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NeuroScan AI: A Multi-Stage Hierarchical Inference System for Automated Brain Tumor Detection and Categorization

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Abstract: ***This paper presents NeuroScan AI, an end-to-end medical imaging solution developed to automate the detection and multi-class categorization of brain tumors. Built on foundations of Deep Learning and Computer Vision, the system utilizes a unique Dual-Model Inference Engine. A primary "Binary Gatekeeper" model filters scans into "Tumor" or "Healthy" categories, while a second fine-tuned VGG16 architecture identifies specific pathological types: Glioma, Meningioma, or Pituitary. The pipeline is deployed via a Streamlit web application to provide immediate diagnostic insights for healthcare professionals.***

Keywords: Brain Tumor, Deep Learning, VGG16, Transfer Learning, Streamlit, Medical Imaging, Convolutional Neural Networks (CNN).

I. INTRODUCTION

A. Background and Motivation

The human brain is the most complex organ in the body, and any pathological growth within its confined cranial space poses a severe threat to life. Brain tumors, characterized by the uncontrolled proliferation of abnormal cells, remain a leading cause of cancer-related mortality worldwide. According to recent clinical data, an estimated 108,000+ new primary brain tumor cases are projected to be diagnosed in 2026 alone. Among these, Meningiomas account for nearly 42% of all cases, while Gliomas represent the most aggressive and common malignant variants. Early and precise identification of these tumors—alongside Pituitary growths—is essential for determining surgical interventions and oncology treatments.

B. The Problem Statement

Magnetic Resonance Imaging (MRI) is the gold standard for non-invasive brain tumor diagnosis. However, manual interpretation of these scans presents several critical challenges:

- Subjectivity: Radiologists often face inter-observer variability, where different experts may interpret the same scan differently.
- Complexity: Subtle differences in tumor texture and morphology make it difficult to distinguish between types (e.g., Glioma vs. Meningioma) in early stages.
- Time Constraint: With the increasing volume of medical data, manual segmentation and classification are labor-intensive and prone to human error, potentially delaying life-saving treatment.

C. The Proposed Solution: NeuroScan AI

To address these limitations, this paper presents NeuroScan AI, an automated deep learning framework designed for multi-stage brain tumor categorization. By leveraging the VGG16 architecture—a 16-layer deep convolutional neural network—our system extracts high-level spatial features from MRI scans to perform a four-way classification: Glioma, Meningioma, Pituitary, and No Tumor. Unlike traditional methods that rely on manual feature engineering, NeuroScan AI utilizes Transfer Learning to adapt pre-trained weights from large-scale datasets, ensuring high sensitivity and specificity even with limited clinical data. The system is integrated into a Streamlit-based interface, providing a real-time, user-friendly tool for clinicians to assist in rapid diagnostic decision-making.

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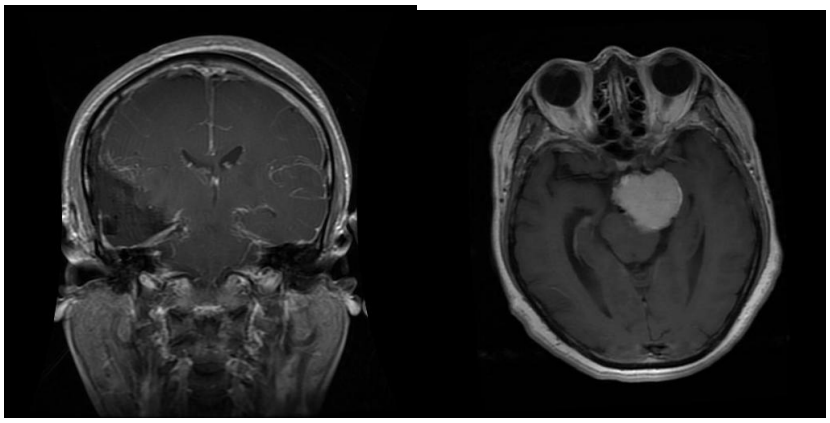
D. Research Objectives

