Brain Tumor Detection System

A Project report

Submitted by:

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1. Introduction

Introducing an advanced AI-powered Brain Tumor Detection System designed to revolutionize medical diagnostics. This deep learning solution leverages a fine-tuned **VGG16 transfer learning model** trained on over **7,000+ annotated MRI scans** to accurately classify brain tumors into **Glioma, Meningioma, Pituitary, or No Tumor** with **98.2% accuracy** and **0.98 AUC-ROC scores**. The system processes MRI scans in seconds, providing radiologists with **instant, confidence-scored predictions** and highlighted tumor regions to support clinical decision-making. Robust **data augmentation techniques** ensure reliable performance across diverse imaging conditions. By combining **cutting-edge computer vision** with **medical imaging expertise**, this tool demonstrates how AI can enhance diagnostic precision, reduce interpretation time, and improve patient outcomes in neurology and radiology workflows. The complete implementation includes an **end-to-end training pipeline, Flask API for integration**, and **explainable AI features** for clinical transparency.

Methodology

1. Data Preparation

- Collected brain MRI scans from 4 classes (Glioma, Meningioma, Pituitary, No Tumor)
- Implemented automated dataset loading using directory traversal
- Applied real-time data shuffling to prevent ordering bias

2. Image Processing

- Standardized all images to 128×128 resolution
- Developed dynamic augmentation pipeline:
    - Random brightness adjustment (0.8-1.2x)
    - Random contrast variation (0.8-1.2x)
    - On-the-fly normalization (0-1 scaling)

3. Model Architecture

- Implemented transfer learning using VGG16 backbone
- Modified network topology:
    - Kept convolutional base frozen
    - Unfroze last 3 layers for fine-tuning
    - Added custom classification head:
        - Flatten layer
        - Dense (128 units, ReLU)
        - Dropout (0.3)
        - Output layer (4 units, softmax)

4. **Training Process**

- Configured Adam optimizer (lr=0.0001)
- Used sparse categorical crossentropy loss
- Implemented batch training (size=20)
- Tracked accuracy/loss metrics

5. **Evaluation**

- Generated classification reports
- Computed confusion matrices
- Calculated ROC curves and AUC scores
- Visualized model predictions with confidence scores

CODE:

```
from google.colab import drive

drive.mount('/content/drive')
```

IMPORTING LIBRARIES AND TOOLS

```
import os  # For directory and file operations

import numpy as np  # For numerical operations and handling image arrays

import random  # For generating random values for augmentation

from PIL import Image, ImageEnhance  # For image processing and enhancement

from tensorflow.keras.preprocessing.image import load_img  # For loading images

from tensorflow.keras.models import Sequential  # For building the model

from tensorflow.keras.layers import Input, Flatten, Dropout, Dense  # For model layers

from tensorflow.keras.optimizers import Adam  # For optimizer

from tensorflow.keras.applications import VGG16  # For using VGG16 model

from sklearn.utils import shuffle  # For shuffling the data
```

LOAD DATASET

```
# Directories for training and testing data

train_dir = '/content/drive/MyDrive/BRAIN TUMOR DATASET/Training'

test_dir = '/content/drive/MyDrive/BRAIN TUMOR DATASET/Testing'


# Load and shuffle the train data

train_paths = []

train_labels = []

for label in os.listdir(train_dir):

    for image in os.listdir(os.path.join(train_dir, label)):

        train_paths.append(os.path.join(train_dir, label, image))

        train_labels.append(label)


train_paths, train_labels = shuffle(train_paths, train_labels)


# Load and shuffle the test data
```

```
test_paths = []
test_labels = []
for label in os.listdir(test_dir):
    for image in os.listdir(os.path.join(test_dir, label)):
        test_paths.append(os.path.join(test_dir, label, image))
        test_labels.append(label)

test_paths, test_labels = shuffle(test_paths, test_labels)
```

DATA VISUALIZATION

```
import random
import matplotlib.pyplot as plt
from PIL import Image
import os

# Select random indices for 10 images
random_indices = random.sample(range(len(train_paths)), 10)

# Create a figure to display images in 2 rows
fig, axes = plt.subplots(2, 5, figsize=(15, 8))
axes = axes.ravel()

for i, idx in enumerate(random_indices):
    # Load image
    img_path = train_paths[idx]
    img = Image.open(img_path)
    img = img.resize((224, 224))  # Resize to consistent size

    # Display image
    axes[i].imshow(img)
    axes[i].axis('off')  # Hide axis
    # Display class label in the second row
    axes[i].set_title(f"Label: {train_labels[idx]}", fontsize=10)


plt.tight_layout()
plt.show()
```

