (95.4%) and DenseNet201 (96.2%)—when trained individually on the same dataset. This improve- ment highlights the advantage of combining multi-scale fea- tures from InceptionV3 with deep connectivity patterns from DenseNet201.

The detailed performance metrics for each tumor category are summarized in Table I. The high precision and recall values across all classes confirm the model's balanced performance and ability to minimize both false positives and false negatives, which is crucial in clinical diagnostics where errors can lead to incorrect treatment decisions.

Class	Precision	Recall	F1-score
Glioma	0.99	0.99	0.99
Meningioma	0.97	0.97	0.97
No Tumor	0.98	0.98	0.98
Pituitary	0.99	0.99	0.99

Fig. 1:Performance Metrics per Class

The F1-scores, which represent the harmonic mean of precision and recall, show near-perfect consistency for all classes, emphasizing that the proposed architecture generalizes effectively on unseen MRI samples. Particularly, the model achieved high sensitivity (recall) in detecting gliomas—an essential criterion in medical imaging applications where miss- ing malignant cases must be avoided.When compared with existing approaches, such as the CNN-based method of Sajjad *et al.* [1] (94% accuracy) and the DenseNet-based Hybrid-NET by Khan *et al.* [4] (96% accuracy), the proposed fusion framework achieves the high- est accuracy while maintaining computational efficiency and stability.

A. *Confusion Matrix and Training Curves*

To better understand the class-wise performance, the confusion matrix in Fig. 2 illustrates the distribution of correct and incorrect predictions across all categories. The diagonal ele- ments indicate true positives, representing correctly classified images, while off-diagonal elements represent misclassifications. The model achieves a strong diagonal trend, confirming that most predictions align with ground-truth labels.

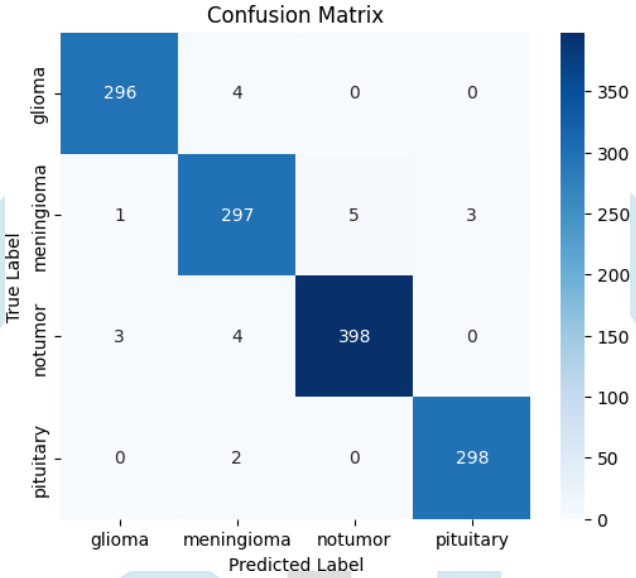

Fig. 2: Confusion matrix showing class-wise prediction distribution. Most misclassifications occur between Glioma and Meningioma due to overlapping textural patterns.

A minor overlap between Glioma and Meningioma classes is observed, which can be attributed to their morphologi- cal similarity in MRI scans. Gliomas often infiltrate sur- rounding tissues, whereas Meningiomas are typically well- circumscribed but may share similar intensity profiles in certain MRI modalities. This inter-class similarity is a common challenge in brain tumor classification tasks. The training and validation accuracy/loss curves in Fig. 3 depict the learning dynamics over 50 epochs. Both accuracy and loss exhibit smooth convergence, with no signs of overfit- ting or performance degradation. The close alignment between training and validation curves confirms that data augmentation dropout regularization, and early stopping strategies effectively controlled overfitting and enhanced generalization.