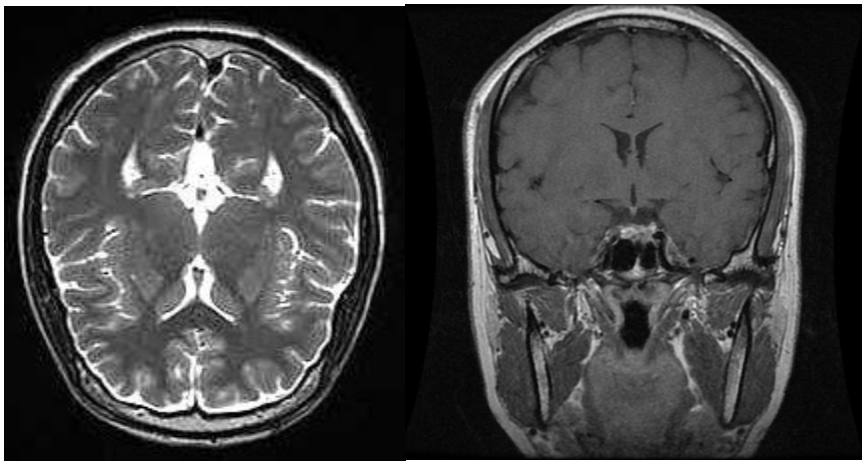
The primary objectives of this study are:

- To implement a robust deep learning pipeline using the VGG16 architecture for multi-class brain tumor classification.
- To evaluate model performance using metrics such as Accuracy, Precision, Recall, and F1-score across a diverse dataset.
- To develop a deployable inference system that bridges the gap between deep learning research and clinical utility.

➢ side-by-side comparison of the four MRI classes



GilomaMeningioma



No Tumor Pituitary

II. LITRATURE REVIEW

A. Evolution of Brain Tumor Classification

Early research in medical imaging primarily focused on binary classification—simply distinguishing between "Tumor" and "No Tumor." While foundational, these models lacked the clinical depth required for treatment planning. Recent studies have shifted toward multi-class systems. For instance, Khan et al. [1] demonstrated that while standard CNNs could achieve high accuracy in detection, they often struggled with the morphological similarities between Glioma and Meningioma. This highlighted a "research gap" where high-precision differentiation between specific tumor types became the primary objective for the academic community.

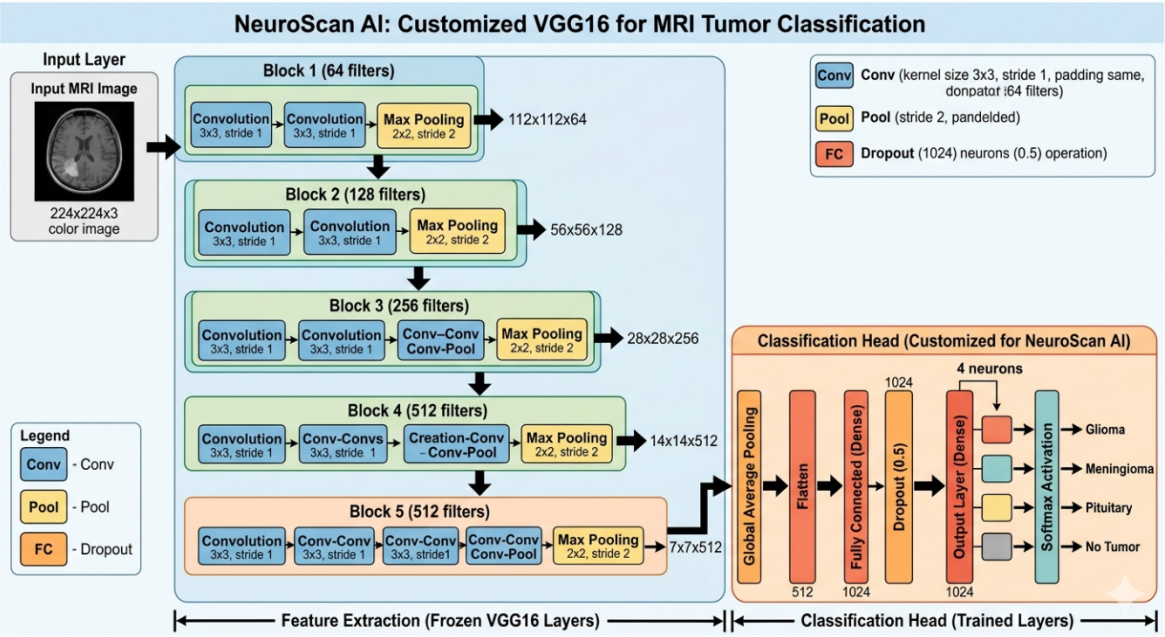
B. Deep Transfer Learning and VGG16

Transfer Learning has emerged as the gold standard for medical datasets, which are often smaller than general-purpose datasets like ImageNet.