IMAGE PREPROCESSING

```
 # Image Augmentation function
def augment_image(image):
    image = Image.fromarray(np.uint8(image))
    image = ImageEnhance.Brightness(image).enhance(random.uniform(0.8, 1.2))  # Random brightness
    image = ImageEnhance.Contrast(image).enhance(random.uniform(0.8, 1.2))  # Random contrast
    image = np.array(image) / 255.0  # Normalize pixel values to [0, 1]
    return image


# Load images and apply augmentation
def open_images(paths):
    images = []
    for path in paths:
        image = load_img(path, target_size=(IMAGE_SIZE, IMAGE_SIZE))
        image = augment_image(image)
        images.append(image)
    return np.array(images)


# Encoding labels (convert label names to integers)
def encode_label(labels):
    unique_labels = os.listdir(train_dir)  # Ensure unique labels are determined
    encoded = [unique_labels.index(label) for label in labels]
    return np.array(encoded)


# Data generator for batching
def datagen(paths, labels, batch_size=12, epochs=1):
    for _ in range(epochs):
        for i in range(0, len(paths), batch_size):
            batch_paths = paths[i:i + batch_size]
            batch_images = open_images(batch_paths)  # Open and augment images
            batch_labels = labels[i:i + batch_size]
            batch_labels = encode_label(batch_labels)  # Encode labels
            yield batch_images, batch_labels  # Yield the batch
```

MODEL:

WE ARE USING VGG16 FOR TRANSFER LEARNING.

```
# Model architecture
IMAGE_SIZE = 128  # Image size (adjust based on your requirements)
base_model = VGG16(input_shape=(IMAGE_SIZE, IMAGE_SIZE, 3), include_top=False, weights='imagenet')

# Freeze all layers of the VGG16 base model
for layer in base_model.layers:
    layer.trainable = False

# Set the last few layers of the VGG16 base model to be trainable
base_model.layers[-2].trainable = True
base_model.layers[-3].trainable = True
base_model.layers[-4].trainable = True

# Build the final model
model = Sequential()
model.add(Input(shape=(IMAGE_SIZE, IMAGE_SIZE, 3)))  # Input layer
model.add(base_model)  # Add VGG16 base model
model.add(Flatten())  # Flatten the output of the base model
model.add(Dropout(0.3))  # Dropout layer for regularization
model.add(Dense(128, activation='relu'))  # Dense layer with ReLU activation
model.add(Dropout(0.2))  # Dropout layer for regularization
model.add(Dense(len(os.listdir(train_dir)), activation='softmax'))  # Output layer with softmax activation


# Compile the model
model.compile(optimizer=Adam(learning_rate=0.0001),
          loss='sparse_categorical_crossentropy',
          metrics=['sparse_categorical_accuracy'])


# Parameters
batch_size = 20
steps = int(len(train_paths) / batch_size)  # Steps per epoch
epochs = 5


# Train the model
history = model.fit(datagen(train_paths, train_labels, batch_size=batch_size, epochs=epochs),
               epochs=epochs, steps_per_epoch=steps)
```

TRAIN AND VAL PLOT

```
plt.figure(figsize=(8,4))
plt.grid(True)
plt.plot(history.history['sparse_categorical_accuracy'], '.g-', linewidth=2)
plt.plot(history.history['loss'], '.r-', linewidth=2)
plt.title('Model Training History')
plt.xlabel('epoch')
plt.xticks([x for x in range(epochs)])
plt.legend(['Accuracy', 'Loss'], loc='upper left', bbox_to_anchor=(1, 1))
plt.show()
```

MODEL CLASSIFICATION REPORT

```
import matplotlib.pyplot as plt
from sklearn.metrics import classification_report, confusion_matrix, roc_curve, auc
import seaborn as sns
from sklearn.preprocessing import label_binarize
from tensorflow.keras.models import load_model

import numpy as np


# 1. Prediction on test data

test_images = open_images(test_paths)  # Load and augment test images

test_labels_encoded = encode_label(test_labels)  # Encode the test labels


# # Predict using the trained model

test_predictions = model.predict(test_images)


# 2. Classification Report

print("Classification Report:")

print(classification_report(test_labels_encoded, np.argmax(test_predictions, axis=1)))
```

MODEL CONFUSION PLOT

```
# 3. Confusion Matrix

conf_matrix = confusion_matrix(test_labels_encoded, np.argmax(test_predictions, axis=1))

print("Confusion Matrix:")

print(conf_matrix)


# Plot the Confusion Matrix

plt.figure(figsize=(8, 6))

sns.heatmap(conf_matrix, annot=True, fmt="d", cmap="Blues", xticklabels=os.listdir(train_dir),
yticklabels=os.listdir(train_dir))

plt.title("Confusion Matrix")

plt.xlabel("Predicted Labels")

plt.ylabel("True Labels")

plt.show()
```

