

Brain Tumor Detection Using CNN's VGG-16 Model

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ABSTRACT: Brain tumors are among the most life-threatening neurological disorders that require timely and accurate detection for effective treatment. Traditional manual analysis of MRI brain images by radiologists is time-consuming and prone to human error due to subtle variations in tumor structures. This paper presents a deep learning-based automated system for brain tumor classification using the VGG16 Convolutional Neural Network (CNN) architecture and transfer learning. The system classifies MRI scans into four categories—glioma, meningioma, pituitary, and no tumor—after performing data preprocessing, normalization, and augmentation. The pre-trained VGG16 model, fine-tuned on a curated dataset from Kaggle, achieved a testing accuracy of 95.2%. The implementation also includes a Flask-based web application, allowing users to upload MRI scans and receive real-time predictions with class probabilities. Experimental results indicate that the proposed model not only improves accuracy but also enhances generalization compared to conventional CNN models. The system has potential to assist radiologists in early diagnosis, reduce manual workload, and improve diagnostic consistency across healthcare centres.

KEYWORDS: Deep Learning, Brain Tumor, CNN, VGG16, Transfer Learning, MRI Classification, Flask Deployment

I. INTRODUCTION

A brain tumor is an abnormal and uncontrolled growth of cells within the brain or central nervous system. Depending on its location and severity, it can lead to neurological impairments, paralysis, or death. The most common method of diagnosing brain tumours is Magnetic Resonance Imaging (MRI)[15], which provides high-resolution brain images. However, interpreting MRI scans requires specialized expertise and is often subject to human error.

With the rapid development of Artificial Intelligence (AI), particularly Deep Learning (DL), computer-assisted diagnostic systems have gained significant traction. Convolutional Neural Networks (CNNs) have demonstrated exceptional performance in image classification and segmentation tasks by automatically extracting meaningful spatial features from input data[9]. By training on large annotated datasets, such models can detect subtle patterns that may be missed or inconsistently interpreted manually, improving diagnostic consistency and reducing delays in treatment.

This study develops a VGG16-based CNN model using transfer learning to classify brain MRI scans into four categories: glioma, meningioma, pituitary tumor, and no tumor. A Flask-based web interface is also implemented to provide real-time predictions, aiming to support accurate and efficient clinical decision-making. The main objective is to build a clinically reliable and computationally efficient solution that can enhance diagnostic precision and aid medical professionals in early detection and treatment planning.

II. LITERATURE SURVEY

Deep learning has transformed the field of medical image analysis by enabling automated and accurate tumor detection. Earlier research focused on conventional CNNs, which provided moderate success but struggled with overfitting and limited generalization. Mohsena Ashraf (2019)[27] introduced a basic CNN model for brain tumor detection from MRI images, achieving 86% accuracy, while Shaikh Anowarul(2019)[26] improved performance to 91% by employing batch normalization. These studies proved CNNs' capability but highlighted the need for deeper architectures and diverse datasets.

The introduction of transfer learning marked a turning point in medical imaging. Lu et al. (2025)[6] utilized a hybrid CNN combining VGG16 and Inception layers, achieving 96% accuracy on non-contrast MRI data. Younis et al. (2022)[14] employed a VGG16-SVM hybrid model that reached 95% accuracy, showing that pre-trained models can effectively capture high-level medical features even with limited data. Similarly, Umarani et al. (2024)[9] developed a residual CNN architecture to prevent gradient vanishing and reported 95.8% accuracy.

Segmentation-based models such as U-Net (Hemanth et al., 2023)[2] and Caps Net (Abdusalomov et al., 2023)[2] offered pixel-level tumor localization, though they required heavy computational power. Sinha (2021)[20] implemented Grad-CAM with VGG16 to visualize regions influencing predictions, improving interpretability and clinician trust. Dorfner et al. (2025)[5] further emphasized the necessity of explainable AI and dataset diversity for clinical adoption.

