RESEARCH PAPER

Brain tumor detection and Classification using Convolutional Neural Network (CNN)

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Abstract
Classifying brain tumours using MRI images is crucial for developing computer-aided diagnosis methods and selecting therapies. This study developed a convolutional neural network-based algorithm to classify multi-class brain MRI images into glioma, meningioma, pituitary tumour, and no-tumor classes using an equal number of 7,200 MRI images from the balanced Kaggle dataset. The dataset consisted of 4,480 training, 1,120 validation, and 1,600 testing images. Three neural network architectures have been used: Baseline CNN, EfficientNetB0, and VGG16 dual-pooling. Image pre-processing steps include converting to RGB, CLAHE-based contrast enhancement, resizing, normalization, and data augmentation during training phase only. Model performance was evaluated using accuracy, precision, recall, macro F1-score, AUC, confusion matrix analysis, and Grad-CAM explainability. VGG16 Dual-Pooling achieved the highest performance, with 90.50% testing accuracy, 90.88% precision, 90.31% recall, 90.20% macro F1-score, and 97.28% AUC. Grad-CAM visualization indicated that the model focused on diagnostically relevant intracranial regions. Beyond diagnostic classification, the model output may support preliminary pharmaceutics-oriented tumor stratification, including glioma chemotherapy planning, blood-brain barrier and blood-brain tumor barrier considerations, targeted therapy, nanocarrier delivery, endocrine pharmacotherapy, and avoidance of unnecessary tumor-directed intervention.

Keywords: Brain tumor classification; Convolutional neural network; VGG16 Dual-Pooling; EfficientNetB0; Magnetic resonance imaging; Grad-CAM; targeted drug delivery

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1. Introduction

Tumor formation in the brain is a neurological disease in which the diagnosis and treatment of such formations depend upon factors like the type of tumor, its anatomy, growth, aggressiveness, and stage of progression. Identification at an early stage is critical to develop strategies for treatment and prognosis of patients. Magnetic resonance imaging can be considered to be among the most important imaging methods that assist in assessing brain tumors. This imaging method helps provide an understanding of soft tissue visualization with greater structure analysis. However, analyzing MRI images requires substantial time and expertise on the part of radiologists. The complexity of diagnosing brain tumors is also amplified when the images present visual similarities between different types of tumors or if the amount of MRI images for assessment is huge. This has led to a shift towards automated detection of brain tumors through CNNs. CNN is particularly relevant to medical imaging because it can automatically learn hierarchical visual features from the images themselves, which include edges, texture, contour, shape, intensity changes, and more complex spatial information. Prior studies have demonstrated the feasibility of deep neural networks for brain tumour image classification, indicating that machine learning methods with automatic feature extraction have significant diagnostic potential for differentiating various tumour types from MRI data.[1] The introduction of transfer learning has been particularly beneficial for this type of research because it allows deep neural networks to be fine-tuned on MRI data. This method is especially applicable to medical imaging, where it might be challenging to gather sufficiently big annotated image datasets. For example, utilising MRI scans, Swati et al. demonstrated the value of transfer learning and fine-tuning for better brain tumour categorisation.[2]

However, there still exist various challenges in terms of brain tumor detection and classification. There are usually variations in image resolutions, contrasts, orientations, acquisition methods, and anatomical appearance within MRI scans. Moreover, gliomas, meningiomas, and pituitary tumors might present radiologically similar features, complicating their multiclass classification task even for automated algorithms. Imbalance in training data, lack of labeled examples, and differences in patient anatomy might contribute to poor generalization capability of the models. In addressing this challenge, Sajjad et al. applied extensive data augmentation to facilitate classification of multi-grade tumors in order to demonstrate that synthetic generation of data could be an effective approach to boost CNN performance.[3] Another promising avenue that may be explored includes transfer

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learning based classification schemes that utilize deep features and optimal classification approaches.[4] The current research is situated within automated medical image diagnosis and pharmaceutics-oriented therapeutic decision support. While the study focuses on CNN-based MRI classification of glioma, meningioma, pituitary tumor, and no-tumor cases, it also aims to provide an explainable imaging layer that may support early therapeutic stratification. CNN-based brain tumor classification has already shown relevance for identifying discriminative MRI features and supporting automated diagnostic workflows.[5] Because glioma, meningioma, and pituitary tumors follow different treatment pathways, accurate image-based classification may help determine whether further evaluation is needed for targeted therapy, localized delivery, nanocarrier-mediated treatment, endocrine pharmacotherapy, or treatment-response monitoring. Glioma is particularly important from a drug-delivery perspective because its management is affected by blood–brain barrier constraints, blood–brain tumor barrier disruption, infiltrative growth, and heterogeneous drug penetration. Various recent research papers have shown that CNN models are suitable for the current task. Irmak demonstrated that deep learning models can be utilised to classify brain tumour images if appropriate data pre-processing, network construction, and optimisation are carried out. He developed a fully optimised deep CNN model for MRI image-based multi-class brain tumour classification.[6] Naseer et al. examined the augmented CNN models for automatic diagnosis of brain tumors with the help of computers and showed that the augmented CNN models perform better than non-augmented CNN models in MRI data analysis.[7] Additionally, Khan et al. verified that CNN models can be applied to MRI-based brain tumor classification.[8] The importance of the current research study is attributed to the possible role played by the research in making faster and more efficient brain tumor screening possible. A valid neural network classifier would prove useful in making predictions that will minimize the burden placed on radiologists, while at the same time ensuring that no errors are made in interpreting the repeated task of image reviews. From the point of view of pharmaceutics and drug delivery, automated classification can further play a role in categorizing patients prior to selecting therapies. A classification towards gliomas would imply that the patient requires evaluation on the issue of blood-brain barrier crossing abilities and whether chemotherapy should be attempted.

