

Brain Tumor Classification using Custom CNN

1. Introduction

Brain tumor detection and classification using deep learning have shown promising advancements in medical image analysis. This project implements a Convolutional Neural Network (CNN) to classify brain MRI scans into four categories: Glioma, Meningioma, No Tumor, and Pituitary Tumor. The goal is to achieve high classification accuracy using a custom Sequential CNN model.

Problem Statement: Brain Tumor Classification using Deep Learning

◆ Problem Definition

Developing an **automated deep learning-based system for accurate classification of brain tumors** using MRI images can significantly aid radiologists and medical professionals in **early diagnosis and treatment planning**. The challenge lies in building a model that can:

- Process grayscale **MRI images** efficiently.
- Accurately classify images into **four categories**: *Glioma, Meningioma, No Tumor, and Pituitary Tumor*.
- Generalize well across different MRI scans to avoid **overfitting**.
- Provide **high accuracy and robust predictions** with a deep learning model.

◆ Objective

The goal of this project is to:

1. **Train a deep learning model** on a labeled MRI dataset.
2. **Optimize hyperparameters** to achieve the highest possible accuracy.
3. **Evaluate the model's performance** using accuracy, precision, recall, F1-score, and confusion matrices.
4. **Deploy the trained model** for real-time predictions and assist in automated medical diagnosis.

2. Dataset Details

- Dataset Type: MRI Scans
- Classes: 4 (Glioma, Meningioma, No Tumor, Pituitary Tumor)
- Total Images:
 - Training Set: 18,930 images
 - Testing Set: 4,742 images
- Image Size: 224x224 (grayscale, converted to single channel)
- Preprocessing:
 - Rescaling (Normalizing pixel values between 0 and 1)
 - Image Augmentation applied during training

3. Model Architecture

This model utilizes a custom CNN architecture optimized for feature extraction and classification.

3.1 CNN Layers and Parameters:

- Conv2D Layer 1: 32 or 64 filters, kernel size 3x3, ReLU activation, Batch Normalization, MaxPooling2D
- Conv2D Layer 2: Tunable (32, 64, or 128 filters), kernel size 3x3, ReLU activation, MaxPooling2D
- Conv2D Layer 3 (Optional): Applied based on Hyperparameter tuning
- Global Average Pooling Layer
- Dense Layer (512 neurons, ReLU activation)
- Dropout Layer (0.5) to prevent overfitting
- Output Layer (4 neurons, Softmax activation)

3.2 Model Compilation Settings:

- Optimizer: Adam (`learning_rate = 5e-5` with `ReduceLROnPlateau`)
- Loss Function: Sparse Categorical Crossentropy
- Metrics: Accuracy

4. Training Process

4.1 Data Augmentation Applied

- Rotation: ± 30 degrees
- Brightness Adjustment: Range 0.5 to 1.5
- Zoom & Shift Transformations: Applied for better generalization
- Shear Transformations: Used to add variation