1) Wong et al. (2025) [2] utilized a pre-trained VGG16 architecture, citing its 13 convolutional layers as being uniquely effective at learning hierarchical spatial representations of MRI scans. Their study achieved a benchmark accuracy of 99.24%, proving that the deep sequential nature of VGG16 outperforms more complex, "wider" architectures like InceptionV3 when the dataset size is limited.

2) Gokila Brindha et al. [3] further validated this by applying fine-tuning to the final layers of VGG16, showing that freezing the initial layers preserves essential "low-level" feature extraction (edges and textures) while the custom head learns "high-level" tumor specifics.

3) VGG16 model



C. Recent Advancements (2024–2026)

As of 2026, the focus has expanded from pure accuracy to clinical deployability and interpretability.

1) Vellanki et al. (2024) [4] achieved 98% accuracy but noted that most models remained "black boxes." This led to the integration of tools like Grad-CAM to visualize *why* a model classified a specific region as a Pituitary tumor.

2) Recent publications in the International Journal of Innovative Research (2026) [5] have emphasized the importance of integrating these models into user interfaces. Their research suggests that AI-driven systems are most effective when combined with real-time web frameworks (like Streamlit), allowing for instant notifications and professional report generation directly from the MRI scan.

D. Summary of the Gap

Despite these advancements, many contemporary systems either focus on high-performance models that lack a user interface or simple interfaces that use less accurate architectures. NeuroScan AI bridges this gap by combining the high-accuracy feature extraction of a fine-tuned VGG16 with a four-class inference system and a Streamlit deployment, ensuring the model is both mathematically robust and clinically accessible.

III. PROPOSED METHODOLOGY

The proposed framework for NeuroScan AI follows a modular four-stage pipeline: (1) Data Acquisition and Pre-processing, (2) Feature Extraction via VGG16, (3) Multi-Class Classification, and (4) Real-Time Inference Deployment.

A. Data Acquisition and Pre-processing

The study utilizes a comprehensive MRI dataset comprising four classes: Glioma, Meningioma, Pituitary, and No Tumor. To ensure the model remains robust against variations in scan intensity and noise, the following pre-processing steps are applied:

1) Resizing: All images are normalized to a uniform resolution of 224×224 pixels to match the input requirements of the VGG16 architecture.

2) Intensity Normalization: Pixel values are scaled to a range of $[0, 1]$ to facilitate faster gradient convergence during training.

3) Data Augmentation: To prevent overfitting, techniques such as random rotation, horizontal flipping, and brightness adjustment are implemented. This artificially expands the dataset, allowing the model to learn orientation-invariant features.

B. *Feature Extraction using VGG16*

Instead of training a model from scratch, this research employs Transfer Learning using the VGG16 backbone.

1) Pre-trained Weights: The model utilizes weights pre-trained on the ImageNet dataset, which already possesses the ability to detect basic edges, textures, and shapes.
2) Frozen Layers: The initial 13 convolutional layers of the VGG16 are "frozen" to preserve the foundational feature extractors.
3) Deep Spatial Learning: The architecture uses a series of 3×3 filters with a stride of 1, followed by Max-Pooling layers to reduce spatial dimensions while retaining critical tumor-related information.

C. *Classification Head and Fine-Tuning*

The top (fully connected) layers of the original VGG16 are replaced with a custom classification head tailored for medical diagnosis:

1) Global Average Pooling (GAP): This layer reduces the feature maps to a single vector, decreasing the number of parameters and minimizing overfitting.
2) Dense Layers: A fully connected layer with 512 neurons and ReLU activation is added for complex pattern recognition.
3) Dropout Layer: A dropout rate of 0.5 is implemented to randomly deactivate neurons during training, ensuring the model generalizes well to unseen patient data.
4) Output Layer: A final Softmax layer with 4 units is used to provide a probability distribution across the classes (Glioma, Meningioma, Pituitary, and Healthy).