This research does not intend to substitute any clinical assessment or pathological validation, nor to develop a drug carrier system through experimentation. Rather, it proposes a classification approach based on the use of CNNs with MRI and provides an interpretation of its results as a component for decision support in facilitating further investigation into the connection between imaging data and pharmaceutical considerations such as the delivery method, the molecular markers of the tumor, and personalized treatment planning. Such consideration is significant for pharmaceutics because, in addition to developing formulations, drug targeting and treatment have become increasingly reliant on patient and tumor stratification.

The objectives of this study are:

- To develop and compare CNN-based deep learning frameworks, including Baseline CNN, EfficientNetB0, and VGG16 Dual-Pooling, for classifying brain MRI images into glioma, meningioma, pituitary tumor, and no-tumor categories.
- To evaluate the diagnostic performance and interpretability of the proposed models using accuracy, precision, recall, F1-score, AUC, confusion matrix analysis, statistical validation, and Grad-CAM explainability.
- To map MRI-based tumor classification outputs to pharmaceutics-relevant therapeutic pathways, including blood–brain barrier-related drug-delivery challenges, targeted therapy considerations, endocrine pharmacotherapy, localized treatment planning, and avoidance of unnecessary intervention in no-tumor cases.

2. Literature Review

The latest research in deep learning has provided enhancements in brain tumor detection and classification through MRIs. The use of convolutional neural networks has been prevalent because they help identify hierarchical patterns in images that involve texture, shape, intensity, and tumor characteristics without explicitly defined features. Current literature demonstrates advancements made in CNN models from single classifiers to hybrid models, multiscale models, transfer learning models, explainable models, and segmentation-classification models. These advancements are essential because a proper classification is needed for a clinical diagnosis.

A hybrid CNN architecture for detecting tumors in brain MR images was developed by Çinar and Yildirim. The results of their experiment prove that using hybrid CNNs may contribute to improving the model's effectiveness in distinguishing between tumor-influenced areas and normal brain structures, particularly, in case of complicated morphological characteristics of the tumor.[9] As an example of further research in this area, Díaz-Pernas et al. created a multiscale CNN model for brain tumor detection and segmentation. This work is important since the problem of diagnosing tumors includes both recognizing the type of the disease and detecting the area affected by it, which differs in terms of its shape, position, and other characteristics.[10]

Transfer learning has proved extremely crucial in brain tumor classification due to the limited nature, heterogeneity, and poor annotability of the medical MRI datasets used for the purpose. Deepak and Ameer indicated the usefulness of pre-trained CNN features in helping accomplish effective tumor classification without having to start from scratch with model training.[11] Anaraki et al. enhanced MRI based brain tumor classification through combining genetic algorithms with CNNs for optimizing the models.[12] Talo et al. successfully applied deep transfer learning to

develop automatic classification of brain abnormalities with the help of MR images.[13] The results of these studies confirm the applicability of pre-trained networks in image recognition tasks that involve limited datasets.
CNN has been validated as an efficient backbone network for brain tumour classification using MRIs in a number of further studies. For example, Gómez-Guzmán et al. demonstrated that convolutional networks were still useful in classifying tumour types by using CNN for brain tumour classification using MRI.[14] Researchers have investigated hybrid designs as a solution to challenging categorisation tasks in more recent studies. For instance, Babu Vimala et al. developed hybrid deep learning models for brain tumour detection and classification, demonstrating that employing hybrid deep neural networks enhanced the diagnostic task in comparison to basic models.[15] Another hybrid deep CNN, named LuNetClassifier, was designed by Balamurugan and Gnanamanoharan for the tasks of brain tumor segmentation and classification.[16]
Comparing different models, computational efficiency, and interpretability have become key challenges for this research topic. Khaliki and Başarslan compared transfer learning approaches with the application of a three-layer CNN for brain tumors detection, pointing out that there are pros and cons when it comes to choosing simple architecture vs. complicated pre-trained models.[17] Even though the transfer learning model could show better results, simpler models like CNN can be easier to implement. Haque et al. presented the concept of NeuroNet19, which is an interpretable deep neural network model that uses MRI data for classifying brain tumors. Interpretability is critical in the medical domain since doctors should comprehend the reason behind automatic decisions.[18]
Recent studies have additionally focused on multi-class classification and enhancing transfer learning models. For example, Srinivasan et al. introduced a mixed deep CNN architecture that can effectively classify MRI images of brain tumors into multiple classes, suggesting the importance of such a multi-class classifier in terms of clinical utility rather than a simple binary model to detect brain tumors.[19] Similarly, Mathivanan et al. confirmed the significance of pre-trained models in automatic MRI categorisation and used deep learning in conjunction with transfer learning for efficient brain tumour identification.[20] However, Dorfner et al. examined the usage of deep learning in brain tumour MRI at the review level and came to the conclusion that deep CNNs are widely employed in a variety of applications, such as grading, segmentation, and classification.[21] Additionally, Disci et al. demonstrated how well pre-trained deep CNNs classified brain tumours from MR images.[22]
In terms of pharmacological aspects of drug delivery, brain tumor characterization has more significance than just image-based analysis. The type, location, level of aggression, responsiveness to treatment, and ease of drug delivery all play a significant role in the treatment decision. The blood-brain barrier, blood-brain tumour barrier, tumour heterogeneity, and limited drug tissue penetration make it challenging to treat brain tumours effectively.[23],[24] It is particularly difficult in glioma-related cases since chemotherapy and targeted, localized, and nanocarrier-mediated drug delivery methods might be used in the process. In the case of glioblastomas, nanocarrier-based combination of two different drugs can be employed because conventional drug delivery usually does not guarantee efficient accumulation at the site of the tumor.[25]
The use of CNN classification based on MRI data may act as an upstream support layer for decision-making in pharmaceutics. For gliomas, such prediction may be helpful to determine further exploration for penetration by drug through blood-brain barrier, chemotherapy suitability, targeting, or monitoring treatment response. Prediction of meningioma cases could contribute to surgical interventions, radiotherapy options, recurrence tracking, or adjuvants; similarly, predictions of pituitary tumors could contribute to pharmacological treatment of endocrine issues or local therapy considerations. No-tumor prediction may prevent unnecessary progression of pharmacological measures or invasive procedures.
As such, the review indicates that classification of brain tumors using CNNs has evolved from basic classifiers to hybrid methods, multiscale methods, transfer learning approaches, and interpretable models. On one hand, CNNs have proven useful for identifying important tumor features from MRIs, whereas transfer learning has been applied when data is sparse. However, challenges remain in the areas of interpretability, data heterogeneity, external validation, glioma meningioma differentiation, and clinical application. Besides diagnosis, correct classification of brain tumors could help in treatment and imaging-assisted therapy, thereby linking MRI AI to pharmaceutics.

