

# Brain Tumor Classification Project Report

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ARTIFICIAL INTELLIGENCE  
BASICS

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[Project Github Link](#)

## Introduction

In this project we focused on the classification of brain tumors using deep learning models. What we deal with are categorized into four classes: glioma, meningioma, pituitary and no tumor.

## Dataset

The dataset consists of MRI brain scans collected. We used the publically available [Kaggle Brain Tumor Classification \(MRI\) Dataset](#).

The images were preprocessed and resized to 150×150 pixels. The dataset is divided into training and testing sets with the following distribution:

### **Training Samples per class:**

- glioma: 1321
- meningioma: 1339
- pituitary: 1595
- no-tumor: 1457

### **Testing Samples per class:**

- glioma: 300
- meningioma: 306
- pituitary: 405
- no-tumor: 300

## Custom CNN Model

### **Training Parameters**

- Input Shape: 150x150x3 (RGB image)
- Optimizer: Adam
- Loss Function: Categorical Crossentropy
- Batch Size: 32
- Number of Epochs: 15 (with early stopping, patience=3)
- Callbacks: EarlyStopping (Helps us prevent overfitting, particularly important in medical imaging.)

# Architecture Details

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 148, 148, 32)	896
batch_normalization (BatchNormalization)	(None, 148, 148, 32)	128
max_pooling2d (MaxPooling2D)	(None, 74, 74, 32)	0
dropout (Dropout)	(None, 74, 74, 32)	0
conv2d_1 (Conv2D)	(None, 72, 72, 64)	18,496
batch_normalization_1 (BatchNormalization)	(None, 72, 72, 64)	256
max_pooling2d_1 (MaxPooling2D)	(None, 36, 36, 64)	0
dropout_1 (Dropout)	(None, 36, 36, 64)	0
conv2d_2 (Conv2D)	(None, 34, 34, 128)	73,856
batch_normalization_2 (BatchNormalization)	(None, 34, 34, 128)	512
max_pooling2d_2 (MaxPooling2D)	(None, 17, 17, 128)	0
dropout_2 (Dropout)	(None, 17, 17, 128)	0
flatten (Flatten)	(None, 36992)	0
dense (Dense)	(None, 128)	4,735,104
dropout_3 (Dropout)	(None, 128)	0
dense_1 (Dense)	(None, 4)	516
Total params: 4,829,764 (18.42 MB)		
Trainable params: 4,829,316 (18.42 MB)		
Non-trainable params: 448 (1.75 KB)		

Summary:

- Conv → Pool → Conv → Pool → Conv → Pool → Flatten → Dense → Dropout → Dense (Output).