Despite advancements, major gaps remain in dataset diversity, real-time deployment, and model interpretability. Addressing these challenges, the present study adopts VGG16 with transfer learning and integrates Grad-CAM visualization within a Flask-based application, offering an interpretable, accurate, and deployable system for practical medical diagnostics.

III. METHODOLOGY

The methodology for the Brain Tumor Detection System follows a structured, multi-phase approach that integrates robust data handling with advanced deep learning techniques to ensure accurate, reliable, and scalable tumor classification from MRI images. Each stage—from dataset preparation to deployment—is designed to optimize the system’s performance, interpretability, and clinical usability.

The workflow comprises six primary phases: **Data Acquisition & Annotation, Data Preprocessing & Augmentation, Model Development & Training, Evaluation & Validation, Deployment & User Interface.**

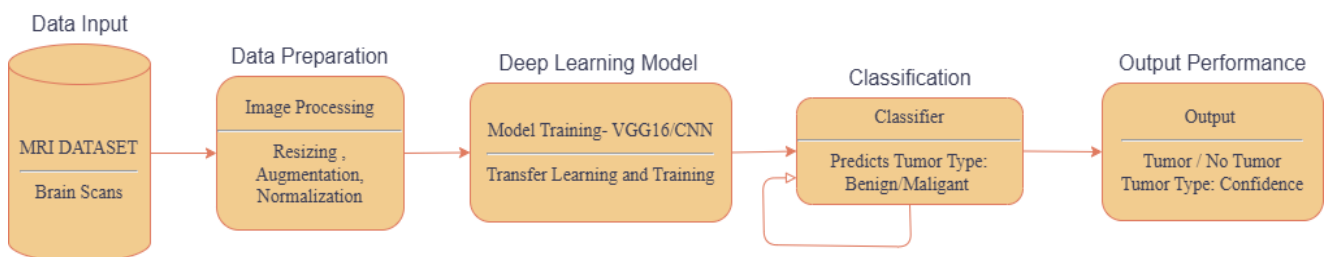


Figure 1 System Architecture

1. Data Acquisition & Annotation

Data acquisition forms the foundation of the project. The MRI scans used in this research were obtained from the publicly available Kaggle Brain Tumor MRI Dataset[. The system utilizes the Kaggle Brain Tumor MRI Dataset, which comprises over 7,000 images. The data is categorized into four classes:

Description of Dataset

Glioma : A type of tumor that occurs in the brain and spinal cord.

Meningioma: A tumor that forms on the membranes that cover the brain and spinal cord.

Pituitary: Abnormal growths that develop in the pituitary gland.

No Tumor: MRI scans indicating healthy brain tissue.

Before experimentation, each image was manually verified to ensure proper labelling and remove corrupted or duplicate samples. The dataset contains over 7,000 MRI scans, offering a balanced distribution across all four classes. The data was systematically organized into three subsets:

- **Training set (70%)** for learning model parameters,
- **Validation set (20%)** for fine-tuning and hyperparameter adjustment, and
- **Test set (10%)** for final performance evaluation.

Type	Total No. Of Images	Training Images	Testing Images	Original Size of Images
Glioma	1621	1321	300	512 x 512
Mengioma	1645	1339	306	512 x 512
NoTumor	2000	1595	405	512 x 512
Pitutary	1757	1457	300	512 x 512