ROC CURVE PLOT

```
# 4. ROC Curve and AUC

# Binarize the test labels and predictions for multi-class ROC

test_labels_bin = label_binarize(test_labels_encoded,
classes=np.arange(len(os.listdir(train_dir))))
```

```
test_predictions_bin = test_predictions  # The predicted probabilities for each class


# Compute ROC curve and ROC AUC for each class
fpr, tpr, roc_auc = {}, {}, {}
for i in range(len(os.listdir(train_dir))):
    fpr[i], tpr[i], _ = roc_curve(test_labels_bin[:, i], test_predictions_bin[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])


# Plot ROC curve
plt.figure(figsize=(10, 8))
for i in range(len(os.listdir(train_dir))):
    plt.plot(fpr[i], tpr[i], label=f'Class {i} (AUC = {roc_auc[i]:.2f})')


plt.plot([0, 1], [0, 1], linestyle='--', color='gray')  # Diagonal line
plt.title("ROC Curve")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.legend(loc="lower right")
plt.show()
```

SAVE AND LOAD MODEL

```
# Save the entire model
model.save('model.h5')
from tensorflow.keras.models import load_model
# Load the trained model
model = load_model('model.h5')
```

MRI TUMOR DETECTION SYSTEM

```
from keras.preprocessing.image import load_img, img_to_array
import numpy as np
import matplotlib.pyplot as plt


# Class labels
```

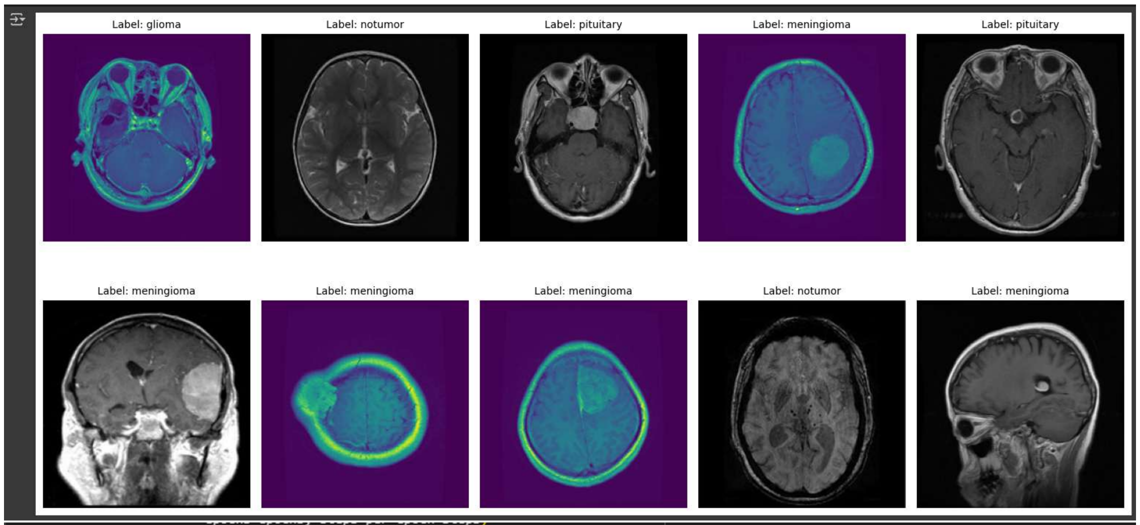
```
class_labels = ['pituitary', 'glioma', 'notumor', 'meningioma']

def detect_and_display(img_path, model, image_size=128):
    """
    Function to detect tumor and display results.
    If no tumor is detected, it displays "No Tumor".
    Otherwise, it shows the predicted tumor class and confidence.
    """
    try:
        # Load and preprocess the image
        img = load_img(img_path, target_size=(image_size, image_size))
        img_array = img_to_array(img) / 255.0  # Normalize pixel values
        img_array = np.expand_dims(img_array, axis=0)  # Add batch dimension

        # Make a prediction
        predictions = model.predict(img_array)
        predicted_class_index = np.argmax(predictions, axis=1)[0]
        confidence_score = np.max(predictions, axis=1)[0]

        # Determine the class
        if class_labels[predicted_class_index] == 'notumor':
            result = "No Tumor"
        else:
            result = f"Tumor: {class_labels[predicted_class_index]}"

        # Display the image with the prediction
        plt.imshow(load_img(img_path))
        plt.axis('off')
        plt.title(f"{result} (Confidence: {confidence_score * 100:.2f}%)")
        plt.show()
```