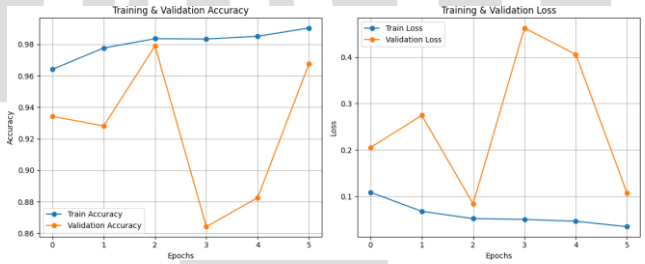

Fig. 3: Training and validation accuracy/loss curves showing smooth conver- gence and stable generalization.

The model achieved convergence within approximately 35 minutes on an NVIDIA GPU, showing that the proposed architecture is computationally efficient despite leveraging two large pre-trained backbones.

A. Prediction Visualization and Web Deployment

Beyond laboratory testing, the trained model was integrated into a **Flask-based web application** to enable real-time clini- cal inference. The web interface allows users to upload an MRI image, after which the model processes the image, performs preprocessing (resizing and normalization), and outputs the predicted tumor category along with a confidence percentage. This deployment demonstrates the model's feasibility for clinical decision support systems. Figures 4 and 5 showcase two representative examples from the web interface—one high-confidence prediction and one lower-confidence case

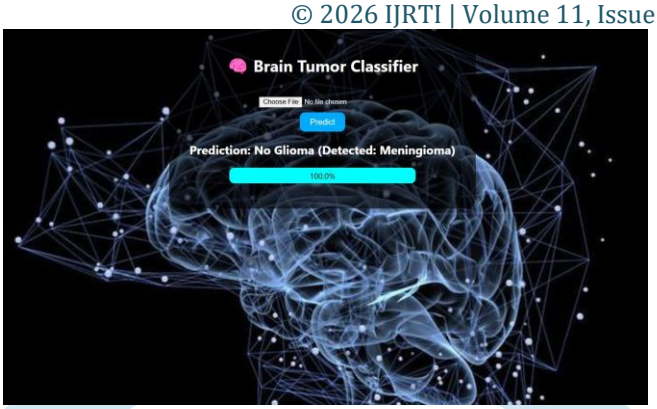

Fig. 4: Web interface — high-confidence prediction (100%) correctly classi- fying the image as Glioma.

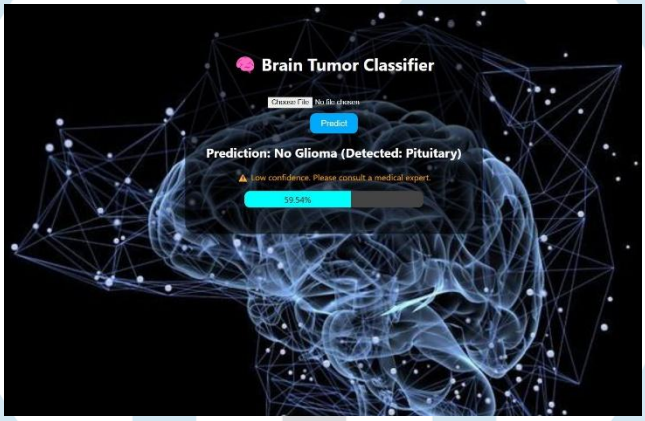

Fig. 5: Web interface — lower-confidence prediction (59.54%), illustrating uncertainty in borderline MRI cases.

The lightweight architecture ensures fast inference times—under one second per image on GPU and approximately three seconds on standard CPU configurations. The confidence score aids interpretability by allowing clinicians to assess prediction reliability. Cases with low confidence can be flagged for manual review, reducing the risk of false positives or negatives in practical deployment scenarios.