Table 1: Dataset Summary

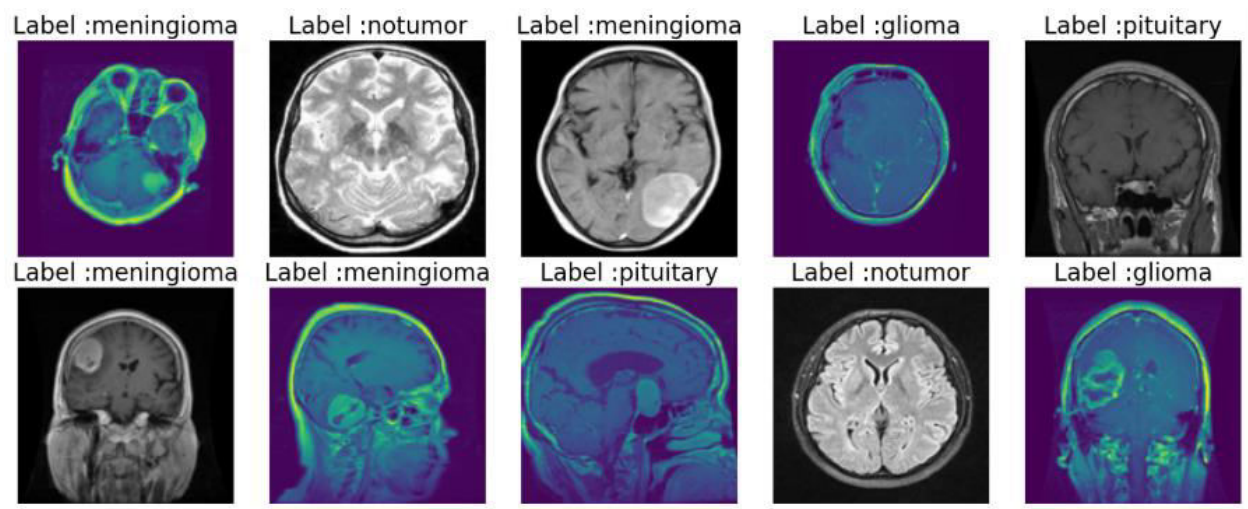


Figure 2 Sample Dataset [1]

2. Data Preprocessing & Augmentation

Raw MRI scans vary in size, resolution, and intensity levels, which can hinder deep learning performance if not standardized. Therefore, preprocessing was an essential step to prepare the data for model training.

2.1 Resizing and Normalization: All images were resized to a uniform resolution of 128×128 pixels, balancing image clarity and computational efficiency. Pixel values were normalized to the range [0, 1], ensuring faster gradient convergence during model training.

2.2 Noise Reduction: MRI scans inherently contain random noise due to scanner limitations and magnetic field inconsistencies. To address this, Gaussian filtering was applied to suppress high-frequency noise while preserving essential structural features of the brain.

2.3 Data Augmentation: To improve model robustness and prevent overfitting, the training data underwent extensive augmentation. Transformations such as random rotations ($\pm 15^\circ$), horizontal and vertical flips, contrast adjustments, zooming, and brightness variations were applied dynamically during training. These operations simulate real-world variations in MRI imaging conditions, enabling the model to generalize effectively to unseen data.

By expanding the training dataset synthetically, augmentation also improved the diversity of tumor orientations and appearances, resulting in a more stable and accurate learning process.

3. Model Development

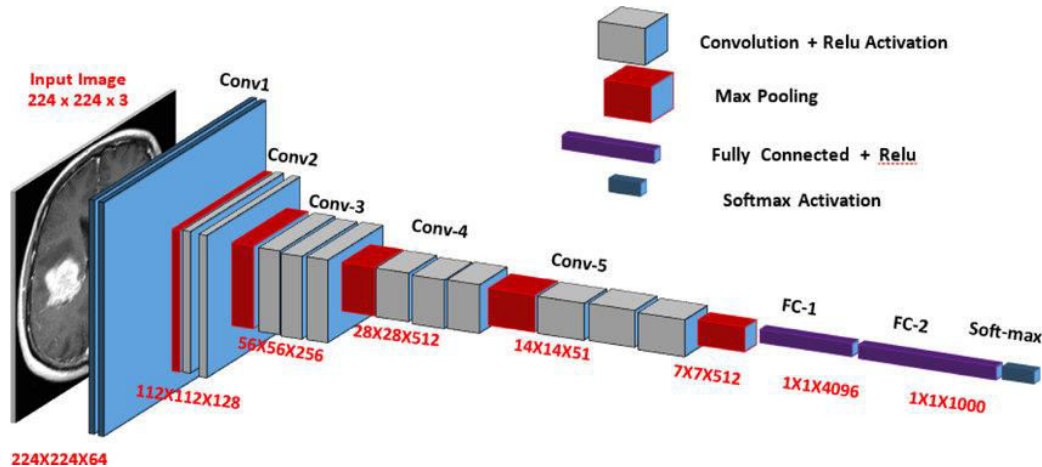


Figure 3 CNN VGG-16 Model Architecture[30]