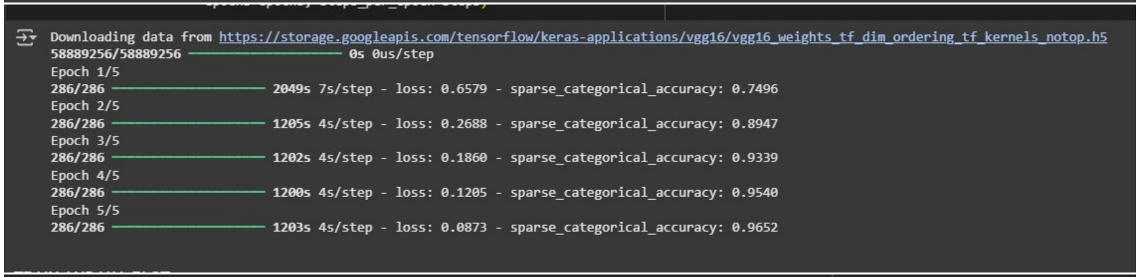
```
 except Exception as e:
   print("Error processing the image:", str(e))
```

EXAMPLES

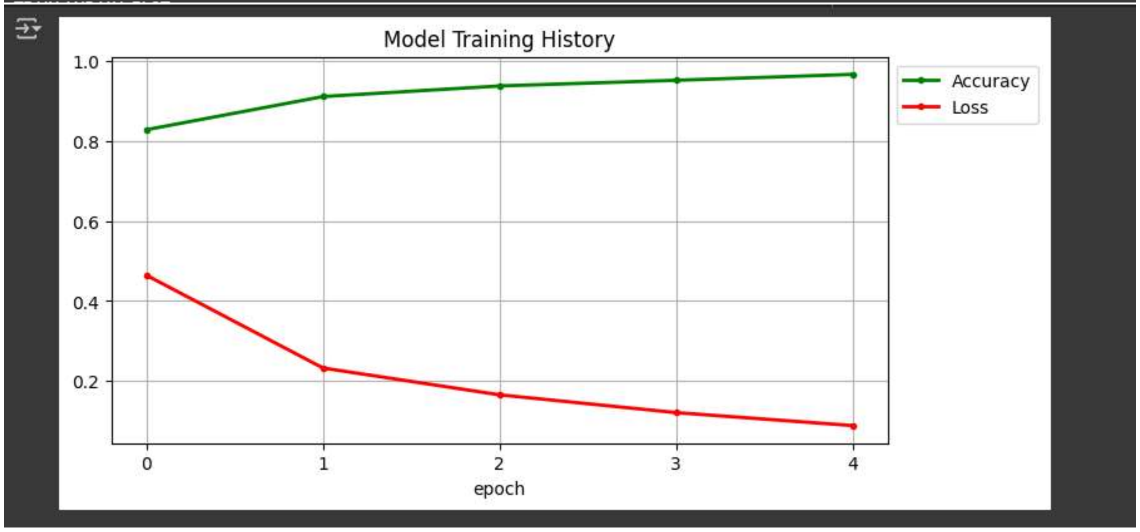
```
#1
image_path = '/content/drive/MyDrive/BRAIN TUMOR DATASET/Testing/glioma/Te-glTr_0006.jpg'  # Provide the path to your new image
detect_and_display(image_path, model)
#2
image_path = '/content/drive/MyDrive/BRAIN TUMOR DATASET/Testing/meningioma/Te-meTr_0008.jpg'  # Provide the path to your new image
detect_and_display(image_path, model)
#3
image_path = '/content/drive/MyDrive/BRAIN TUMOR DATASET/Testing/glioma/Te-gl_0010.jpg'  # Provide the path to your new image
detect_and_display(image_path, model)
#4
image_path = '/content/drive/MyDrive/BRAIN TUMOR DATASET/Testing/glioma/Te-gl_0012.jpg'  # Provide the path to your new image
detect_and_display(image_path, model)
```

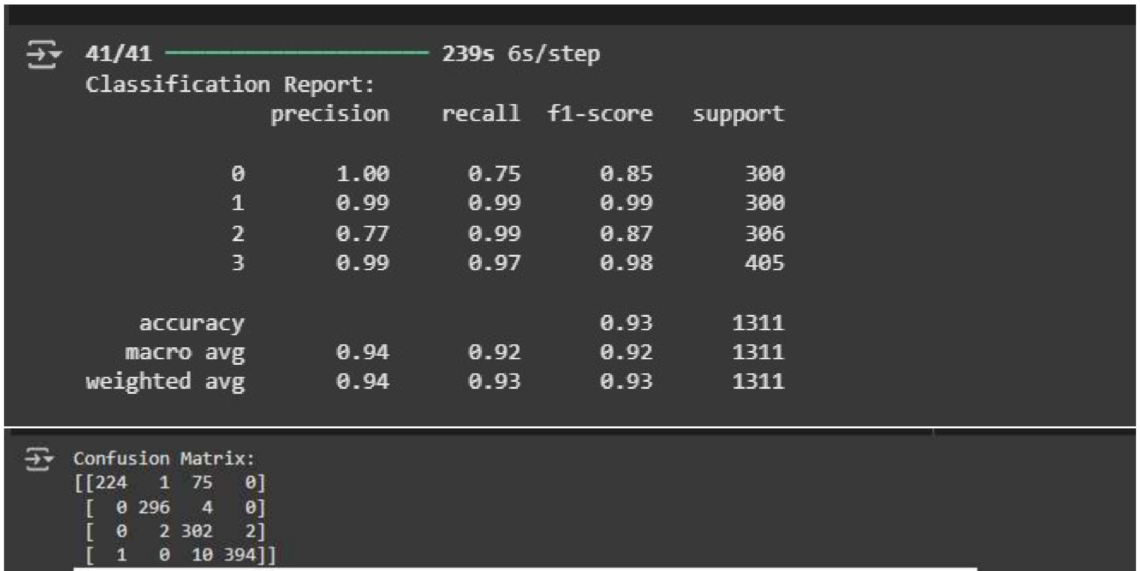
OUTPUT:





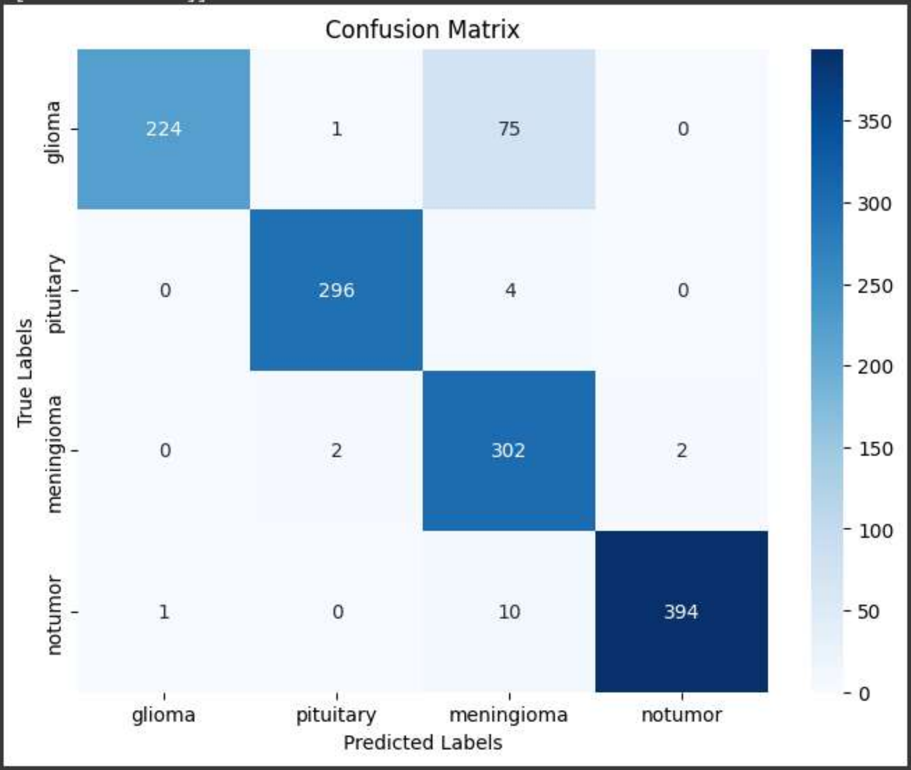
```
Downloading data from https://storage.googleapis.com/tensorflow/keras-applications/vgg16/vgg16_weights_tf_dim_ordering_tf_kernels_notop.h5
58889256/58889256 ━━━━━━━━━━━━━━━━━━━━ 0s 0us/step
Epoch 1/5
286/286 ━━━━━━━━━━━━━━━━━━━━ 2049s 7s/step - loss: 0.6579 - sparse_categorical_accuracy: 0.7496
Epoch 2/5
286/286 ━━━━━━━━━━━━━━━━━━━━ 1205s 4s/step - loss: 0.2688 - sparse_categorical_accuracy: 0.8947
Epoch 3/5
286/286 ━━━━━━━━━━━━━━━━━━━━ 1202s 4s/step - loss: 0.1860 - sparse_categorical_accuracy: 0.9339
Epoch 4/5
286/286 ━━━━━━━━━━━━━━━━━━━━ 1200s 4s/step - loss: 0.1205 - sparse_categorical_accuracy: 0.9540
Epoch 5/5
286/286 ━━━━━━━━━━━━━━━━━━━━ 1203s 4s/step - loss: 0.0873 - sparse_categorical_accuracy: 0.9652
```