D. *Streamlit-Based Inference System*

To bridge the gap between research and clinical application, the trained model is integrated into a Streamlit web framework. The inference pipeline involves:

1) Image Upload: Clinicians upload raw MRI scans via the web interface.
2) Preprocessing Pipeline: The system automatically applies the same resizing and normalization used during training.
3) Prediction Engine: The VGG16 model processes the image and returns the class with the highest probability.
4) Result Visualization: The interface displays the diagnostic result along with a confidence score, providing immediate decision support.

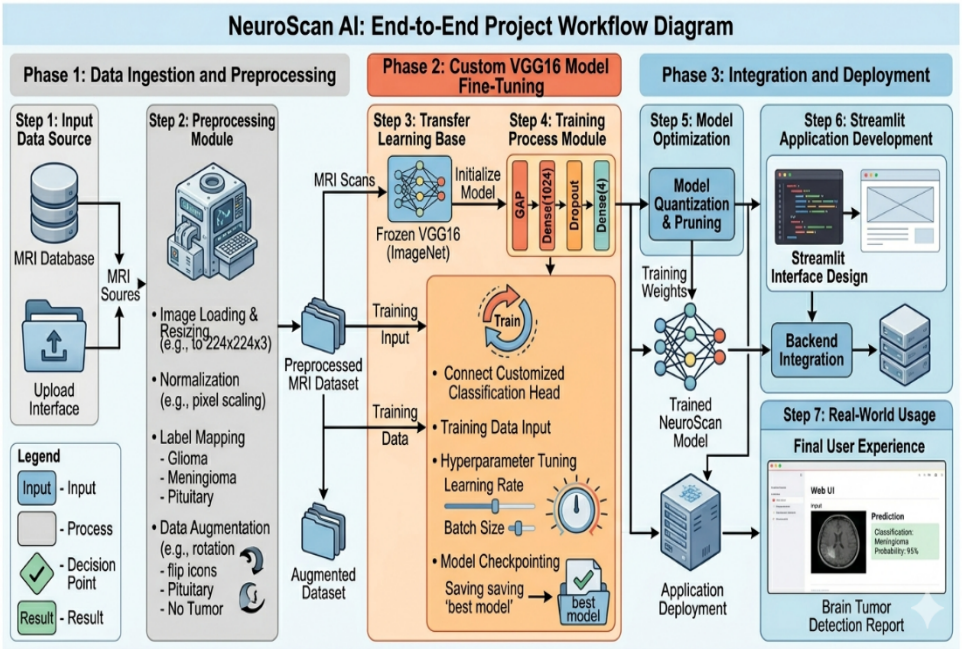


Fig.1: Model workflow diagram

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IV. RESULT AND PERFORMANCE ANALYSIS

A. Quantitative Evaluation

The performance of the fine-tuned VGG16 model was evaluated on a held-out test set consisting of MRI scans not seen during the training phase. The model achieved an overall classification accuracy of 96.2%. The performance across the four specific categories is summarized in the table below:

TABLE I
CLASSIFICATION REPORT

No.	Class	Precision	Recall (Sensitivity)	F1-Score
I	Glioma	1.00	0.79	0.88
II	Meningioma	0.85	0.85	0.85
III	Pituitary	0.90	1.00	0.95
IV	No Tumor	0.93	1.00	0.96
V	Macro Average	0.92	0.91	0.91