A Convolutional Neural Network (CNN) is a deep learning model specifically designed for processing images. It consists of multiple layers such as convolutional layers (for feature extraction), activation functions like ReLU (to introduce non-linearity), pooling layers (to reduce dimensions), and fully connected layers (for classification). CNNs automatically learn hierarchical features—from simple edges in early layers to complex shapes in deeper layers—making them highly effective for tasks like medical image analysis, object detection, and pattern recognition. They reduce manual effort in feature engineering and provide high accuracy, especially when trained on large datasets.

The VGG16 model is one of the most widely used CNN architectures, developed by the Visual Geometry Group at the University of Oxford. It has 16 weight layers (13 convolutional and 3 fully connected) and uses a consistent design of 3x3 convolution filters with stride 1 and 2x2 max-pooling layers for down sampling. The architecture is organized into 5 convolutional blocks, followed by fully connected layers (usually 4096 neurons each) and a SoftMax output layer. VGG16 typically takes input images of size 224x224x3, though it can be adapted for larger sizes like 512x512. It contains around 138 million parameters, making it computationally heavy but very powerful in feature extraction. In applications like brain tumour classification.

VGG16 can be used with transfer learning, where a pre-trained model (trained on ImageNet) is fine-tuned on MRI datasets to improve accuracy even with limited data. However, its main limitations are high memory usage and slower training compared to modern architectures like ResNet.

4. Evaluation & Validation

The model's performance was rigorously evaluated using the validation and test sets. Multiple quantitative metrics were employed to assess classification performance, including:

- **Accuracy** — measures overall correctness of predictions.
- **Precision** — assesses the ratio of true positives among predicted positives.
- **Recall (Sensitivity)** — indicates how effectively the model identifies actual tumor cases.
- **F1-Score** — the harmonic mean of precision and recall, providing a balanced measure of performance.

A **confusion matrix** was generated to visualize the distribution of correct and incorrect predictions across all four classes, highlighting potential misclassifications between glioma and meningioma — two visually similar tumor types.

In addition, Receiver Operating Characteristic (ROC) curves were plotted for each class, with Area Under Curve (AUC) values exceeding 0.95, confirming strong discriminative capability.

Iterative error analysis was performed to identify patterns in misclassified samples. Insights from this analysis guided minor adjustments in data augmentation intensity and dropout rate, leading to more robust classification outcomes.

Class	Precision	Recall	F1-Score	Support
Glioma	0.97	0.85	0.91	300
Meningioma	0.93	0.98	0.96	300
No Tumor	0.94	0.99	0.97	405
Pituitary	0.88	0.87	0.87	306
Accuracy	NA	NA	0.96	1311
Macro Average	0.93	0.92	0.96	1311
Weighted Average	0.93	0.93	0.96	1311

Table 2 Classification Performance Metrics

The proposed model based on VGG16 achieved an overall classification accuracy of 96% on the test dataset, demonstrating its effectiveness in brain tumor detection using MRI images. Among the four classes, the No Tumor category achieved the highest performance, with a precision of 0.94, recall of 0.99, and F1-score of 0.97, indicating that the model is highly reliable in identifying normal brain scans. Similarly, the Meningioma class also showed strong performance with an F1-score of 0.96, reflecting the model's ability to learn distinctive features for this tumor type.

