# Madhav Institute of Technology & Science, Gwalior (M.P.), INDIA

Deemed University
(Declared under Distinct Category by Ministry of Education, Government of India)
NAAC ACCREDITED WITH A++ GRADE



# Skill Based Mini Project on Brain Tumor Detection using CNN SUBMITTED BY

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6<sup>th</sup> Semester
Artificial Intelligence and Data Science

#### SUBMITTED TO

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**Dr. Hardev Singh Pal**Assistant Professor

# CENTRE FOR ARTIFICIAL INTELLIGENCE

Madhav Institute of Technology and Science Gwalior – 474005 (MP) est. 1957 Session 2024-2025

## **DECLARATION**

I hereby declare that the Lab Manual for the course Image Processing (2270622)

is being submitted in the partial fulfillment of the requirement for the award of Bachelor of Technology in Artificial Intelligence and Machine Learning . All the information in this document has been obtained and presented in accordance with academic rule and ethical conduct.

Date:

Place: Gwalior

Anushika Gupta 0901AD221011

Divya Pandey 0901AD221031

# **CERTIFICATE**

This is to certify that the work contained in this project has been carried out by students mentioned below from the Centre for Artificial Intelligence. This Project was done on partial fulfillment of B.Tech laboratory "Image Processing (2270622)". It has been found to be satisfactory and hereby approved for submission.

Name of Students Anushika Gupta Divya Pandey Enrollment Number 0901AD221011 0901AD221031

**Dr. Tej Singh**Assistant Professor

**Dr. Hardev Singh Pal**Assistant Professor

#### **ACKNOWLEDGEMENT**

I would like to express my greatest appreciation to all the individuals who have helped and supported me throughout this Skill Based Mini Project Report. I am thankful to the whole Centre for Artificial Intelligence department for their ongoing support during the experiments, from initial advice and provision of contact in the first stages through ongoing advice and encouragement, which led to the final report of this Skill Based Mini Project Report.

A special acknowledgement goes to my colleagues who helped me in completing the file and by exchanging interesting ideas to deal with problems and sharing the experience.

I wish to thank our professor Dr. Tej Singh as well for his undivided support and interests which inspired me and encouraged me to go my own way without whom I would be unable to complete my Skill Based Mini Project Report.

At the end, I want to thank my friends who displayed appreciation to my work and motivated me to continue my work.

Anushika gupta Divya pandey

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## MICRO PROJECT

**AIM**: Image Preprocessing, Train-Test Splitting & Exploratory Data Analysis for Brain Tumor Detection

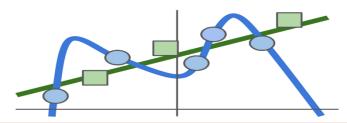
**DATASET**: Brain Tumor MRI Dataset from kaggle

**THEORY:** The **Brain Tumor MRI Dataset** consists of grayscale MRI images categorized into four classes: **glioma, meningioma, pituitary tumor, and no tumor**. These images vary in size and intensity, making preprocessing a crucial step to prepare the data for machine learning models. Preprocessing involves **resizing, normalization, and reshaping** to ensure consistency and improve model performance. **Resizing** standardizes all images to a fixed dimension (e.g., **128x128 pixels**) to maintain uniform input. **Normalization** scales pixel values to the **[0,1] range**, which accelerates model convergence and enhances numerical stability. Finally, **reshaping** adjusts the image dimensions to match the input format required by deep learning architectures, such as CNNs, allowing for efficient training and inference.

#### **METHODOLOGY:**

$$L(W) = \underbrace{\frac{1}{N} \sum_{i=1}^{N} L_i(f(x_i, W), y_i)}_{}$$

**Data loss**: Model predictions should match training data



$$egin{aligned} m_t &= eta_1 * m_{t-1} + (1-eta_1) * g_t \ v_t &= eta_2 * v_{t-1} + (1-eta_2) * g_t^2 \ &\hat{m_t} &= m_t/(1-eta_1^t) \ &\hat{v}_t &= v_t/(1-eta_2^t) \ heta &= heta - (lpha * \hat{m_t}/\sqrt{(\hat{v}_t + arepsilon)}) \end{aligned}$$