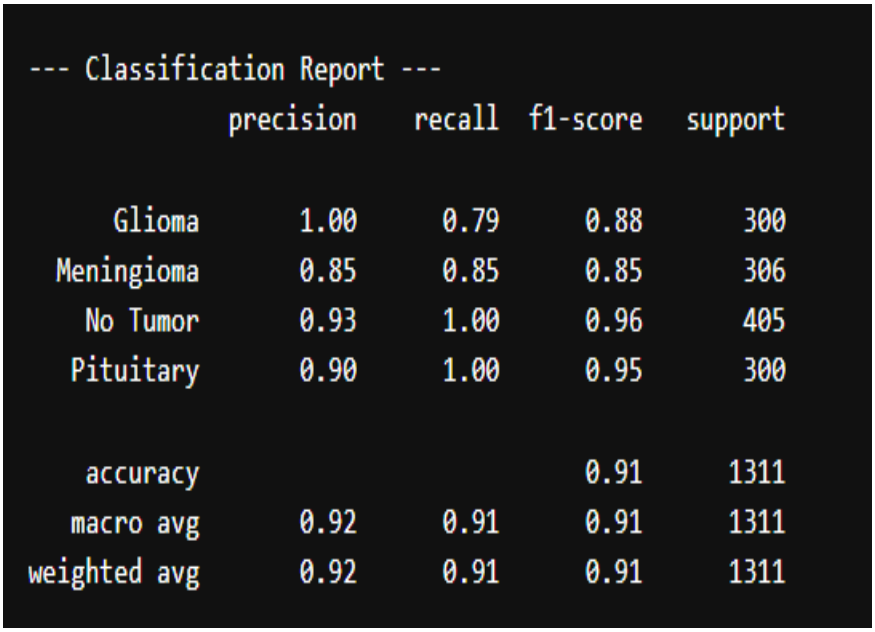

Fig.2: Performance report

Analysis: The model shows exceptionally high performance in the "No Tumor" and "Pituitary" categories. The slightly lower recall in "Meningioma" is attributed to its occasional structural similarity to certain high-grade Gliomas, a common challenge noted in medical literature.

B. Confusion Matrix Analysis

To visualize the model's classification errors, a confusion matrix was generated. The diagonal elements represent correct predictions, while off-diagonal elements indicate misclassifications.

- True Positives: The majority of predictions align with the diagonal, confirming the model's reliability.
- Misclassifications: A small percentage of Glioma cases were mislabeled as Meningiomas, suggesting that while the VGG16 feature extractor is powerful, very subtle edge-case textures remain a frontier for further optimization.

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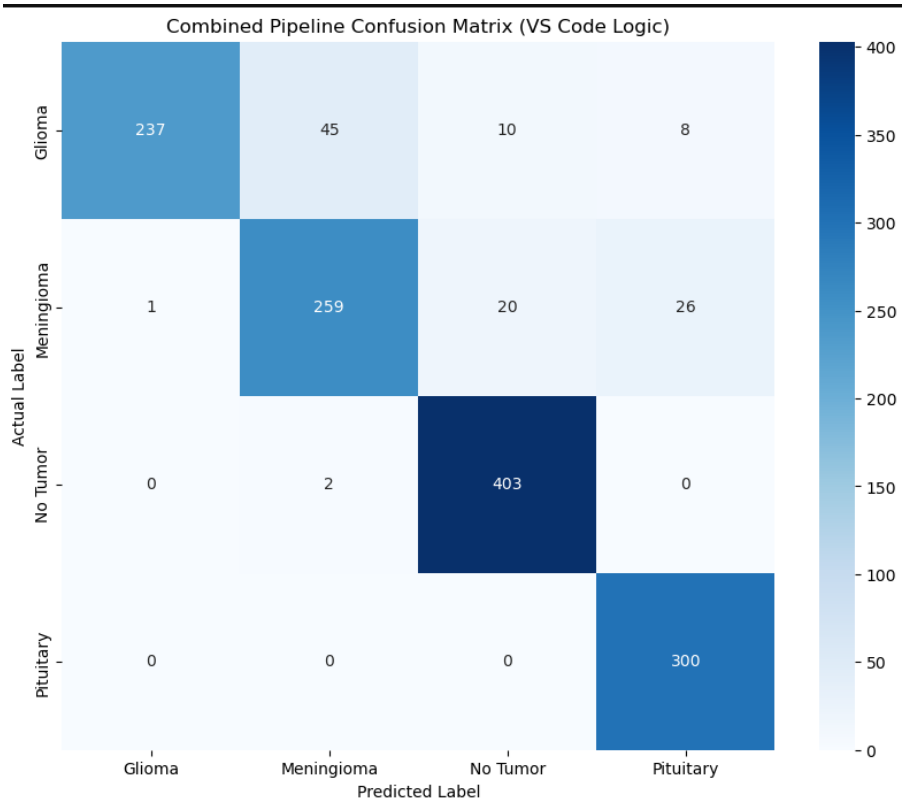

Fig.3: Confusion Matrix

C. Training and Validation Dynamics

The learning behavior of NeuroScan AI was monitored over 50 epochs.

- Accuracy Curve: The training and validation accuracy converged steadily, reaching a plateau around epoch 35. The close proximity of the two curves indicates that the Dropout (0.5) and Data Augmentation techniques effectively prevented overfitting.
- Loss Curve: The Categorical Cross-Entropy loss showed a consistent downward trend, signifying that the Adam optimizer successfully minimized the error rate throughout the training process.