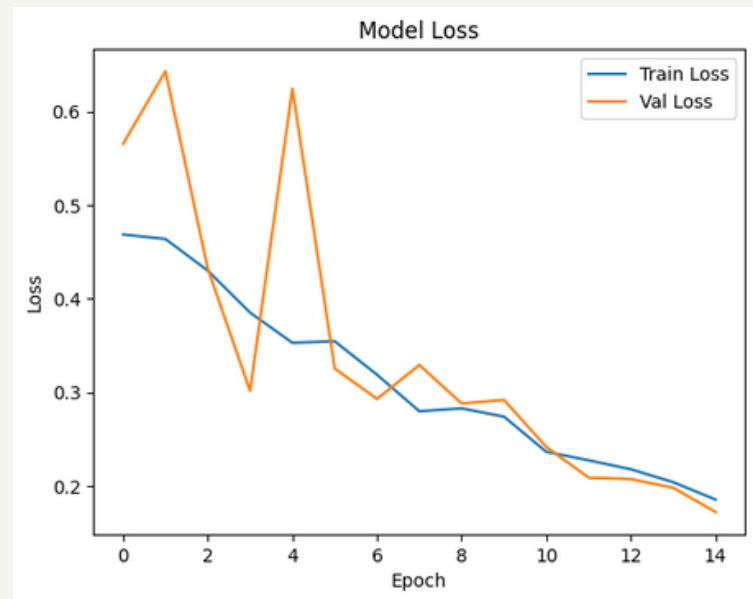
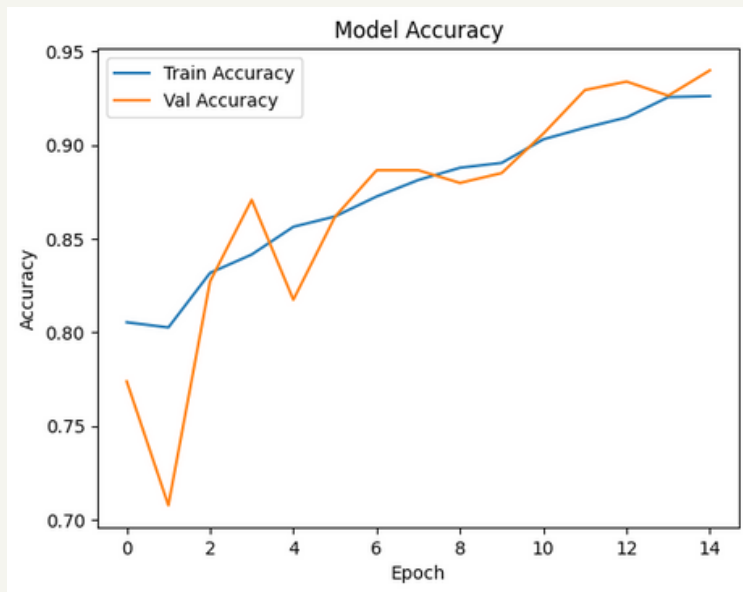
Total Parameters:

- 4,829,764

# Performance Metrics

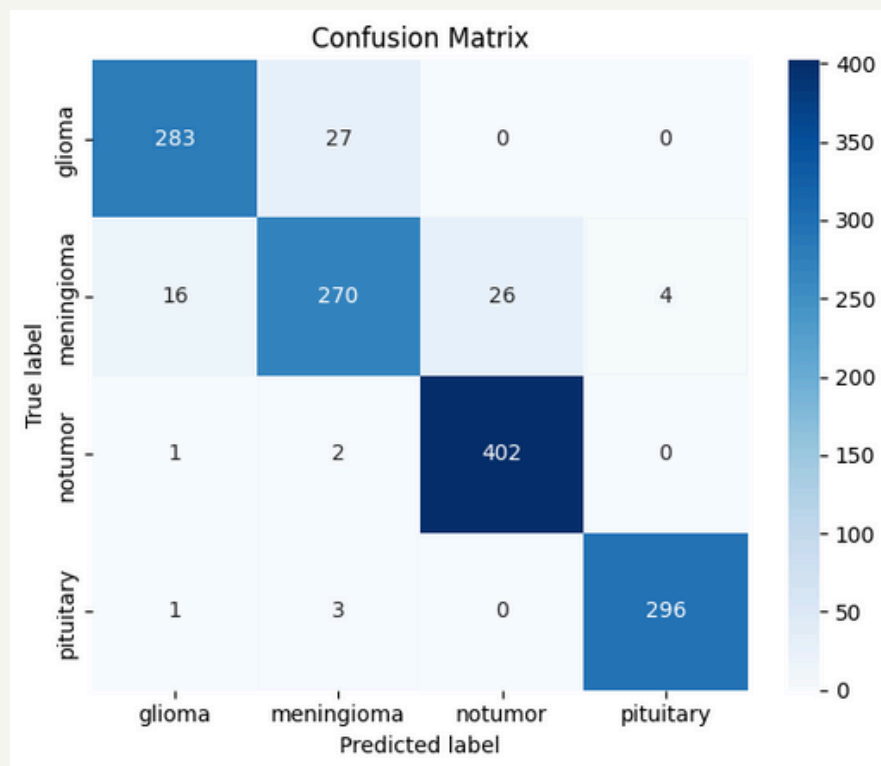
	precision	recall	f1-score	support
glioma	0.9402	0.9129	0.9264	310
meningioma	0.8940	0.8544	0.8738	316
notumor	0.9393	0.9926	0.9652	405
pituitary	0.9867	0.9867	0.9867	300
accuracy			0.9399	1331
macro avg	0.9400	0.9366	0.9380	1331
weighted avg	0.9394	0.9399	0.9393	1331