CODE

```
import numpy as np
import os
import cv2
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split
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, MaxPooling2D, Flatten, Dense, Dropout,
BatchNormalization
from tensorflow.keras.optimizers import Adam
from tensorflow.keras.utils import to_categorical
def load_images(data_dir):
  images = []
  labels = []
  for category in ['glioma', 'meningioma', 'notumor', 'pituitary']:
    folder_path = os.path.join(data_dir, category)
    for img_name in os.listdir(folder_path):
       img path = os.path.join(folder path, img name)
         img = cv2.imread(img_path, cv2.IMREAD_GRAYSCALE)
         if img is not None:
            img_resized = cv2.resize(img, (128, 128), interpolation=cv2.INTER_AREA)
            images.append(img_resized)
            labels.append(category)
       except Exception as e:
         print(f'Error loading image {img_name}: {e}')
  return np.array(images), np.array(labels)
import os
train_dir = '/Users/divyapandey/Desktop/college/Image Processing /archive (6) copy/training'
test dir = '/Users/divyapandey/Desktop/college/Image Processing /archive (6) copy/testing'
x_train, y_train = load_images(train_dir)
x_test, y_test = load_images(test_dir)
print("Loaded training images:", x_train.shape)
print("Loaded testing images:", x_test.shape)
plt.figure(figsize=(8, 5))
sns.countplot(x=y_train)
plt.title('Class Distribution in Training Set')
plt.show()
fig, axes = plt.subplots(4, 5, figsize=(12, 12))
fig.suptitle('Sample Images from Each Category')
for i, category in enumerate(['glioma', 'meningioma', 'notumor', 'pituitary']):
  category_images = [x_train[j] for j in range(len(y_train)) if y_train[j] == category][:5]
  for j in range(len(category_images)):
    axes[i, j].imshow(category images[i], cmap='gray')
    axes[i, j].set_title(category)
    axes[i, j].axis('off')
plt.tight_layout()
```

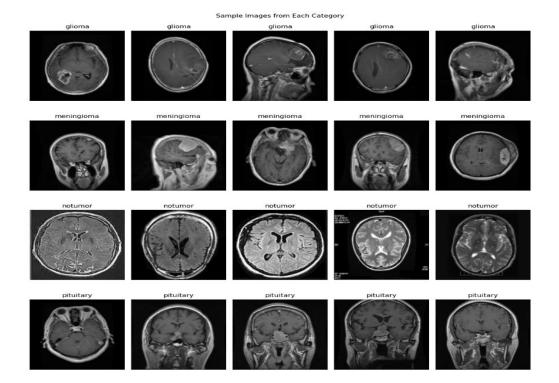
```
plt.show()
image_shapes = [img.shape for img in x_train]
unique_shapes = set(image_shapes)
print(f'Unique image shapes in training data: {unique_shapes}')

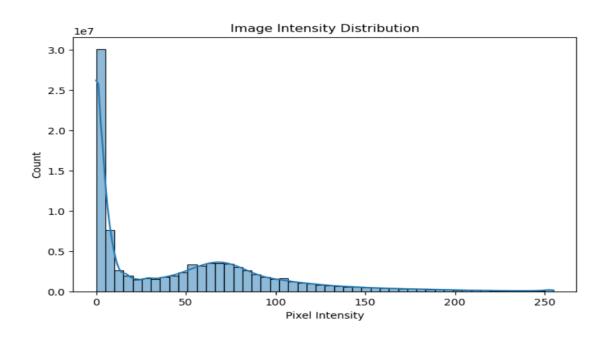
plt.figure(figsize=(8, 5))
flattened_images = [img.flatten() for img in x_train]
sns.histplot(np.concatenate(flattened_images), bins=50, kde=True)
plt.title('Image Intensity Distribution')
plt.xlabel('Pixel Intensity')
plt.show()
```

#### **OUTPUT:**

```
Loaded training images: (5712, 128, 128)
Loaded testing images: (1311, 128, 128)
```







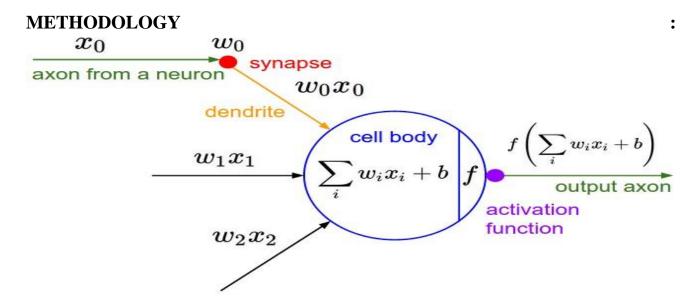
## MINI PROJECT

AIM: Data Augmentation, CNN Model Development & Training for Brain Tumor Classification