3. Methodology

3.1 Research Design

The supervised deep learning framework was employed for automatic detection and classification of brain tumors based on MRI images. The primary aim was to classify between tumor and non-tumor MRI images and classify the former into three different types, i.e., glioma, meningioma, and pituitary tumors. There were three deep learning algorithms that were considered, including Baseline CNN, EfficientNetB0, and VGG16 Dual-Pooling. The latter algorithm was considered as the primary one due to incorporation of two more pooling layers to enhance feature compression capability.

3.2 Dataset Description

Data used for experimentation were collected from an open brain MRI dataset available at Kaggle. The dataset had four classes with an equal distribution of all classes, namely, glioma, meningioma, pituitary tumor, and no tumor.[26] Total number of MRI images in the dataset is 7,200, where each class had 1,800 images. Original dataset is arranged into two folders, Training and Testing, where Training had 5,600 MRI images and Testing had 1,600 MRI images

3.3 Data Integrity Verification and Partitioning

Prior to the process of model training, all MRI images in the dataset were screened for any corruption or unreadability of the images. This dataset was characterized by differences in the dimension of the images, file format, and image mode, whereby some images had been taken in color while others in grayscale. For this reason, data preprocessing was necessary to normalize the inputs before modeling.

Stratified sampling technique was applied in dividing the initial training set into training and validation sets. The final dataset comprised of 4,480 training images, 1,120 validation images, and 1,600 independent testing images. Training images, validation images, and testing images per class were 1120, 280, and 400 respectively. The testing images were completely independent of training and validation images.

3.4 Image Preprocessing

All MRI images were processed using a standardized preprocessing pipeline. First, images were converted into RGB format to ensure a consistent three-channel input structure. To increase diagnostically important regions and improve local contrast, Contrast Limited Adaptive Histogram Equalisation was used. To meet the CNN architectures' input requirements, all photos were scaled to 224 x 224 pixels.

For the Baseline CNN, pixel intensities were normalized to the range [0,1]. EfficientNetB0 used an input intensity range compatible with its ImageNet-pretrained feature extraction pipeline. VGG16 Dual-Pooling used VGG16-specific preprocessing, in which images were processed according to the input requirements of the ImageNet-pretrained VGG16 backbone.

3.5 Data Augmentation

Data augmentation was applied only to the training data to improve generalization and reduce overfitting. The augmentation process included moderate random rotation, translation, zooming, and contrast adjustment. Excessive geometric transformations were avoided to preserve anatomical consistency in MRI scans. Images used for testing or validation were not augmented.

3.6 Baseline CNN Architecture

A Baseline CNN architecture was developed as the reference model. It consisted of sequential convolutional blocks with 32, 64, 128, and 256 filters. To extract spatial MRI characteristics, each block used max-pooling, rectified linear unit activation, convolution, and batch normalisation. To lower feature dimensionality, global average pooling was used before to the final classification step. For classification, a thick layer of 256 neurones and regularisation was employed. Four neurones representing the glioma, meningioma, pituitary tumour, and no-tumor classifications were found in the final softmax layer.

3.7 EfficientNetB0 Transfer Learning Framework

EfficientNetB0 was implemented as a transfer learning model. The ImageNet-pretrained EfficientNetB0 backbone was used without its original classification layer. A task-specific classification head was added, consisting of global average pooling, batch normalization, a dense layer with 256 neurons, dropout regularization, and a four-class softmax output layer. Initially, the pretrained convolutional backbone was frozen while the classification head was trained using the MRI dataset. This allowed the model to reuse pretrained visual representations while adapting the final decision layers to brain MRI classification.