## ACCURACY vs. ITERATION / LOSS vs. ITERATION



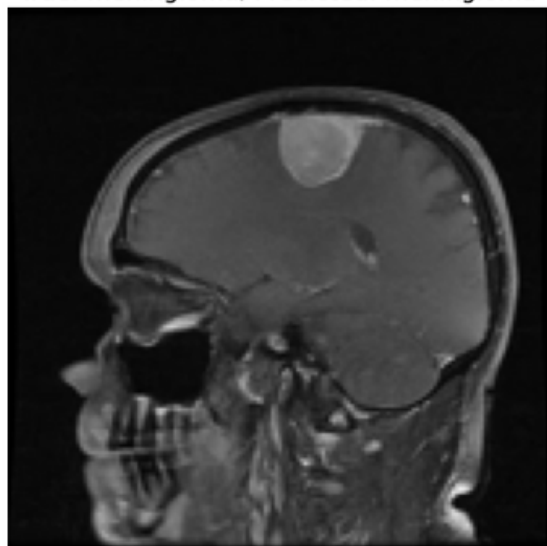
Our customized CNN model was 93% accurate in brain tumor classification after 14 epochs. The training accuracy shows steady improvement while validation accuracy fluctuates, particularly in epochs 2-4. Loss curves also follow this pattern, training loss declining smoothly to 0.18 while validation loss fluctuates. By the final epochs, both metrics join very closely, indicating good balance between fitting training data and generalizing to unseen examples, though occasional plateaus suggest room for optimization.

## CONFUSION MATRIX

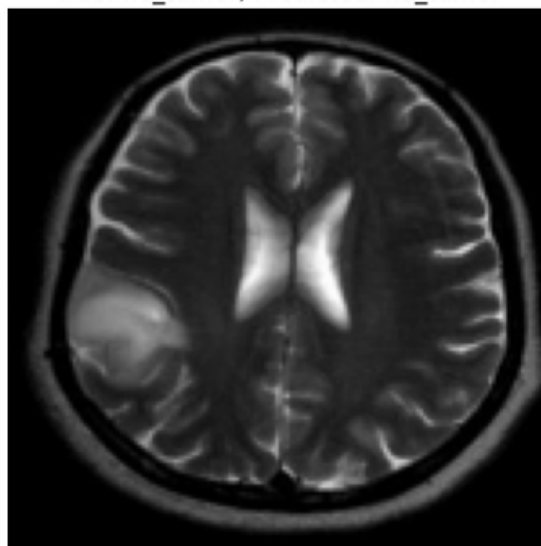


## TEST IMAGE PREDICTIONS

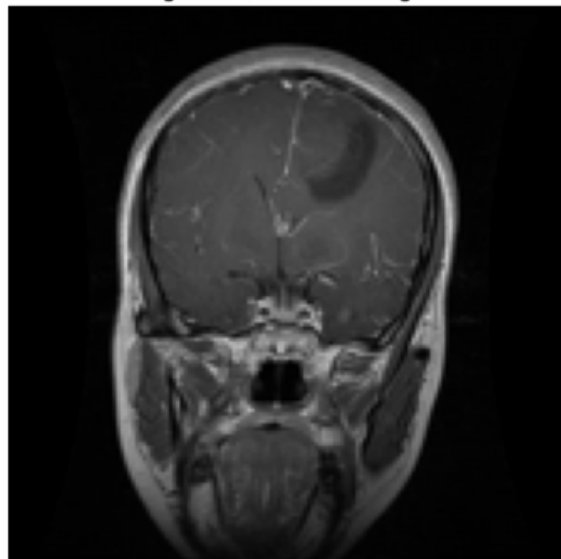
True: meningioma, Predicted: meningioma



True: no\_tumor, Predicted: no\_tumor



True: glioma, Predicted: glioma



# Transfer Learning Model VGG-16

## Architecture Details

Layer (type)	Output Shape	Param #
vgg16 (Functional)	(None, 4, 4, 512)	14,714,688
flatten_1 (Flatten)	(None, 8192)	0
dense_2 (Dense)	(None, 256)	2,097,408
dropout_4 (Dropout)	(None, 256)	0
dense_3 (Dense)	(None, 4)	1,028