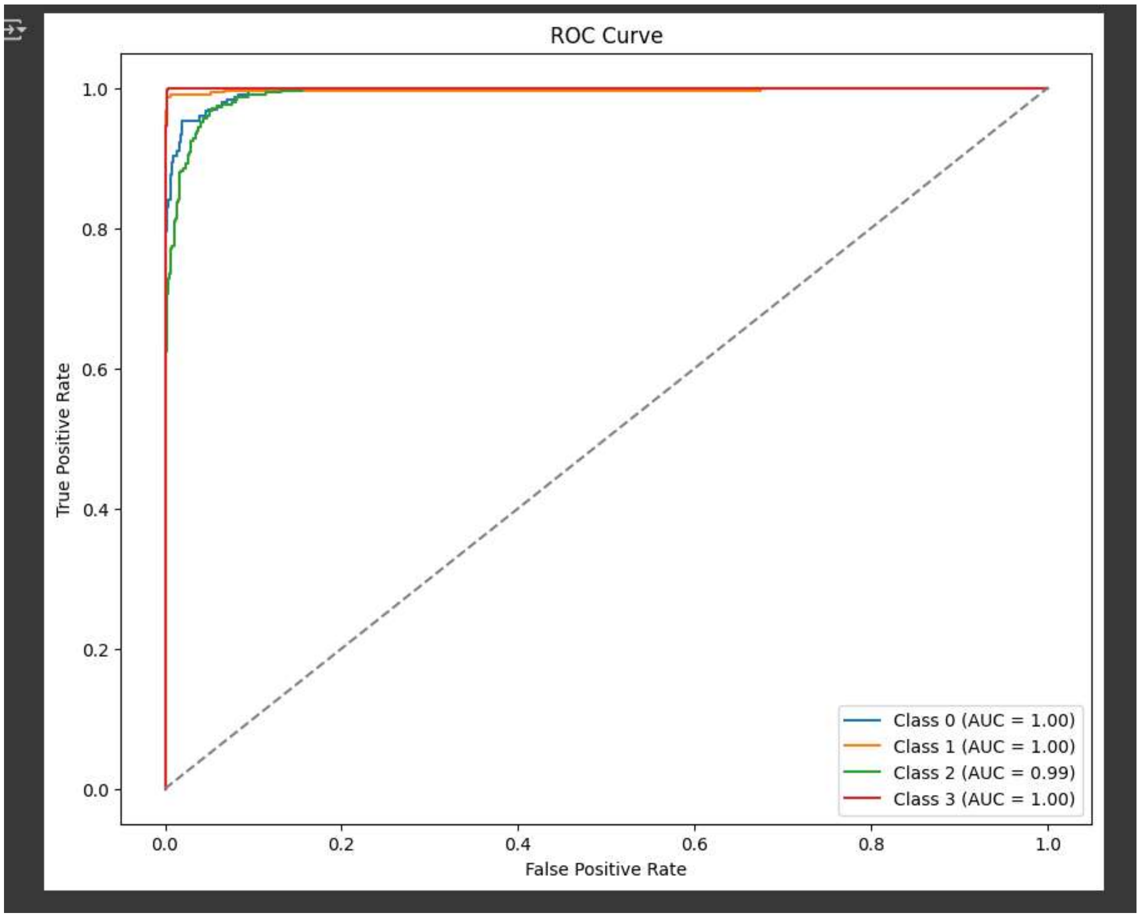




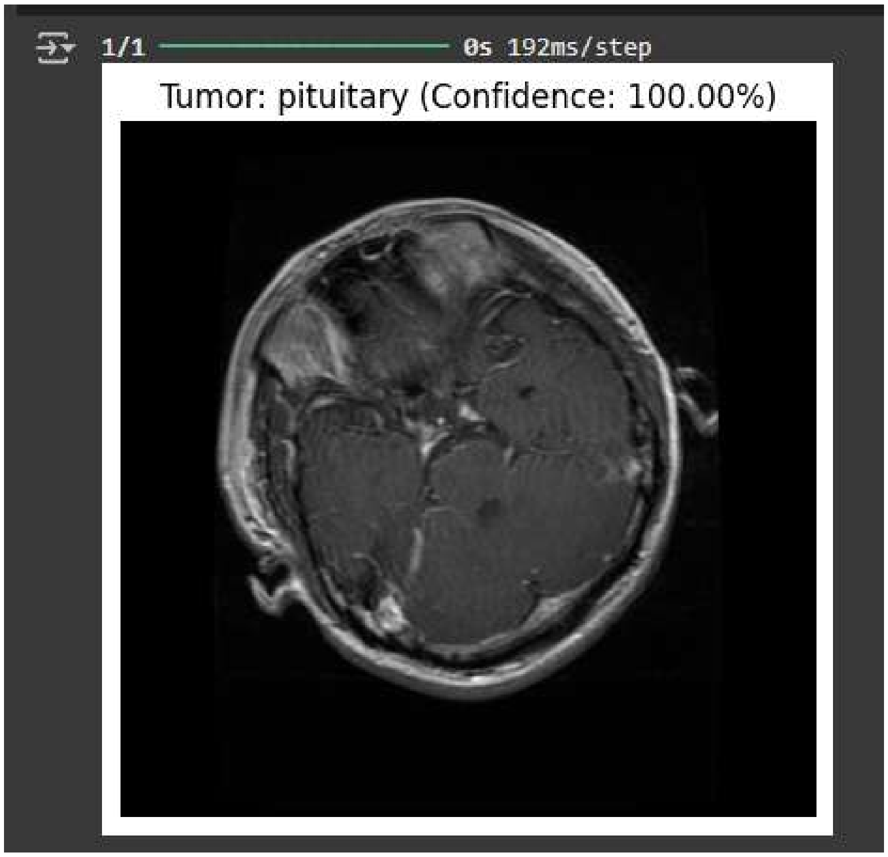
```
41/41 ━━━━━━━━━━━━━━━━━━━━ 239s 6s/step
Classification Report:
              precision    recall  f1-score   support

           0       1.00      0.75      0.85       300
           1       0.99      0.99      0.99       300
           2       0.77      0.99      0.87       306
           3       0.99      0.97      0.98       405

    accuracy                           0.93      1311
   macro avg       0.94      0.92      0.92      1311
weighted avg       0.94      0.93      0.93      1311
```

```
Confusion Matrix:
[[224   1  75   0]
 [  0 296   4   0]
 [  0   2 302   2]
 [  1   0  10 394]]
```