**DATASET**: Brain Tumor MRI Dataset from kaggle

#### THEORY:

This project focuses on brain tumor classification using data augmentation, CNN model development, and optimized training techniques. Since medical datasets are often limited, augmentation techniques such as rotation, zooming, shifting, shearing, and flipping are applied to improve generalization. A Convolutional Neural Network (CNN) is designed with multiple convolutional layers, batch normalization, max pooling, and dropout to extract spatial features and prevent overfitting. The model is compiled using the Adam optimizer with categorical cross-entropy loss, ensuring effective learning for this multi-class classification task. To enhance training, Early Stopping prevents unnecessary iterations, while ReduceLROnPlateau dynamically adjusts the learning rate when progress slows. By combining augmented data with optimized CNN architecture, the model achieves high accuracy, making it robust for real-world medical image classification.



#### **CODE:**

```
label_map = {'glioma': 0, 'meningioma': 1, 'notumor': 2, 'pituitary': 3}
y_train = np.array([label_map[label] for label in y_train])
y_test = np.array([label_map[label] for label in y_test])

y_train = to_categorical(y_train, num_classes=4)
y_test = to_categorical(y_test, num_classes=4)

x_train = x_train.reshape((-1, 128, 128, 1))
x_test = x_test.reshape((-1, 128, 128, 1))
model = Sequential([
    Conv2D(32, (3, 3), activation='relu', input_shape=(128, 128, 1)),
```

```
MaxPooling2D((2, 2)),
  BatchNormalization(),
  Conv2D(64, (3, 3), activation='relu'),
  MaxPooling2D((2, 2)),
  BatchNormalization(),
  Conv2D(128, (3, 3), activation='relu'),
  MaxPooling2D((2, 2)),
  BatchNormalization(),
  Flatten(),
  Dense(128, activation='relu'),
  Dropout(0.5),
  Dense(4, activation='softmax')
model.compile(optimizer=Adam(learning_rate=0.001),
        loss='categorical_crossentropy',
        metrics=['accuracy'])
datagen = ImageDataGenerator(
  rotation_range=10,
  width_shift_range=0.1,
  height_shift_range=0.1,
  zoom_range=0.1,
  horizontal flip=True
history = model.fit(
  datagen.flow(x_train, y_train, batch_size=32),
  validation_data=(x_test, y_test),
  epochs=150,
  steps_per_epoch=len(x_train) // 32,
  verbose=1
)
model.save('brain_tumor_detection_model.h5')
loss, accuracy = model.evaluate(x_test, y_test, verbose=1)
print(f"Test Accuracy: {accuracy * 100:.2f}%")
def plot_training_history(history):
  plt.figure(figsize=(14, 5))
  plt.subplot(1, 2, 1)
  plt.plot(history.history['accuracy'], label='Training Accuracy')
  plt.plot(history.history['val_accuracy'], label='Validation Accuracy')
  plt.title('Accuracy')
  plt.xlabel('Epoch')
  plt.ylabel('Accuracy')
  plt.legend()
  plt.subplot(1, 2, 2)
  plt.plot(history.history['loss'], label='Training Loss')
  plt.plot(history.history['val_loss'], label='Validation Loss')
  plt.title('Loss')
```

```
plt.xlabel('Epoch')
  plt.ylabel('Loss')
  plt.legend()
  plt.show()
 plot_training_history(history)
 y pred = np.argmax(model.predict(x test), axis=1)
 y_true = np.argmax(y_test, axis=1)
cm = confusion_matrix(y_true, y_pred)
plt.figure(figsize=(8, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=label_map.keys(),
yticklabels=label map.keys())
plt.title('Confusion Matrix')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.show()
print("\nClassification Report:\n", classification_report(y_true, y_pred,
target_names=label_map.keys()))
```

