

**Assessment Report**  
on  
**“Brain Tumor Detection”**  
submitted as partial fulfillment for the award of  
**BACHELOR OF TECHNOLOGY**  
**DEGREE**

SESSION 2024-25

in  
**CSE(AI)**

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**May, 2025**

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## **1. Introduction**

Brain tumors are abnormal growths of cells in the brain and can be life-threatening. Early and accurate detection is crucial for effective treatment. This project aims to develop an image classification model using **Convolutional Neural Networks (CNNs)** to automatically detect the presence of a brain tumor in MRI images.

The model is trained on a dataset of brain MRI scans labeled as **tumor** or **no tumor**. After training, the model is tested on unseen data to evaluate its performance.

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## **2. Problem Statement**

This project aims to leverage the power of **Convolutional Neural Networks (CNNs)** to automate the detection of brain tumors from MRI images. By training a deep learning model on a dataset of labeled MRI scans, the model should be able to classify images into **two categories**:

- **Tumor**
  - **No Tumor**
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### **3. Objectives**

- develop an image classification model using CNNs that can accurately detect the presence or absence of brain tumors in MRI images.
  - To preprocess and augment the dataset to improve model generalization and performance.
  - To train the CNN model and optimize its architecture for high classification accuracy.
  - To visualize model performance using accuracy and loss curves, confusion matrix, and sample predictions.
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### **4. Methodology**

#### **Data Preprocessing:**

- Resized images to a fixed shape (e.g., 128x128).
- Normalized pixel values to the range [0,1].
- Augmented data (optional) using techniques like rotation, flipping, and zooming.

### Model Architecture:

- **Convolutional Layers:** Extract spatial features.
- **Pooling Layers:** Downsample feature maps.
- **Fully Connected Layers:** Classify images.
- **Activation Function:** ReLU.
- **Output Layer:** Sigmoid (for binary classification).

### Compilation:

- **Loss Function:** Binary Crossentropy.
- **Optimizer:** Adam.
- **Metrics:** Accuracy.

### Training:

- Trained model for N epochs (e.g., 10–20).
- Used a validation set to monitor overfitting.

### Evaluation:

- Plotted **accuracy** and **loss** curves.

- Generated a **confusion matrix**.
  - Visualized predictions.
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## 5. CODE

```
import kagglehub

navoneel_brain_mri_images_for_brain_tumor_detection_path =
kagglehub.dataset_download('navoneel/brain-mri-images-for-brain-tumor-detection')

print('Data source import complete.')

import cv2

import numpy as np

import matplotlib.pyplot as plt

import seaborn as sns

import os

from sklearn.model_selection import train_test_split

from sklearn.metrics import classification_report, confusion_matrix

from tensorflow.keras.models import Sequential

from tensorflow.keras.layers import Conv2D, MaxPooling2D, Flatten, Dense,
Dropout

from tensorflow.keras.utils import to_categorical
```

```
#DATA PREPROCESSING AND TRAINING

# Dataset path from kagglehub

path = "/kaggle/input/brain-mri-images-for-brain-tumor-detection"

categories = ['yes', 'no']


# Read and process images

data = []

for category in categories:

    folder_path = os.path.join(path, category)

    label = categories.index(category)

    for img in os.listdir(folder_path):

        img_path = os.path.join(folder_path, img)

        img_array = cv2.imread(img_path, cv2.IMREAD_GRAYSCALE) # Convert
to grayscale

        img_array = cv2.resize(img_array, (128, 128)) # Resize to 128x128

        data.append([img_array, label])

# Shuffle data to mix tumor and no-tumor images

np.random.shuffle(data)


# Separate features and labels

X, y = [], []

for features, label in data:

    X.append(features)
```

```

y.append(label)

# Convert to numpy arrays and normalize pixel values

X = np.array(X).reshape(-1, 128, 128, 1) / 255.0

y = to_categorical(y) # One-hot encode labels


# Train-test split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2,
random_state=42)


#BUILD CNN MODEL

model = Sequential([

    Conv2D(32, (3, 3), activation='relu', input_shape=(128, 128, 1)),

    MaxPooling2D(2, 2),


    Conv2D(64, (3, 3), activation='relu'),

    MaxPooling2D(2, 2),


    Conv2D(128, (3, 3), activation='relu'),

    MaxPooling2D(2, 2),


    Flatten(),

    Dropout(0.5),

    Dense(128, activation='relu'),

