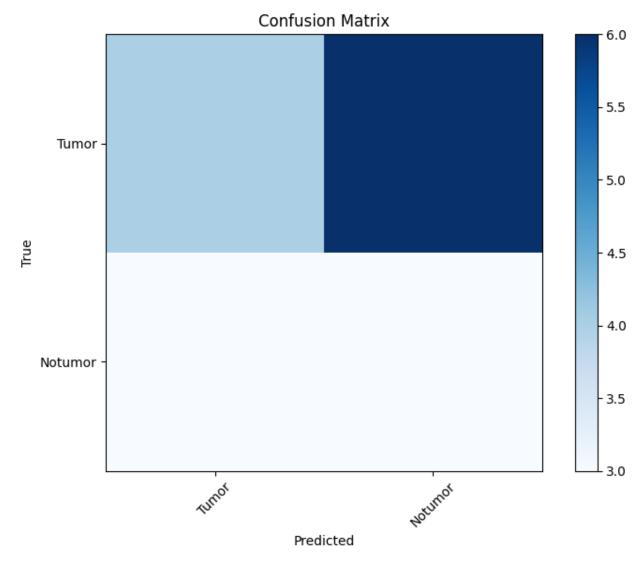
```
import os
import numpy as np
import matplotlib.pyplot as plt
from sklearn.metrics import confusion matrix, classification report
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Conv2D, BatchNormalization,
MaxPooling2D, Dropout, Flatten, Dense
# Define parameters
image size = (128, 128)
batch size = 32
num epochs = 10
# max photos per class = 30
train data dir = '/content/drive/MyDrive/brain tumor/Training'
test data dir = '/content/drive/MyDrive/brain tumor/Testing'
class labels = os.listdir(train data dir)
# Data augmentation for training data
train datagen = ImageDataGenerator(
   rescale=1.0/255,
   shear range=0.2,
    zoom range=0.2,
   horizontal flip=True
# Rescale the pixel values for the test data (no augmentation)
test datagen = ImageDataGenerator(rescale=1.0/255)
# Load training data with a maximum of 30 photos per class
train generator = train datagen.flow from directory(
    train data dir,
   target size=image size,
   batch size=batch size,
    class mode='categorical',
    subset='training',
    shuffle=True,
```

```
seed=42,
    interpolation='nearest'
# Load test data with a maximum of 30 photos per class
test_generator = test_datagen.flow_from directory(
    test data dir,
   target size=image size,
   batch size=batch size,
    class mode='categorical',
    shuffle=True,
   seed=42,
    interpolation='nearest'
# Create the CNN model
model = Sequential()
# Convolutional layer 1
model.add(Conv2D(32, (3, 3), input shape=(image size[0], image size[1],
3)))
model.add(BatchNormalization())
model.add(MaxPooling2D(pool size=(2, 2)))
# Convolutional layer 2
model.add(Conv2D(64, (3, 3)))
model.add(BatchNormalization())
model.add(MaxPooling2D(pool size=(2, 2)))
# Convolutional layer 3
model.add(Conv2D(128, (3, 3)))
model.add(BatchNormalization())
model.add(MaxPooling2D(pool size=(2, 2)))
# Convolutional layer 4
model.add(Conv2D(256, (3, 3)))
model.add(BatchNormalization())
model.add(MaxPooling2D(pool size=(2, 2)))
# Flatten the feature maps
```

```
model.add(Flatten())
# Fully connected layer 1 with 512 nodes
model.add(Dense(512, activation='relu'))
model.add(BatchNormalization())
# Fully connected layer 2 with 256 nodes
model.add(Dense(256, activation='relu'))
model.add(BatchNormalization())
# Output layer with softmax activation for multi-class classification
model.add(Dense(len(class labels), activation='softmax'))
# Compile the model
model.compile(loss='categorical crossentropy',
              optimizer='adam',
              metrics=['accuracy'])
# Train the model
history = model.fit(
    train generator,
    steps per epoch=train generator.samples // batch size,
    epochs=num epochs,
    validation data=test_generator,
    validation steps=test generator.samples // batch size
# Evaluate the model on the test data
test loss, test accuracy = model.evaluate(test generator)
print(f'Test Loss: {test loss:.4f}')
print(f'Test Accuracy: {test accuracy:.4f}')
# model.save("braintumor.h5")
# Get the true labels and predicted labels
true labels = test generator.classes
predictions = model.predict(test generator)
# Calculate the confusion matrix
confusion_mtx = confusion_matrix(true_labels, np.argmax(predictions,
axis=-1))
```

```
# Plot the confusion matrix
def plot confusion matrix(cm, classes):
  plt.figure(figsize=(8, 6))
  plt.imshow(cm, interpolation='nearest', cmap=plt.cm.Blues)
  plt.title('Confusion Matrix')
  plt.colorbar()
  tick marks = np.arange(len(classes))
  plt.xticks(tick marks, classes, rotation=45)
  plt.yticks(tick marks, classes)
  plt.xlabel('Predicted')
  plt.ylabel('True')
  plt.tight layout()
plot confusion matrix(confusion mtx, class labels)
plt.show()
['Tumor', 'Notumor']
Found 54 images belonging to 2 classes.
Found 16 images belonging to 2 classes.
Epoch 1/10
1/1 [=============================] - 18s 18s/step - loss: 0.9638 - accuracy: 0.5455
Epoch 2/10
Epoch 3/10
Epoch 4/10
Epoch 5/10
Epoch 6/10
Epoch 7/10
Epoch 8/10
Epoch 9/10
Epoch 10/10
1/1 [=================================] - 0s 487ms/step - loss: 0.3127 - accuracy: 0.8125
Test Loss: 0.3127
Test Accuracy: 0.8125
1/1 [=======] - 0s 429ms/step
```



```
import os
import numpy as np
import matplotlib.pyplot as plt  # Add Matplotlib for image display
from tensorflow.keras.preprocessing.image import load_img, img_to_array
from tensorflow.keras.models import load_model

# Define parameters
image_size = (150, 150)
model_path = '/content/drive/MyDrive/brain_tumor/braintumor.h5'

# Load the trained model
model = load_model(model_path)
```

```
# Function to predict if an image contains a brain tumor or not
def predict brain tumor(image path):
    # Load and preprocess the image
    img = load img(image path, target size=image size)
    img = img to array(img)
   img = np.expand dims(img, axis=0)
    img = img / 255.0 # Rescale the pixel values
    # Make predictions
   prediction = model.predict(img)
    # Class labels (assuming two classes: "No Tumor" and "Tumor")
   class labels = ["No Tumor", "Tumor"]
    # Get the predicted class label and probability
   predicted class = class labels[np.argmax(prediction)]
   probability = prediction[0][np.argmax(prediction)]
   return predicted class, probability, img
# Example usage:
image path =
'/content/drive/MyDrive/brain tumor/Training/Notumor/Tr-no 0016.jpg'
predicted class, probability, img = predict brain tumor(image path)
print(f'Predicted Class: {predicted class}\nProbability:
{probability:.4f}')
# Display the input image
plt.imshow(img[0])
plt.title(f'Predicted Class: {predicted class}\nProbability:
{probability:.4f}')
plt.axis('off')
plt.show()
1/1 [=======] - 0s 187ms/step
```

Predicted Class: No Tumor

Probability: 0.9948

Predicted Class: No Tumor Probability: 0.9948