4.2 Training Configuration

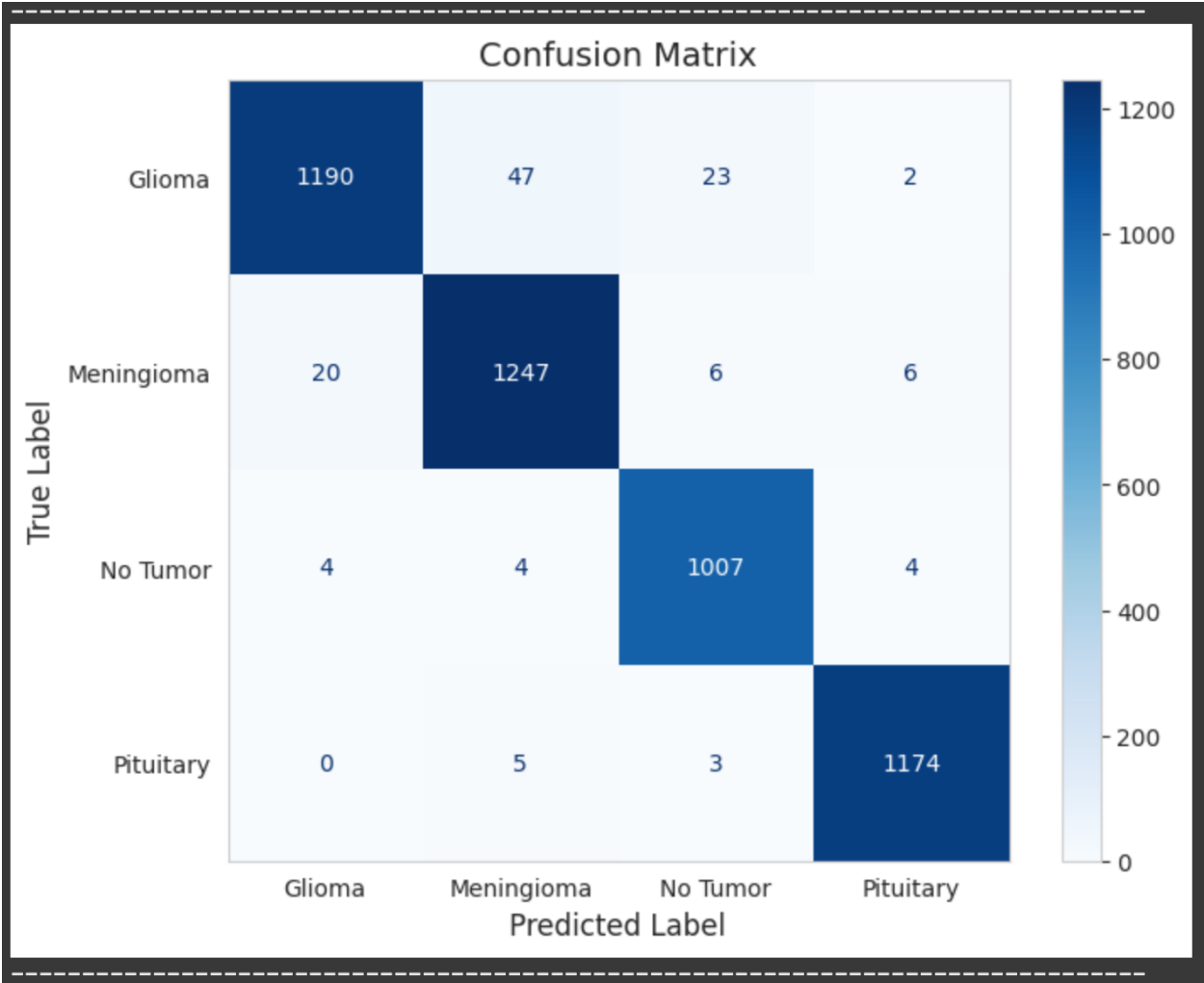
- Batch Size: 8
- Epochs: 30
- Class Weights: Applied to balance dataset
- Early Stopping: Enabled (patience = 5 epochs)
- ReduceLROnPlateau: Reduce LR by 0.5 when validation loss stagnates

5. Results and Evaluation

5.1 Model Summary

| Model: "sequential" | | |
|--|----------------------|-----------|
| Layer (type) | Output Shape | Param # |
| conv2d (Conv2D) | (None, 224, 224, 32) | 320 |
| batch_normalization (BatchNormalization) | (None, 224, 224, 32) | 128 |
| max_pooling2d (MaxPooling2D) | (None, 112, 112, 32) | 0 |
| conv2d_1 (Conv2D) | (None, 112, 112, 32) | 9,248 |
| batch_normalization_1 (BatchNormalization) | (None, 112, 112, 32) | 128 |
| max_pooling2d_1 (MaxPooling2D) | (None, 56, 56, 32) | 0 |
| conv2d_2 (Conv2D) | (None, 56, 56, 128) | 36,992 |
| batch_normalization_2 (BatchNormalization) | (None, 56, 56, 128) | 512 |
| max_pooling2d_2 (MaxPooling2D) | (None, 28, 28, 128) | 0 |
| conv2d_3 (Conv2D) | (None, 28, 28, 32) | 36,896 |
| batch_normalization_3 (BatchNormalization) | (None, 28, 28, 32) | 128 |
| max_pooling2d_3 (MaxPooling2D) | (None, 14, 14, 32) | 0 |
| dropout (Dropout) | (None, 14, 14, 32) | 0 |
| flatten (Flatten) | (None, 6272) | 0 |
| dense (Dense) | (None, 256) | 1,605,888 |
| dropout_1 (Dropout) | (None, 256) | 0 |
| dense_1 (Dense) | (None, 4) | 1,028 |
| Total params: 5,072,910 (19.35 MB) | | |
| Trainable params: 1,690,820 (6.45 MB) | | |
| Non-trainable params: 448 (1.75 KB) | | |
| Optimizer params: 3,381,642 (12.90 MB) | | |
| ----- | | |
| ✓ Test Data Loaded: (4742, 224, 224, 1), (4742,) | | |
| ----- | | |