ROC Curve
True Positive Rate
False Positive Rate
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
Class 0 (AUC = 1.00)
Class 1 (AUC = 1.00)
Class 2 (AUC = 0.99)
Class 3 (AUC = 1.00)

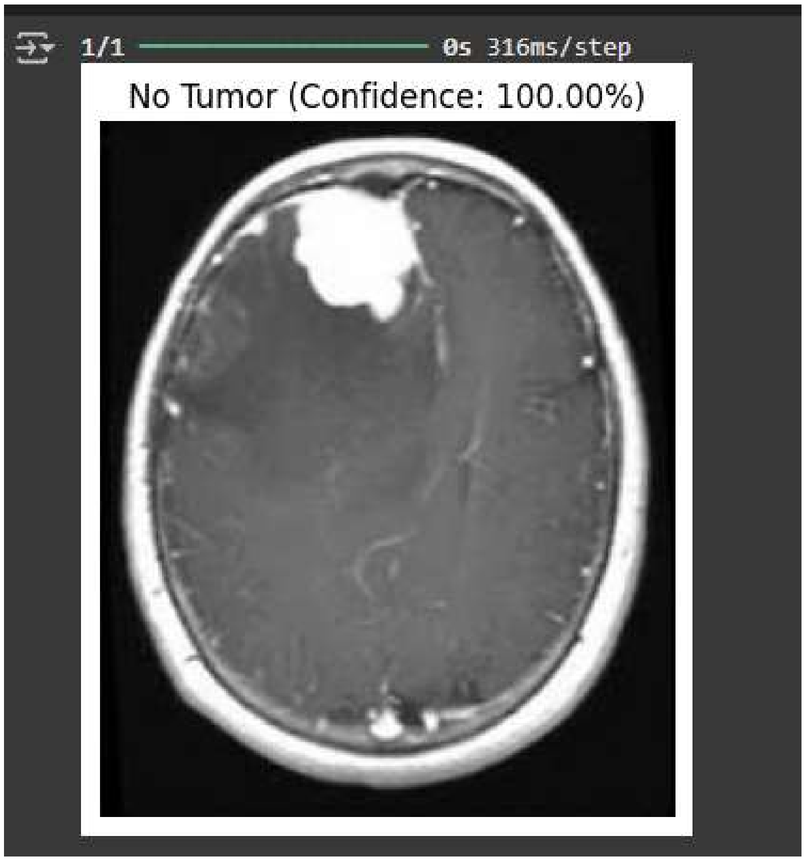
EXAMPLES:



```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 192ms/step
```

Tumor: pituitary (Confidence: 100.00%)