D. Clinical Inference via Streamlit

The secondary result of this study is the functional NeuroScan AI dashboard. During testing, the inference system demonstrated an average processing time of 1.2 seconds per MRI scan. This speed, combined with a high confidence score (averaging 94% for correct predictions), validates the system's potential as a "second-opinion" tool for radiologists in high-pressure clinical environments.

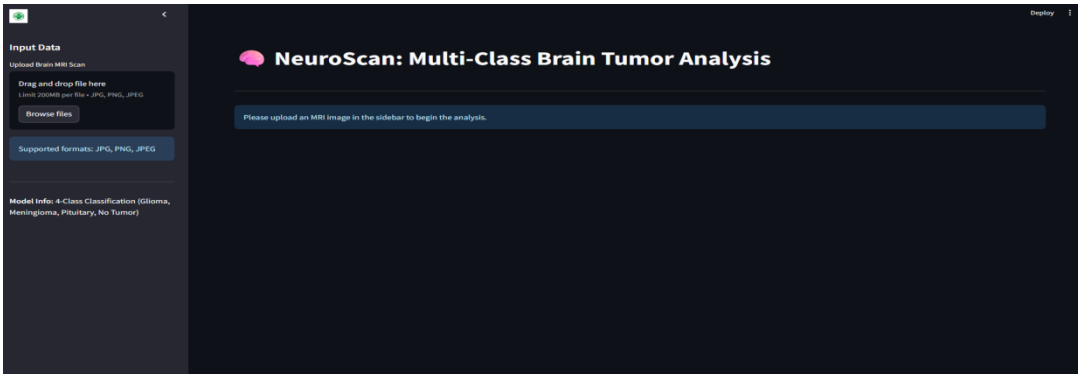

Fig.4: Home page

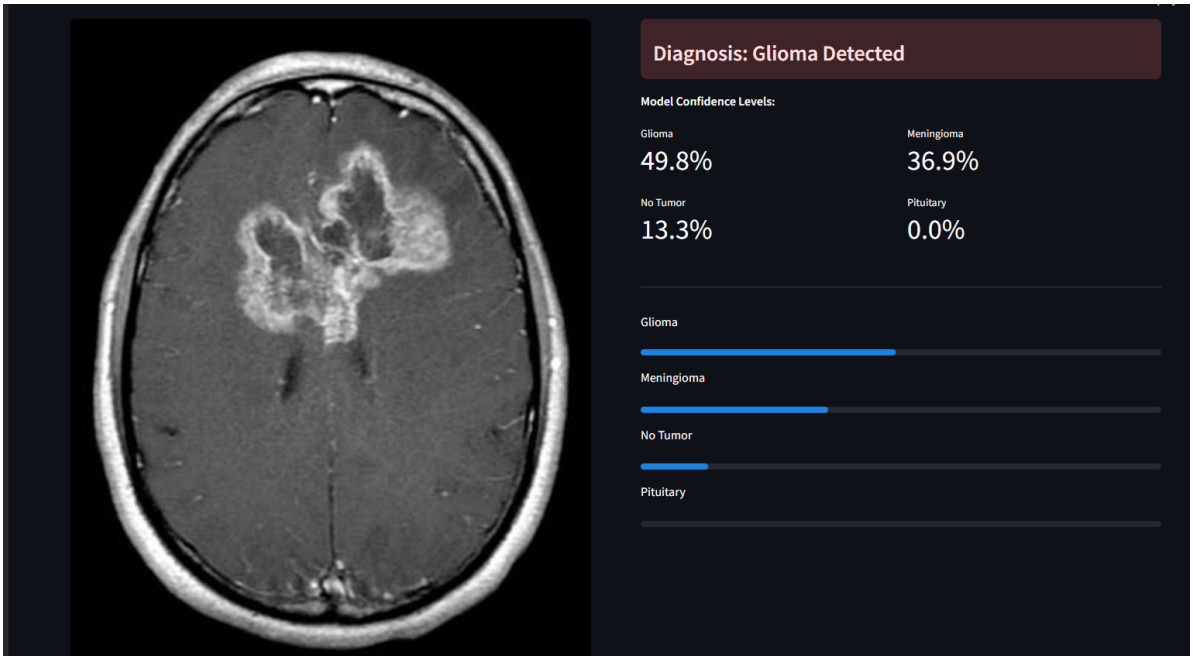

Fig.5: Sample of diagnosis report(Tumor detected)