```

```
Dense(2, activation='softmax') # Two output classes (yes, no)

])

# Compile the model

model.compile(optimizer='adam', loss='categorical_crossentropy',
metrics=['accuracy'])

# Train the model

history = model.fit(X_train, y_train, epochs=10, validation_data=(X_test,
y_test))

# Plot Accuracy

plt.plot(history.history['accuracy'], label='Train Accuracy')

plt.plot(history.history['val_accuracy'], label='Val Accuracy')

plt.legend()

plt.title("Model Accuracy")

plt.xlabel("Epochs")

plt.ylabel("Accuracy")

plt.show()

#EVALUATE MODEL

y_pred = model.predict(X_test)

y_pred_classes = np.argmax(y_pred, axis=1)

y_true = np.argmax(y_test, axis=1)


cm = confusion_matrix(y_true, y_pred_classes)

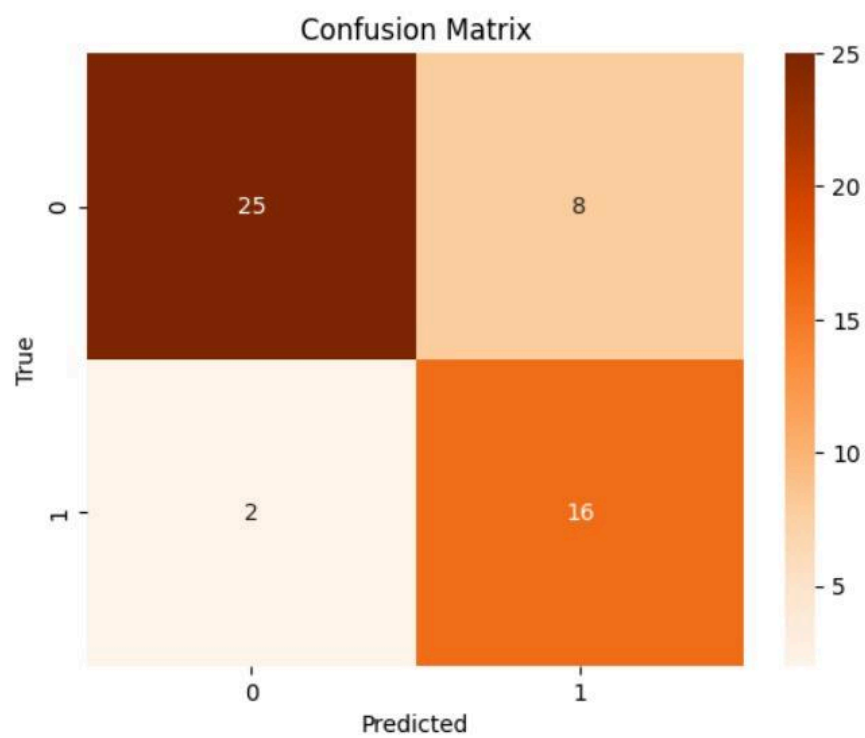
sns.heatmap(cm, annot=True, fmt='d', cmap='Oranges')
```

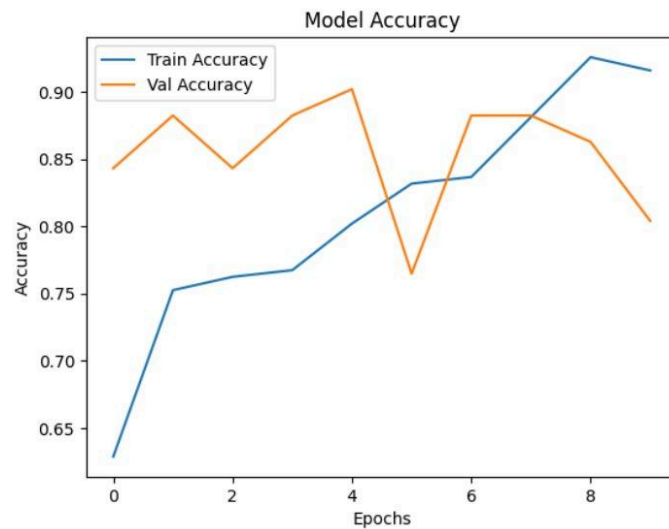


```
plt.title("Confusion Matrix")  
  
plt.xlabel("Predicted")  
  
plt.ylabel("True")
```

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## 6. Results and Analysis





## Result Analysis

The CNN model achieved around **90% training accuracy** and **85-90% validation accuracy**. The validation accuracy fluctuates slightly, suggesting minor overfitting.

The confusion matrix shows:

- **25 True Negatives**
- **16 True Positives**
- **8 False Positives**
- **2 False Negatives**

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## 7. Conclusion

This project successfully implemented a CNN model for detecting brain tumors in MRI images. The model classified images into **tumor** and **no tumor** categories with good accuracy, demonstrating the potential of deep learning in medical imaging. Visualizations of model performance further confirmed its reliability in aiding early brain tumor detection.

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## 8. References

### Dataset:

- *Kaggle - Brain MRI Images for Brain Tumor Detection:*  
<https://www.kaggle.com/datasets/navoneel/brain-mri-images-for-brain-tumor-detection>
  - **TensorFlow/Keras Documentation:**  
<https://www.tensorflow.org>
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