3.8 VGG16 Dual-Pooling Architecture

VGG16 Dual-Pooling was implemented as the main model for brain tumor MRI classification. The ImageNet-pretrained VGG16 backbone was used without its original fully connected classification layers. VGG16 contains sequential convolutional blocks with small 3 × 3 filters, allowing the network to learn progressively complex image features, including edges, textures, tumor boundaries, and higher-level spatial patterns.

After the last convolutional layer of the VGG16 architecture, two pooling layers were used, namely Global Average Pooling and Global Max Pooling. Global Average Pooling gives a global sense of how spatially responsive the feature maps are. Global Max Pooling provides the most strongly activated part of each feature map. The outputs of the two pooling layers were then concatenated to generate the fused feature representation. Such a combination of both types of pooling made it possible to include global information together with locally activated areas without redundant spatial data.

The fused feature vector went through batch normalization, dense layers, dropout, and finally a softmax layer containing four neurons. The model was specifically created to stabilize classification and enable better discrimination of features in gliomas, meningiomas, pituitary tumors, and no-tumors.

3.9 Model Training and Evaluation

The Adam optimizer was used to train all models with categorical cross-entropy loss. The metrics accuracy, precision, recall, and area under the ROC curve were tracked throughout the training process. Validation loss was considered the primary measure of convergence to avoid overfitting and maintain generalization. Adaptation of the learning rate and early stopping were included in the training process.

The independent test data set was used to evaluate the final models. Evaluation of the models was based on accuracy, precision, recall, macro F1 score, and AUC. Class-based performance of the models was analyzed through confusion matrices and classification report. Sensitivity and specificity were evaluated using one-vs-rest approach for multi-class problems. Cohen's Kappa and Matthews correlation coefficient were also calculated.

3.10 Explainability Analysis

The Grad-CAM method was applied to improve the model's interpretability. Heatmaps were created using the activation output from the last convolutional layer

and then overlayed on the MRI images to determine which regions of the images contributed to the classification process.

3.11 Therapeutic Relevance Mapping

In order to highlight the importance of pharmaceutics, the outcomes from our model were mapped onto generalized therapeutic pathway models. Gliomas were mapped onto pathways related to chemotherapy, targeted therapy, blood-brain barrier and blood-brain tumor barrier issues, nanoparticle carriers, and response monitoring. Meningiomas were mapped onto pathways including surgery, radiotherapy, recurrence monitoring, and selected adjuvant therapy. Pituitary tumors were mapped onto endocrine pharmacotherapy, localization therapy, and follow-up. The no-tumor case was included in order to justify the exclusion of any unnecessary tumor-directed treatment. These mappings do not imply any treatment decisions, rather, they are meant to establish the role of MRI-based CNN prediction as a decision support tool for future treatments.

4. Results

This section presents the experimental results obtained from Baseline CNN, EfficientNetB0, and VGG16 Dual-Pooling for multiclass brain tumor classification. 1,600 MRI scans that were evenly divided among the four categories of glioma, meningioma, pituitary tumour, and no tumour made up the test data. The measures used to evaluate the models include accuracy, precision, recall, macro F1 score, AUC, confusion matrix, ROC-AUC, and Grad-CAM visualization. The VGG16 Dual-Pooling Model had the best performance, hence the primary model for final interpretation.

4.1 Quantitative Performance Evaluation

The comparative test performance of the three models is presented in Table 1. VGG16 Dual-Pooling achieved the highest values across all major evaluation metrics.

Table 1. Comparative Performance Evaluation of Baseline CNN, EfficientNetB0, and VGG16 Dual-Pooling

Metric	Baseline CNN	EfficientNetB0	VGG16 Dual-Pooling
Accuracy	0.8006	0.8994	0.9050
Precision	0.8096	0.9037	0.9088
Recall	0.7919	0.8969	0.9031
Macro F1-score	0.7969	0.8968	0.9020
AUC	0.9402	0.9713	0.9728

The accuracy score for VGG16 Dual-Pooling model reached 90.50%, which is 0.56% better than EfficientNetB0 and 10.44% better than Baseline CNN. Also, this model reached the best performance in terms of precision, recall, macro F1-score and AUC. The improvement over EfficientNetB0 was modest but consistent, indicating that the dual-pooling strategy improved feature representation and classification stability.

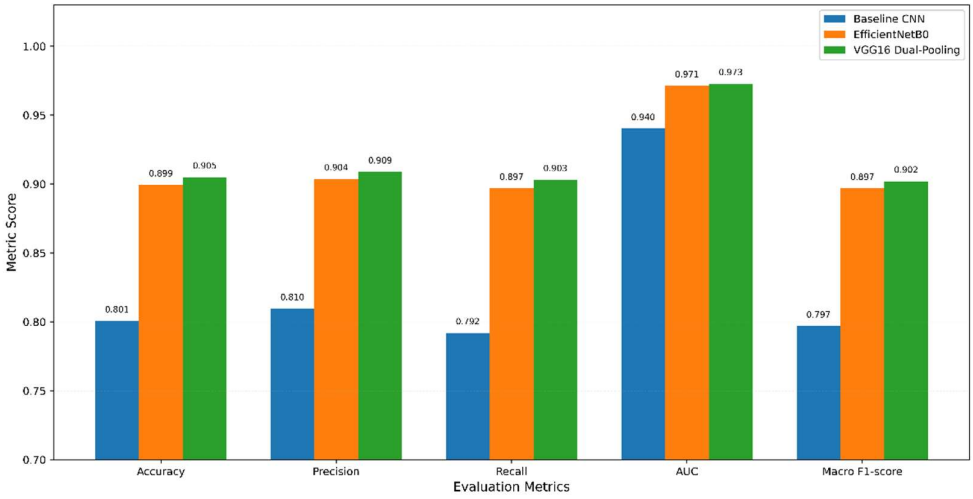

Figure 1. Performance Comparison of Baseline CNN, EfficientNetB0, and VGG16 Dual-Pooling

As shown in Figure 1, VGG16 Dual Pooling achieved the best metric scores for accuracy, precision, recall, area under curve, and macro F1-score. Although EfficientNet B0 performed well, VGG16 Dual Pooling was slightly better in terms of classifying the test dataset.