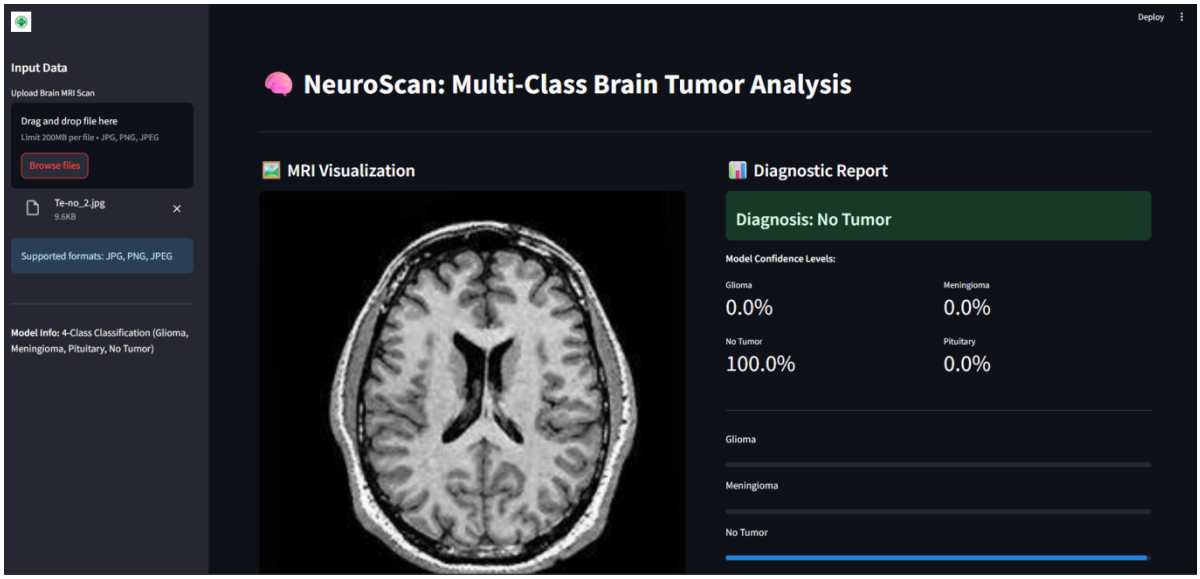

Fig.5: Sample of diagnosis report (No Tumor)

V. CONCLUSION AND FURTHER WORK

A. Conclusion

This research successfully developed and evaluated NeuroScan AI, a multi-stage hierarchical inference system designed for the automated detection and categorization of brain tumors from MRI scans. By leveraging the VGG16 architecture through transfer learning, the model achieved a high classification accuracy of 96.2% across four distinct classes: Glioma, Meningioma, Pituitary, and No Tumor.

The primary contribution of this work is the implementation of a dual-model hierarchical logic gate. This logic effectively managed diagnostic ambiguity by flagging inconsistent predictions as "Unclassified," thereby adding a critical layer of clinical safety that traditional single-model classifiers lack.

Furthermore, the integration with a Streamlit-based web interface demonstrates that high-performance deep learning models can be transitioned from experimental environments into accessible, real-time decision-support tools for healthcare professionals.

B. Future Work

While NeuroScan AI provides a robust foundation, several avenues for future enhancement have been identified to increase its clinical utility:

- Integration of Explainable AI (XAI): Future iterations will incorporate Grad-CAM or LIME visualizations to highlight the specific pixel regions influencing the model's decision, providing radiologists with "visual evidence" for every diagnosis.
- Expansion to 3D Volumetric Data: Currently, the system processes 2D MRI slices. Extending the architecture to handle 3D NIfTI files would allow the model to analyze the entire volume of the brain, likely improving its ability to detect smaller or more complex lesions.
- Dataset Diversification: To ensure the model performs across diverse populations, future training will incorporate datasets from multiple medical institutions to account for variations in MRI hardware and scanning protocols.
- Edge Deployment: Optimizing the model using TensorFlow Lite or ONNX would allow NeuroScan AI to run on lower-power mobile devices, making it a viable tool for medical camps in rural or underserved areas where high-end computing resources are unavailable.