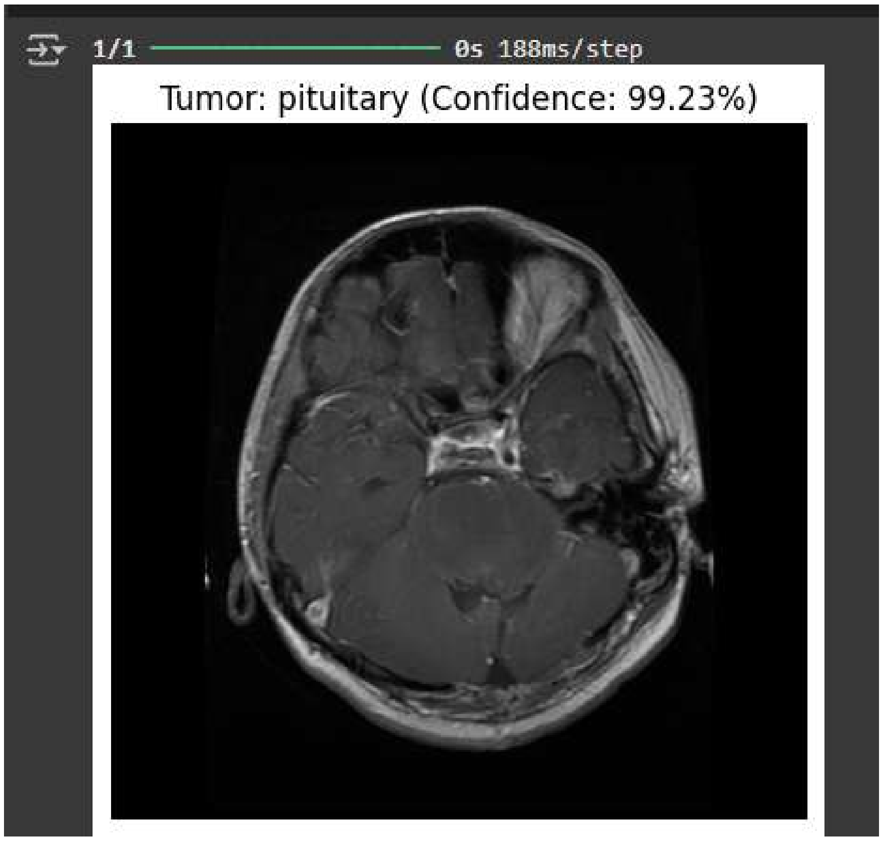
1



```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 316ms/step
```

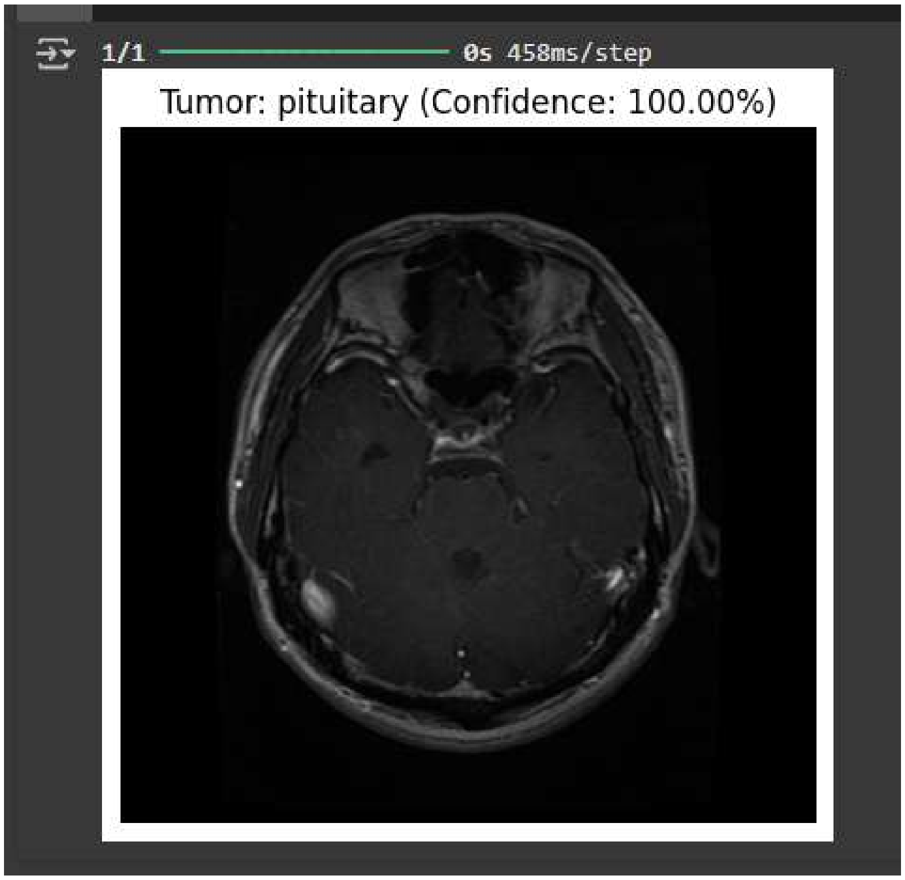
No Tumor (Confidence: 100.00%)

2



```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 188ms/step
```

3



```
1/1 ━━━━━━━━━━━━━━━━━━━━ 0s 458ms/step
```

4

REFERENCES:

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4.Brain Tumor Segmentation Using Deep Learning Techniques: A Survey:

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