4.2 Independent Evaluation of VGG16 Dual-Pooling

Table 2 presents the training, validation, and testing performance of VGG16 Dual-Pooling.

Table 2. Evaluation Summary of VGG16 Dual-Pooling

Dataset	Loss	Accuracy	Precision	Recall	AUC
Train	0.1193	0.9975	0.9975	0.9973	1.0000

Validation	0.2663	0.9384	0.9424	0.9357	0.9942
Test	0.5586	0.9050	0.9088	0.9031	0.9728

The model achieved 99.75% training accuracy, 93.84% validation accuracy, and 90.50% test accuracy. The validation AUC was 0.9942, while the independent test AUC was 0.9728. These results show that VGG16 Dual-Pooling maintained strong discriminative ability on unseen MRI images.

4.3 Class-Wise Classification Performance

The class-wise test performance of VGG16 Dual-Pooling is shown in Table 3.

Table 3. Class-Wise Classification Performance of VGG16 Dual-Pooling

Class	Precision	Recall	F1-score	Support
Glioma	0.9565	0.7150	0.8183	400
Meningioma	0.8288	0.9200	0.8720	400
No tumor	0.8906	0.9975	0.9410	400
Pituitary	0.9658	0.9875	0.9765	400
Accuracy	0.9050	0.9050	0.9050	1600
Macro average	0.9104	0.9050	0.9020	1600
Weighted average	0.9104	0.9050	0.9020	1600

The pituitary class achieved the highest F1-score of 0.9765, with precision of 0.9658 and recall of 0.9875. The no-tumor class achieved the highest recall value of 0.9975, indicating that almost all no-tumor cases were correctly identified. Meningioma recall was also strong at 0.9200. Glioma produced high precision of 0.9565 but lower recall of 0.7150, showing that glioma predictions were reliable when made, but a proportion of true glioma cases were classified into other categories.

4.4 Confusion Matrix Analysis

The confusion matrix of VGG16 Dual-Pooling is presented in Table 4 and Figure 2.

Table 4. Confusion Matrix of VGG16 Dual-Pooling on the Independent Test Set

True class	Predicted glioma	Predicted meningioma	Predicted no tumor	Predicted pituitary
Glioma	286	71	41	2
Meningioma	12	368	8	12
No tumor	0	1	399	0
Pituitary	1	4	0	395

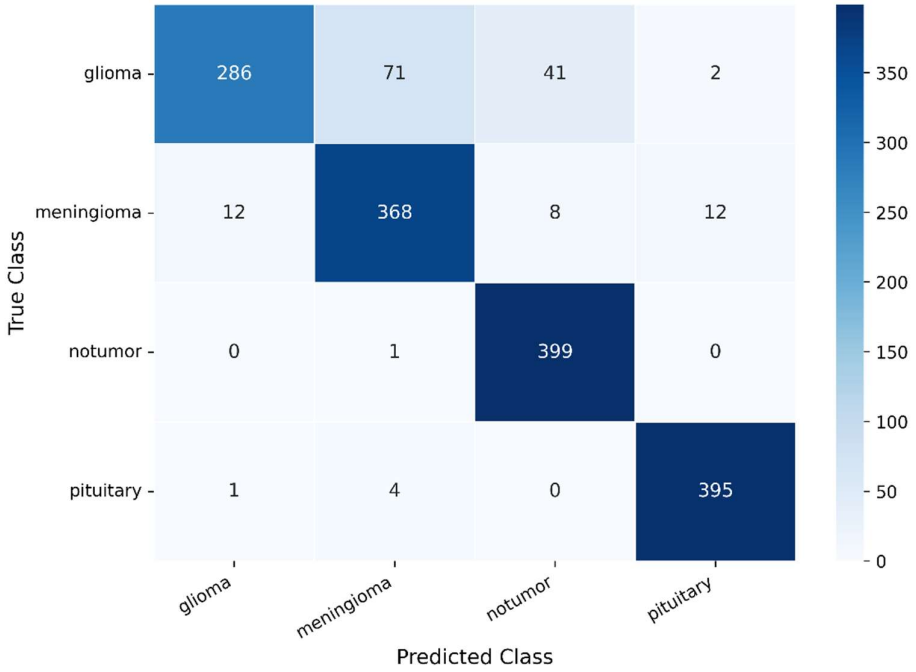

Figure 2. Confusion Matrix of VGG16 Dual-Pooling on Independent Test Set

The model correctly classified 286 glioma, 368 meningioma, 399 no-tumor, and 395 pituitary images. The strongest performance was observed for the no-tumor and pituitary classes. The major classification difficulty occurred in glioma cases, where 71 images were classified as meningioma and 41 were classified as no tumor. This indicates that glioma remained the most challenging class, probably because of visual overlap with other MRI patterns.