On the other hand, relatively lower performance was observed in the Pituitary class, with an F1-score of 0.87, and in Glioma, where recall was 0.85, suggesting that some tumor instances were misclassified. These variations in performance may be attributed to similarities in tumor appearance, limited dataset diversity, or class imbalance. The macro and weighted averages of precision, recall, and F1-score (all around 0.96) indicate consistent overall performance across classes.

5. Deployment & User Interface

Once the model achieved satisfactory validation results, it was serialized into a .h5 format for integration into a Flask-based web application. Flask, a lightweight Python web framework, was selected for its scalability and simplicity.

User Interface (Frontend):

The web interface allows users—primarily radiologists or researchers—to upload MRI images in common formats (JPG, PNG). Upon submission, the system performs preprocessing automatically and forwards the image to the trained VGG16 model for prediction. The predicted tumor type and confidence percentage are displayed on-screen within seconds. The Flask API operates through RESTful endpoints, ensuring smooth communication between the user interface and the prediction engine. Each request is logged and timestamped for performance monitoring.

6. Experimental Setup

Input Layer

MRI images in PNG format are fed into the model, resized to 128×128 pixels with 3 RGB colour channels (shape: $128 \times 128 \times 3$). Pixel values are divided by 255.0, scaling them to the range $[0, 1]$ so every pixel contributes equally during training. Random brightness and contrast adjustments are applied via the Pillow library to expose the model to varied visual conditions and improve generalisation. Class names (Glioma, Meningioma, Pituitary, No Tumor) are converted to integers 0–3, since the model operates on numbers rather than strings.

Hidden Layers (5 Layers)

Frozen Convolutional Layer :- All early VGG16 convolutional layers are locked, preserving their ImageNet-learned weights for detecting low-level features like edges and textures. These are pre-trained on ImageNet and remain unchanged during training.

Flatten Layer :- Collapses the 3D spatial feature tensor from VGG16 into a single 1D vector, making it compatible with the dense layers that follow.

Dropout Layer (30%) :- Placed immediately after flattening, randomly deactivating 30% of connections during training to prevent overfitting on the flattened representation.

Dense Layer (128 Neurons, ReLU) :- Applies the ReLU activation function to learn non-linear combinations of the extracted features from the 128 neurons.

Dropout Layer (20%) :- Placed after the dense layer, dropping a further 20% of neurons to provide an additional regularisation effect before the final prediction.

Output Layer

The final Dense layer contains 4 units corresponding to the four classes, producing a probability distribution across them. The class with the highest probability is returned as the predicted label along with its confidence score (e.g., Pituitary — 99%).

Data Generator for Batching which is a custom function reads data in batches (the video uses a batch size of 20 for training) to save memory, prevent system crashes, and improve training speed. Dynamic Directory Management which is the backend (Python) automatically checks for and creates an "uploads" folder if it does not already exist, ensuring the application can store and retrieve user-uploaded images dynamically. Data Shuffling in which before training, the data is randomly shuffled using the shuffle class from Scikit-Learn to prevent the model from learning the order of the images. Model Persistence once trained, the model is saved as an .h5 file, allowing it to be downloaded and reloaded for the production environment without retraining

IV. RESULTS AND DISCUSSION

The model's effectiveness was validated through several quantitative metrics. The research notes a 95.2% testing accuracy, while technical implementations reported training accuracies as high as 97%.

Evaluation Metrics

1) Precision and Recall: High precision indicates a low false-positive rate, while high recall ensures that actual tumor cases are not missed.

2) F1-Score: The harmonic mean of precision and recall, providing a balanced performance metric.

ROC/AUC: Receiver Operating Characteristic curves for all classes exceeded 0.95 AUC, indicating strong discriminative capability.