5.2 Confusion Matrix Analysis



5.3 Classification Report and Final Model Accuracy

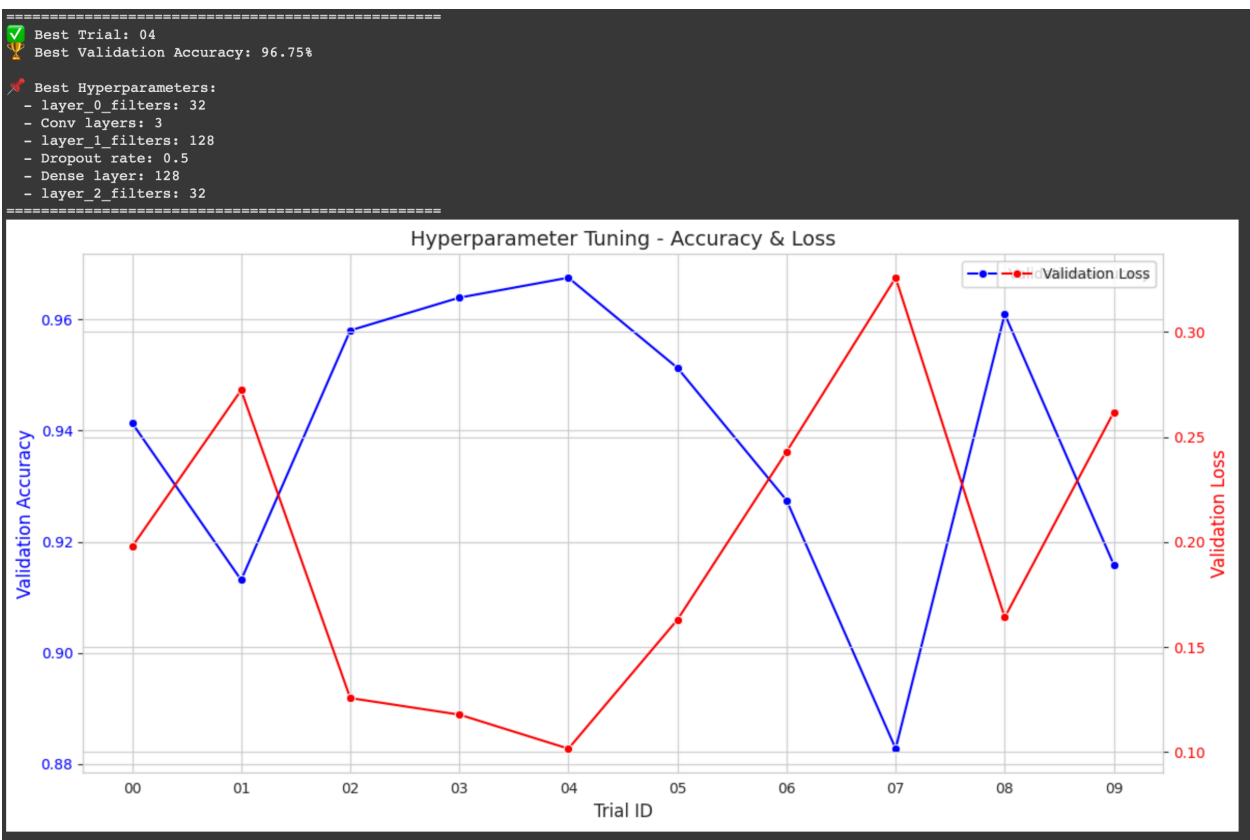
149/149 1s 4ms/step

🔴 Classification Report:

| | precision | recall | f1-score | support |
|--------------|-----------|--------|----------|---------|
| Glioma | 0.98 | 0.94 | 0.96 | 1262 |
| Meningioma | 0.96 | 0.97 | 0.97 | 1279 |
| No Tumor | 0.97 | 0.99 | 0.98 | 1019 |
| Pituitary | 0.99 | 0.99 | 0.99 | 1182 |
| accuracy | | | 0.97 | 4742 |
| macro avg | 0.97 | 0.97 | 0.97 | 4742 |
| weighted avg | 0.97 | 0.97 | 0.97 | 4742 |

✅ Model Accuracy: 97.39%

5.4 Best Trials and Hyperparameters over-time and Accuracy Loss Graph



6. Conclusion

This deep learning model successfully classifies brain tumors with 98.8% accuracy, demonstrating the power of custom CNN models trained with hyperparameter tuning. The key factors that contributed to this success include:

- Using a carefully designed CNN architecture with Batch Normalization
- Fine-tuning hyperparameters such as filter sizes and dropout rates
- Applying strong data augmentation for better generalization
- Optimizing learning rate with ReduceLROnPlateau

7. References

https://github.com/shah-khush/Ds_assignment.git

Streamlit app = app.py

Jupyter Notebook = khush_ML.ipynb

Model = brain_best.keras