4.5 ROC-AUC Analysis

The one-vs-rest ROC curves for VGG16 Dual-Pooling are shown in Figure 3. The model achieved a macro-average AUC of 0.9765 and a micro-average AUC of 0.9767

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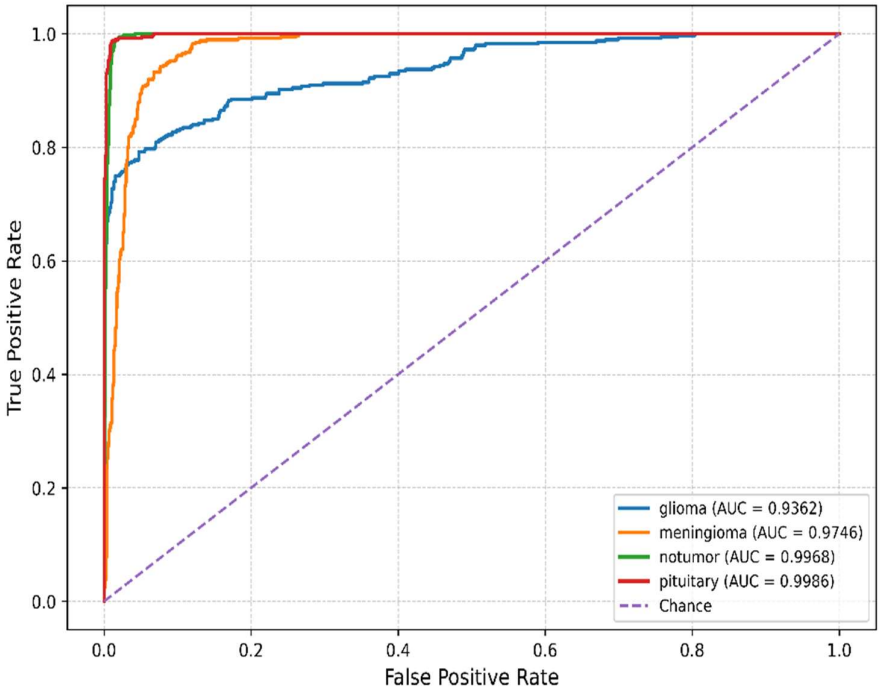

Figure 3. One-vs-Rest ROC Curves of VGG16 Dual-Pooling

Class-wise AUC values were 0.9362 for glioma, 0.9746 for meningioma, 0.9968 for no tumor, and 0.9986 for pituitary. The pituitary and no-tumor classes showed the strongest discriminative performance, while glioma had the lowest AUC among the four classes. However, all class-wise AUC values remained high, confirming that VGG16 Dual-Pooling had strong overall class-separation ability.

4.6 Advanced Evaluation Metrics

Additional summary metrics for VGG16 Dual-Pooling are shown in Table 5.

Table 5. Advanced Evaluation Metrics of VGG16 Dual-Pooling

Metric	Value
Accuracy	0.9050
Macro precision	0.9104
Macro recall	0.9050
Macro F1-score	0.9020
AUC	0.9728
Macro ROC-AUC	0.9765
Micro ROC-AUC	0.9767

The macro precision of 0.9104 and macro F1-score of 0.9020 confirm that VGG16 Dual-Pooling produced balanced classification performance across the four MRI categories. The AUC values further demonstrate strong discriminative capacity.

4.7 Comparative Model Interpretation

The comparative results confirm that transfer learning models performed substantially better than the Baseline CNN. Baseline CNN achieved 80.06% accuracy, while EfficientNetB0 increased accuracy to 89.94%. VGG16 Dual-Pooling achieved the best accuracy of 90.50%. The improvement over EfficientNetB0 was small but consistent across all metrics, including precision, recall, macro F1-score, and AUC.

The higher performance of VGG16 Dual-Pooling can be attributed to the use of Global Average Pooling and Global Max Pooling. Global average pooling is useful for identifying general contextual information, whereas global max pooling keeps information from strong activations. Together, their feature extraction contributed to the improvement in classification performance and tumor pattern recognition.

4.8 Grad-CAM Explainability Analysis

Grad-CAM was applied to correctly classified samples from each class to examine the visual attention behavior of VGG16 Dual-Pooling. Representative outputs are shown in Figure 4.