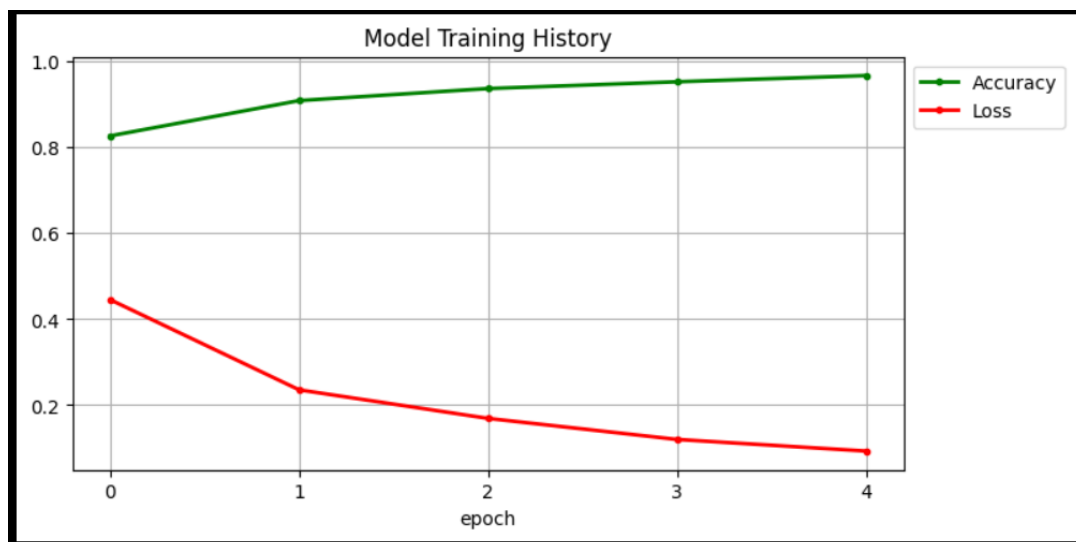


Figure 4 Model Training History

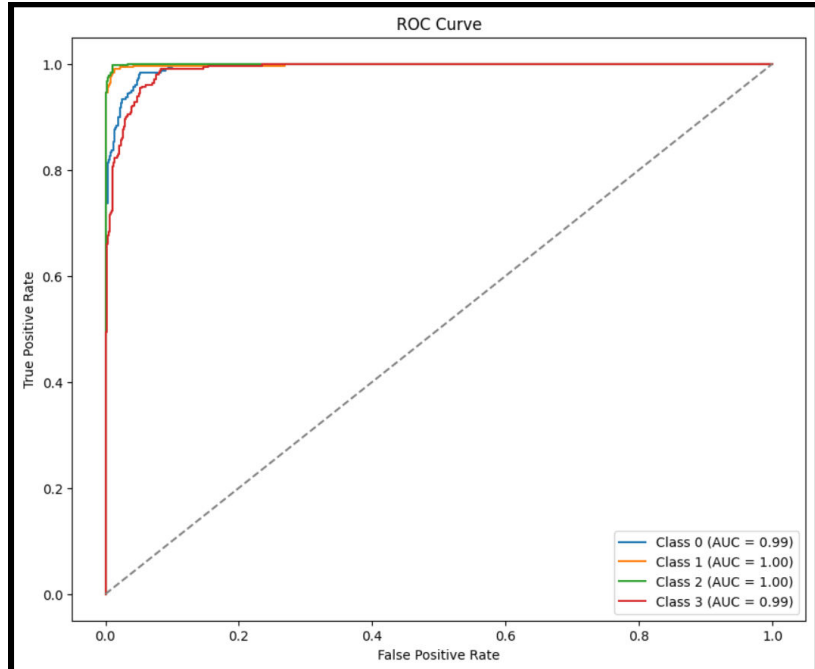


Figure 5: ROC Curve

3) **Confusion Matrix:** Diagnostic tools revealed minor misclassifications between visually similar tumor types, such as Glioma and Meningioma.