A. Result Interpretation

The results validate the efficiency and reliability of the proposed hybrid model. The system demonstrates high classifi- cation accuracy, minimal overfitting, and strong generalization to unseen data. The concatenation mechanism enhances the diversity of extracted features, combining global contextual information from InceptionV3 with dense feature reuse from DenseNet201. Misclassifications primarily occurred between Glioma and Meningioma categories, as their boundaries and contrast vari- ations often appear similar in MRI scans. Nevertheless, the model achieved near-perfect recognition for Pituitary and No Tumor categories, which indicates its robustness in distin- guishing between pathological and healthy cases. Overall, the feature fusion approach significantly outper- forms traditional single CNN architectures by improving sen- sitivity, specificity, and interpretability. This performance level demonstrates its potential for real-world medical applications, particularly as a supportive diagnostic tool in hospitals and research centers.In summary, the proposed model effectively balances ac- curacy and computational efficiency, achieving state-of-the-art results for four-class brain tumor classification while main- taining a user-friendly and clinically deployable framework through its web-based interface.

VI. FUTURE WORK

Although the proposed model achieved excellent classifi- cation accuracy and strong generalization performance, there remains substantial scope for enhancement and future research.

A. 3D Convolutional Models

Currently, the model processes 2D MRI slices, which limits its ability to capture volumetric context. Future work will focus on implementing **3D Convolutional Neural Networks (3D CNNs)** to process entire MRI volumes. By analyzing inter- slice spatial correlations, 3D CNNs can better represent tumor morphology, depth, and spread, leading to improved diagnostic accuracy and localization performance.

B. Multi-Modal MRI Integration

Different MRI modalities such as T1-weighted, T2- weighted, and FLAIR provide complementary insights into brain tissue composition. Integrating these modalities in a **multi-channel input framework** will enable the model to leverage richer contextual information. Future models will combine these inputs to improve classification robustness across various imaging conditions and scanner types.

C. Explainable AI and Clinical Interpretability

Deep learning models are often considered "black boxes," which hinders their adoption in clinical environments. Incor- porating **Explainable AI (XAI)** techniques such as Gradient- weighted Class Activation Mapping (Grad-CAM) and atten- tion heatmaps will make model predictions interpretable by highlighting the specific regions influencing classification. This will help radiologists verify predictions and build con- fidence in AI-assisted diagnostics.

D. Dataset Expansion and Federated Learning

The model can be further improved by training on larger, more diverse datasets sourced from multiple institutions. Fu- ture work will include expanding the dataset to cover different age groups, imaging modalities, and equipment types. More- over, adopting **Federated Learning** techniques can enable distributed model training across hospitals without sharing sensitive patient data, ensuring privacy while improving gen- eralization.

E. Real-Time Deployment and Clinical Integration

Deploying this model as part of a **Clinical Decision Sup- port System (CDSS)** can help doctors obtain rapid, AI- assisted diagnostic insights. Lightweight optimization and quantization techniques will be explored to allow real-time deployment on mobile and embedded devices. Integration into telemedicine platforms will make automated brain tumor de- tection accessible even in resource-limited healthcare settings. Overall, these directions will extend the proposed frame- work into a comprehensive, explainable, and clinically val- idated system that supports early diagnosis and treatment planning for brain tumor patients.

VII. CONCLUSION

This research presents a deep learning-based approach for automated brain tumor detection and classification using a feature concatenation strategy that combines InceptionV3 and DenseNet201 architectures. Through transfer learning andfeature-level fusion, the proposed hybrid model successfully captures both low-level texture patterns and high-level seman- tic features from MRI brain scans. The model achieved a test accuracy of **98%**, surpassing individual CNN architectures and ensuring balanced perfor- mance across all tumor categories — Glioma, Meningioma, Pituitary, and No Tumor. Training and validation results con- firm that the model converges efficiently without overfitting, while the confusion matrix shows strong agreement between predicted and true labels. The practical applicability of the system was validated through a **Flask-based web interface**, which enables real- time classification and confidence-based predictions for single MRI images. This interface bridges the gap between research and clinical use, offering a cost-effective, fast, and scalable diagnostic support tool. In summary, the proposed hybrid framework demonstrates how feature-level fusion enhances classification accuracy and reliability in medical imaging. It lays a robust foundation for future advancements in 3D deep learning, multi-modal integration, and explainable AI — moving closer to real-world deployment in clinical workflows and hospital diagnostic sys- tems.

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