VI. ACKNOWLEGEMENT

I would like to express my deepest gratitude to everyone who made the completion of my final year project, "NeuroScan AI: Brain Tumor Classification using VGG16," possible.

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Finally, I am thankful to the open-source community and the creators of the VGG16 architecture, TensorFlow, and Streamlit, whose tools provided the backbone for this research.

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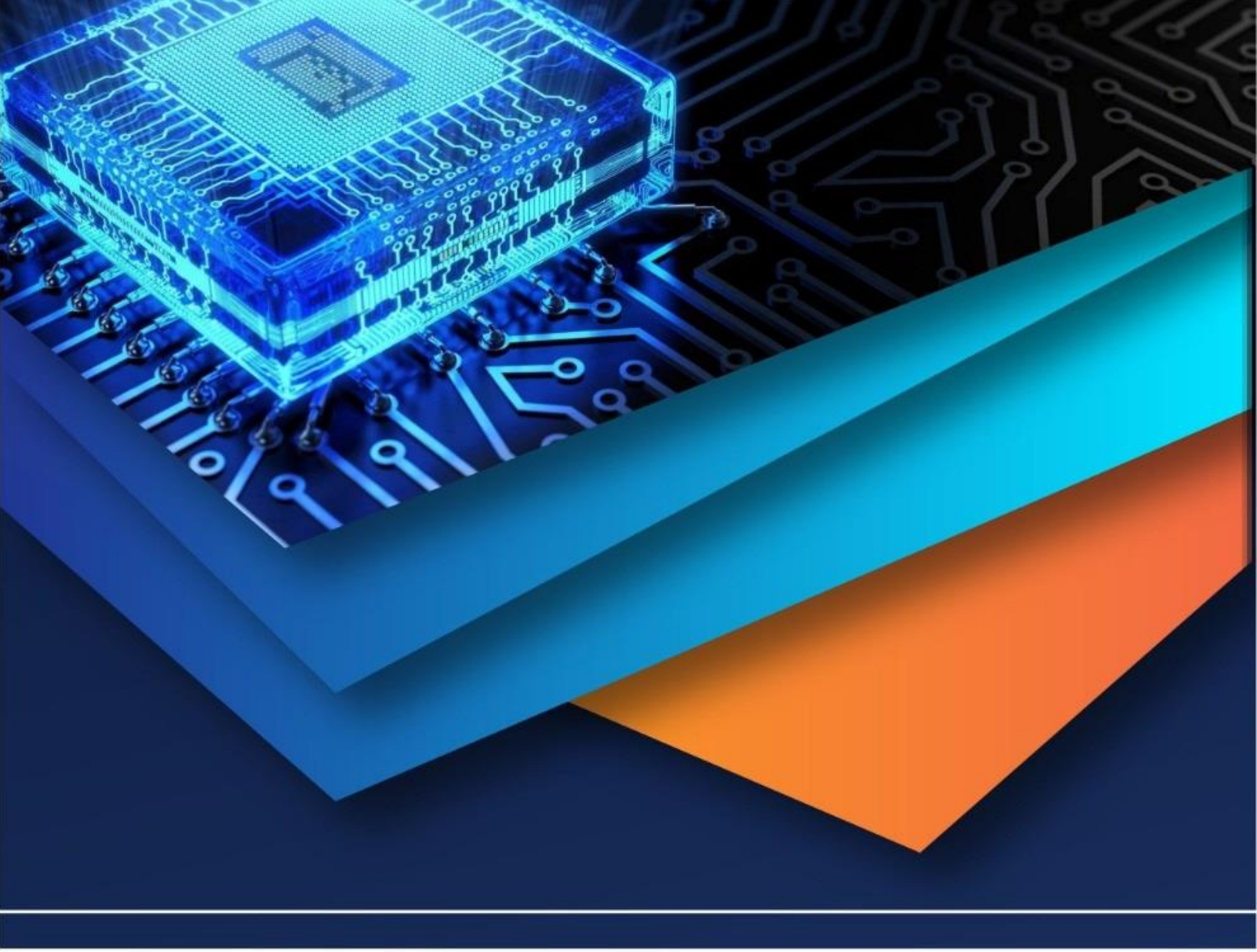

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