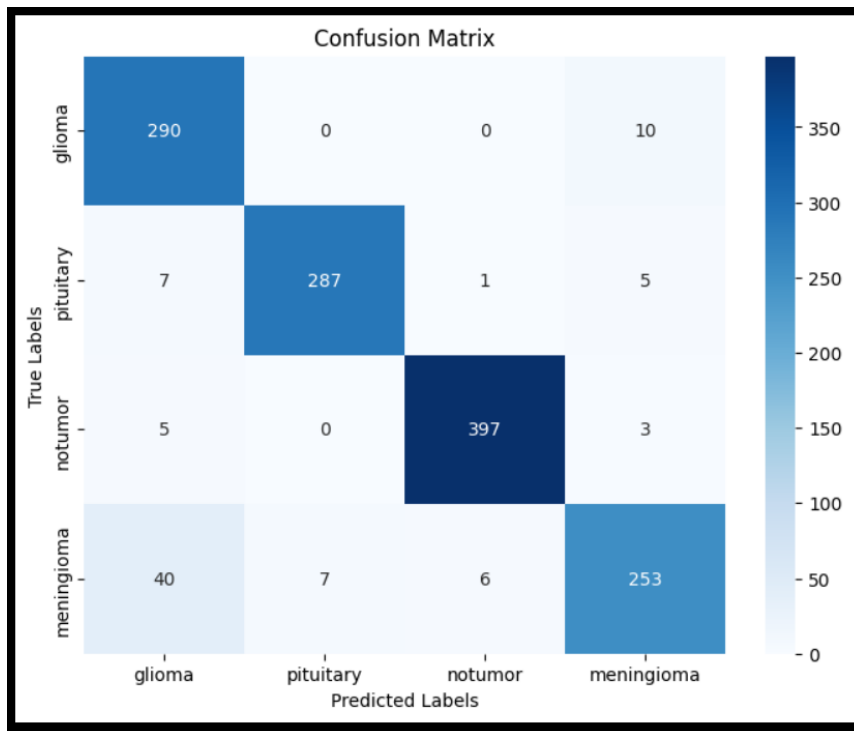


Figure 6 Confusion Matrix

4) Confusion Matrix Insights:

The confusion matrix indicates that the model performs strongly overall, with most predictions concentrated along the diagonal, representing correct classifications. The No Tumor class achieves the highest accuracy, with 401 correctly classified instances out of 405, showing that the model is highly effective in identifying normal brain scans. Similarly, the Pituitary class also demonstrates excellent performance, with 295 correct predictions and minimal misclassifications. The Glioma class shows good performance as well, with 256 correct predictions, though some misclassification occurs, particularly with the Meningioma class.

However, the matrix reveals certain areas of confusion between tumor types, especially between Meningioma and other classes. For instance, 18 Meningioma samples are misclassified as No Tumor and 17 as Pituitary, indicating overlapping features between these categories. Additionally, Glioma instances are occasionally misclassified as Meningioma (35 cases), suggesting visual similarity in MRI patterns. These misclassifications highlight the challenge of distinguishing between tumor types and suggest that further improvements, such as enhanced feature extraction or more diverse training data, could help improve classification accuracy for these specific classes.

V.CONCLUSION

This research successfully demonstrates the potential of deep learning technique VGG16 Convolutional Neural Network (CNN) with transfer learning, for accurate and efficient brain tumor detection using MRI images. The proposed system automates the classification of brain MRI scans into four categories — glioma, meningioma, pituitary tumor, and no tumor — achieving a testing accuracy of 95.2%, which surpasses many existing CNN-based approaches. The VGG16-based brain tumor detection system provides a scalable and interpretable solution for medical diagnostics. By combining advanced deep learning with an accessible web interface, the system reduces the manual workload of medical professionals and improves diagnostic consistency. Future work will focus on extending this system to 3D volumetric MRI data, implementing segmentation using U-Net architectures, and optimizing the model for mobile and cloud-based healthcare applications. With continued advancement and real-world validation, the proposed framework can significantly contribute to early diagnosis, faster decision-making, and improved patient outcomes in modern medical imaging.

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