Total params: 16,813,124 (64.14 MB)  
Trainable params: 2,098,436 (8.00 MB)  
Non-trainable params: 14,714,688 (56.13 MB)

## Training Parameters

### Training Parameters

#### Phase 1: Initial Training

- Loss Function: Categorical Crossentropy
- Optimizer: Adam
- Epochs: 15
- Batch Size: 32
- EarlyStopping (patience=3)

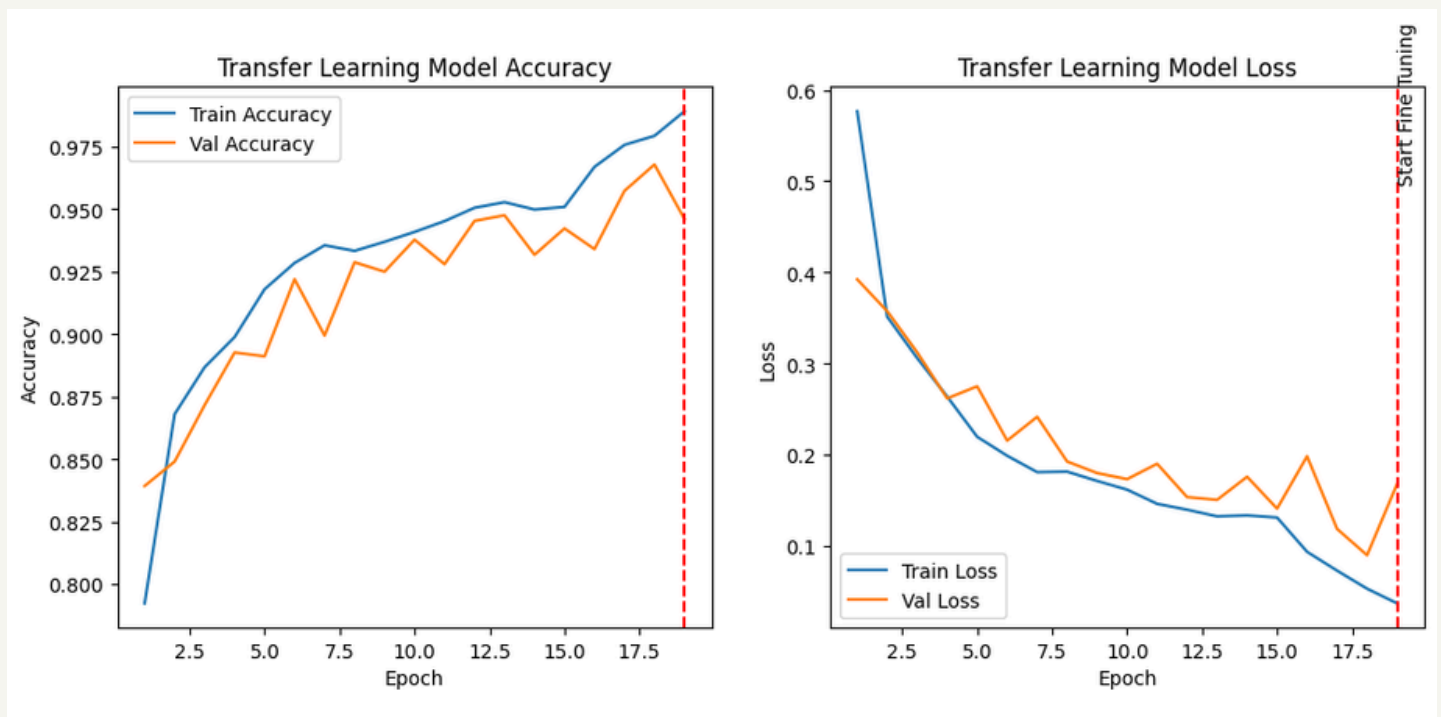
#### Phase 2: Fine-Tuning

- Last 4 VGG16 layers unfrozen
- Learning Rate: 1e-5
- Optimizer: Adam
- Epochs: 4
- Batch Size: 32
- During fine-tuning, the last 4 layers of the VGG16 base model were unfrozen and trained. This allowed the model to adjust high-level feature representations specifically for the brain tumor classification task.