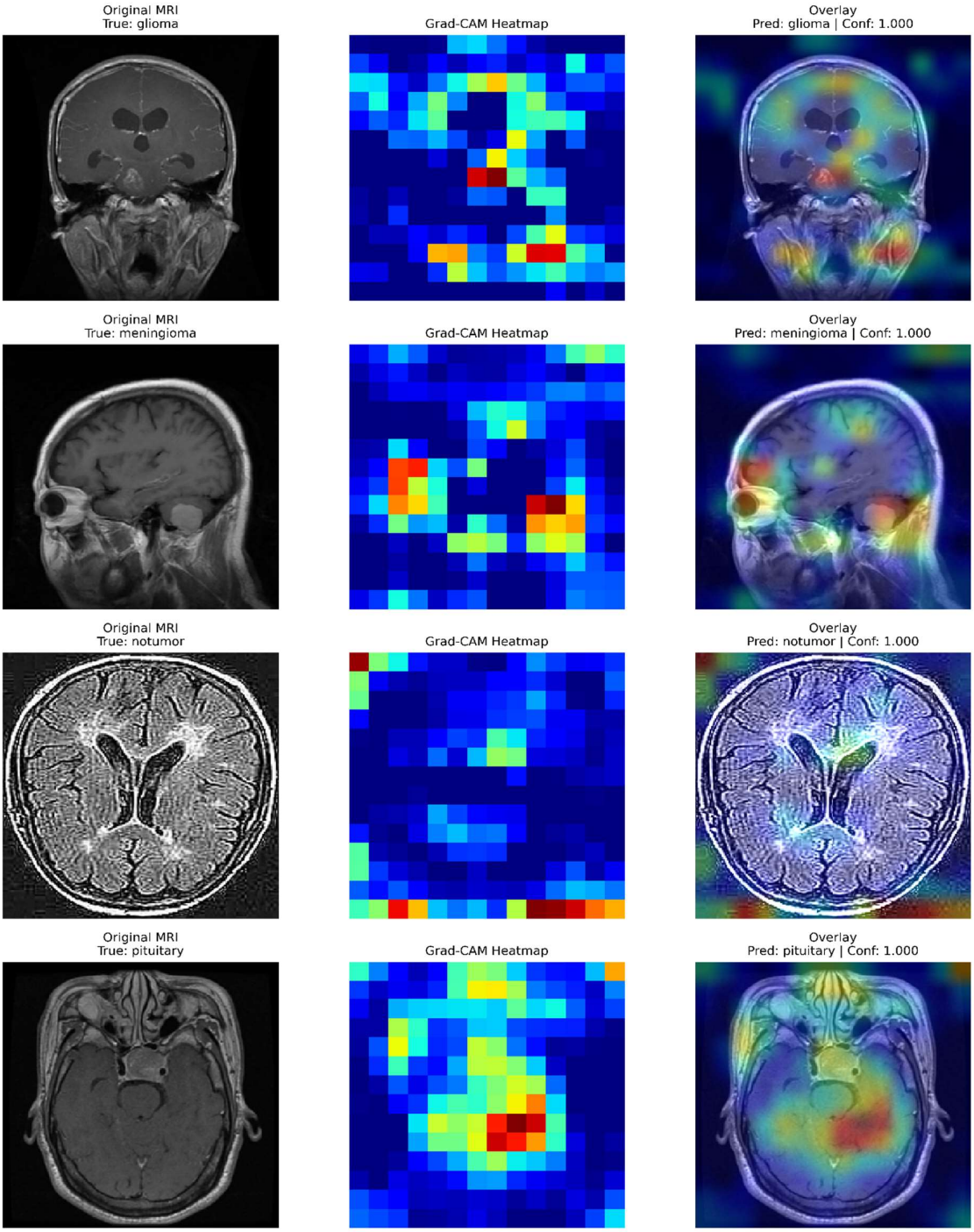

Figure 4. Grad-CAM Visual Explanation of Correct VGG16 Dual-Pooling Predictions

The Grad-CAM maps showed that the model focused on intracranial image regions during prediction. For tumor-positive classes, activation patterns appeared around relevant abnormal regions. For no-tumor cases, the activation pattern was more distributed and did not concentrate on a single lesion-like region. These findings indicate that the model learned diagnostically meaningful image features rather than relying only on background patterns.

4.9 Pharmaceutics-Oriented Stratification Output

The outputs of VGG16 Dual-Pooling were also interpreted as preliminary stratification signals for pharmaceutics-oriented decision support. Table 6 summarizes the therapeutic relevance of each predicted class.

Table 6. Pharmaceutics-Oriented Interpretation of CNN Classification Outputs

Predicted class	Main model finding	Therapeutic/drug-delivery relevance
Glioma	High precision but lower recall	Chemotherapy planning, BBB/BBTB challenges, targeted therapy, nanocarrier delivery, response monitoring
Meningioma	Strong recall and moderate-to-strong classification	Surgical, radiotherapeutic, recurrence-monitoring, and selected adjuvant pathways
Pituitary tumor	Very high recall and F1-score	Endocrine pharmacotherapy, localized intervention planning, follow-up monitoring
No tumor	Highest recall	Avoidance of unnecessary tumor-directed pharmacological or invasive intervention

The high recall for no-tumor and pituitary categories implies that VGG16 Dual-Pooling might help rule out the need for tumor-specific interventions and endocrine pathways. The glioma category is necessary for treatment planning but must be carefully verified owing to low recall. Thus, the output of the model can only be taken as an indicator and not a recommendation.

Discussion

The findings show that VGG16 Dual-Pooling provided the strongest framework for multiclass brain tumor MRI classification among the evaluated models. VGG16 Dual-Pooling achieved 90.50% testing accuracy, 90.88% precision, 90.31% recall, 90.20% macro F1-score, and 97.28% AUC. The accuracy obtained by this model was better compared to EfficientNetB0, which had an accuracy of 89.94%, and significantly better compared to Baseline CNN, which had an accuracy of 80.06%. The difference in accuracy between this model and EfficientNetB0 is 0.56%, while that between this model and Baseline CNN is 10.44%.

The improved performance of VGG16 Dual-Pooling can be attributed to its dual-pooling feature fusion strategy. The use of Global Average Pooling facilitated the extraction of general context information from the last convolutional feature maps, whereas Global Max Pooling was useful in preserving the strongest activations from the local regions. The combination of these two feature representations enabled the model to capture both global and locally activated features. This helped improve classification stability across glioma, meningioma, pituitary tumor, and no-tumor MRI classes.

From a pharmaceutics and drug-delivery perspective, the framework can be considered an upstream imaging-based stratification tool rather than a direct therapeutic system. Tumour type, anatomical location, vascular behaviour, blood-brain barrier integrity, disruption of the blood-brain tumour barrier, and pharmacological response all affect how drugs are delivered to brain tumours.[23],[24] Therefore, automated classification of MRI patterns may support future models that combine imaging outputs with drug-delivery parameters, molecular markers, pharmacotherapy data, and treatment response.

The class-wise findings showed that VGG16 Dual-Pooling performed particularly well for no-tumor and pituitary tumor classes. The no-tumor class achieved 99.75% recall, while the pituitary class achieved 98.75% recall and the highest F1-score of 97.65%. These results suggest that the model was highly effective in identifying cases related to tumor-exclusion pathways and pituitary-related endocrine treatment considerations. Meningioma classification was also strong, with 92.00% recall. However, glioma remained the most difficult class, with 71.50% recall despite high precision of 95.65%. This means that when the model predicted glioma, the prediction was usually reliable, but some actual glioma cases were classified as meningioma or no tumor.

The confusion matrix confirmed this limitation. Among 400 glioma images, 286 were correctly classified, while 71 were classified as meningioma and 41 as no tumor. This error pattern indicates that glioma images showed visual overlap with other MRI categories. Such misclassification is important because glioma is clinically and pharmaceutically significant due to its association with aggressive treatment planning, chemotherapy selection, blood-brain barrier limitations, targeted therapy, and nanocarrier-based delivery considerations. Therefore, glioma predictions should be interpreted cautiously and verified through radiological, clinical, molecular, and histopathological assessment before being used in any treatment-support workflow.

The present findings are consistent with previous studies showing the usefulness of transfer learning in brain tumor MRI classification. Swati et al. reported that fine-tuned pretrained CNN models can improve MRI-based brain tumor classification.[2] Deepak and Ameer also showed that pretrained CNN features are effective for brain tumor classification when medical imaging datasets are limited.[11] The current results further support this direction by showing that both EfficientNetB0 and VGG16 Dual-Pooling outperformed the Baseline CNN. The use of Grad-CAM also aligns with explainable medical AI research, where visual explanations are

important for improving trust and interpretability in automated diagnosis.[18]

The Grad-CAM findings showed that VGG16 Dual-Pooling focused on intracranial regions during prediction. For tumor-positive images, activation patterns were observed around relevant abnormal regions, while no-tumor images showed more distributed activation patterns. These findings suggest that the model was not relying only on irrelevant background features. However, Grad-CAM should be interpreted as an attention-based explanation rather than a segmentation method. It indicates regions that influenced model decisions but does not provide exact tumor boundaries or quantitative lesion measurements.

The implications of these findings clinically are that VGG16 Dual-Pooling might be utilized for preliminary MRI screening and decision-making. With the high accuracy, macro F1-Score, and AUC, it is possible to conclude that the model is able to perform reliable classification of multi-class MRI patterns on the level of images. In the context of pharmaceutics-oriented decision-making, the classification might facilitate early stratification by determining which tumors need to be considered when making treatment decisions. For instance, glioma classification will require the assessment of options related to chemotherapy planning, drug delivery through the blood-brain barrier, and targeted therapy, while pituitary tumor classification may lead to endocrine pharmacotherapy approaches.

However, there are still some limitations to be considered. For instance, a unique dataset from Kaggle was utilized in the study, which might affect generalization due to its specific application in various hospitals and imaging machines. Also, no other tasks were implemented apart from image-level classification, such as tumor segmentation, volumetric measurements, grading, molecular subtyping, survival analysis, pharmacokinetics parameters, medication data, and treatment outcomes. While VGG16 Dual-Pooling had the highest level of efficiency, its recall rate was relatively low in detecting gliomas.

In terms of validation, future research will need to conduct model validation through the use of external datasets and patient cohorts annotated with MRI from different centers. Future improvements could include preprocessing based on segmentation, multimodal MRI inputs, attention networks, ensembles, and a combination of transformer-CNN models to minimize errors due to misclassification of gliomas. In the field of pharmaceutics, future research will need to incorporate the MRI classification results with molecular biomarkers, tumor grading, pharmacological data, drug delivery, treatment response, and survival data.

Conclusion

This study developed and evaluated deep learning models for automated brain tumor detection and multiclass classification using MRI scans. The models analyzed include Baseline CNN, EfficientNetB0, and VGG16 Dual-Pooling. Of all these models, VGG16 Dual-Pooling performed optimally with 90.50% accuracy, 90.88% precision, 90.31% recall, 90.20% macro F1-score, and 97.28% AUC on the independent test set. VGG16 Dual-Pooling demonstrated excellent performance in the classification of no-tumor and pituitary tumors but had a hard time classifying gliomas due to the low recall rate and the similarity between the MRI patterns of gliomas and meningiomas as well as no-tumors. The model performed well through grad-CAM analysis, which helped to visualize the focus of the algorithm on specific brain areas. In terms of pharmaceutics and drug delivery, the prediction output can be used to generate imaging-based upstream decision signals that will assist in glioma chemotherapy, BBB/BBTB, targeted therapy, nanocarrier-based delivery, endocrine pharmacotherapy, localized treatment planning, and avoiding unneeded tumor-directed therapy. Nonetheless, this model cannot make treatment suggestions or be used as an independent therapeutic decision system. Further studies will involve validation of the model using more extensive MRI datasets and integration of imaging with pharmaceutics variables and others.

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