## Performance Metrics

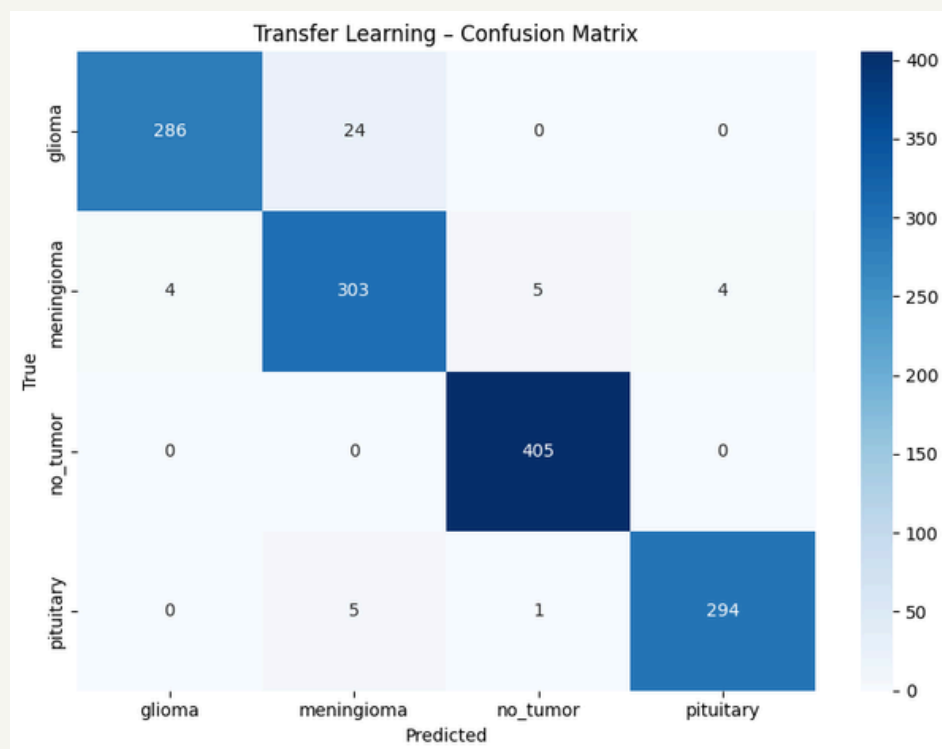
Classification Report:				
	precision	recall	f1-score	support
glioma	0.9862	0.9226	0.9533	310
meningioma	0.9127	0.9589	0.9352	316
no_tumor	0.9854	1.0000	0.9926	405
pituitary	0.9866	0.9800	0.9833	300
accuracy			0.9677	1331
macro avg	0.9677	0.9654	0.9661	1331
weighted avg	0.9686	0.9677	0.9677	1331
Macro Avg Precision: 0.9677				
Macro Avg Recall: 0.9654				
Macro Avg F1-score: 0.9661				
Weighted Avg Precision: 0.9686				
Weighted Avg Recall: 0.9677				
Weighted Avg F1-score: 0.9677				

## ACCURACY vs. ITERATION / LOSS vs. ITERATION



Our transfer learning model, built on the VGG16 architecture, achieved an impressive 96.7% accuracy in brain tumor classification after 19 epochs, including a fine-tuning phase. Initially, the training accuracy rose rapidly, with validation accuracy also improving but showing slight fluctuations. During fine-tuning, both metrics aligned more closely, with validation accuracy peaking around 96%. The training loss steadily declined to below 0.05, while validation loss also dropped significantly, reaching a minimum of 0.08. The close convergence of loss and accuracy curves in later epochs indicates strong generalization, and fine-tuning helped refine the model's performance without overfitting.

## CONFUSION MATRIX



## TEST IMAGE PREDICTIONS