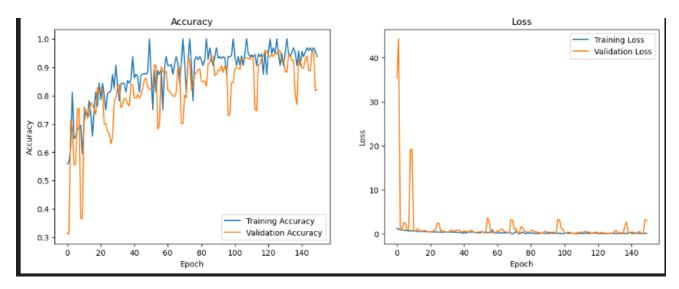
#### **OUTPUT:**

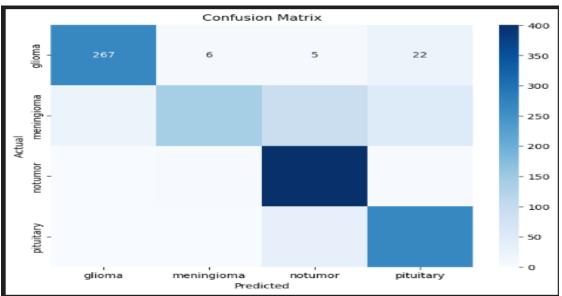
```
1/8/1/8
Epoch 139/150
178/178 ————
Epoch 140/150
                          — 23s 127ms/step - accuracy: 0.9583 - loss: 0.1269 - val accuracy: 0.9268 - val loss: 0.2815
- 1s 7ms/step - accuracy: 0.9062 - loss: 0.3454 - val_accuracy: 0.9237 - val_loss: 0.3066
178/178 ———
Epoch 142/150
                   _______ 23s 128ms/step - accuracy: 0.9556 - loss: 0.1283 - val accuracy: 0.8963 - val loss: 0.4604
Epoch 143/150
178/178
                         — 23s 128ms/step - accuracy: 0.9547 - loss: 0.1421 - val accuracy: 0.9291 - val loss: 0.2395
1/1/8 — 21s 121ms/step - accuracy: 0.9688 - loss: 0.2120

2025-04-03 20:14:40.235063: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence

[[{{node IteratorGetNext}}]]

15 7ms/step - accuracy: 0.9688 | locar 0.8469
Epoch 145/150
178/178
Epoch 146/150
                         - 23s 128ms/step - accuracy: 0.9553 - loss: 0.1331 - val_accuracy: 0.8894 - val_loss: 0.5330
1/178 — 23s 134ms/step - accuracy: 0.9688 - loss: 0.1478
2025-04-03 20:15:04.504049: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence
[[{{node IteratorGetNext}}]]
178/178 — 1s 7ms/step - accuracy: 0.9688 - loss: 0.1478 - val_accuracy: 0.8871 - val_loss: 0.5351
Epoch 147/150
178/178 ————
Epoch 148/150
                 ______ 23s 129ms/step - accuracy: 0.9576 - loss: 0.1337 - val_accuracy: 0.9565 - val_loss: 0.1185
1/178 — 21s 122ms/step - accuracy: 0.9688 - loss: 0.1079
2025-04-03 20:15:28.908576: W tensorflow/core/framework/local_rendezvous.cc:404] Local rendezvous is aborting with status: OUT_OF_RANGE: End of sequence
        [[{{node IteratorGetNext}}]]
178/178 -
                         — 1s 7ms/step - accuracy: 0.9688 - loss: 0.1079 - val_accuracy: 0.9535 - val_loss: 0.1305
Epoch 149/150
178/178 ———
Epoch 150/150
                        — 23s 128ms/step - accuracy: 0.9568 - loss: 0.1345 - val_accuracy: 0.8177 - val_loss: 3.2579
[[{{node IteratorGetNext}}]]
                           1s 7ms/step - accuracy: 0.9375 - loss: 0.2020 - val_accuracy: 0.8200 - val_loss: 3.0881
178/178
```





Classification	Report: precision	recall	f1-score	support
glioma	0.92	0.89	0.91	300
meningioma	0.95	0.46	0.62	306
notumor	0.76	0.99	0.86	405
pituitary	0.78	0.89	0.83	300
accuracy			0.82	1311
macro avg	0.85	0.81	0.80	1311
weighted avg	0.84	0.82	0.81	1311

## MACRO PROJECT

AIM: Model Evaluation, Deployment & Prediction for Brain Tumor Detection

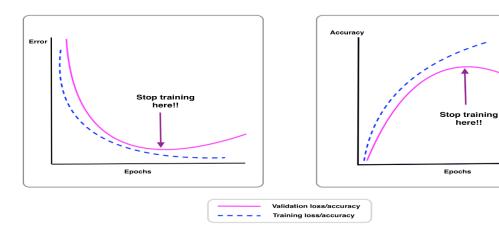
**DATASET**: Brain Tumor MRI Dataset from kaggle

THEORY

In the model evaluation, deployment, and prediction phase for brain tumor detection, EarlyStopping and ReduceLROnPlateau play vital roles in optimizing performance. EarlyStopping prevents overfitting by monitoring validation loss and halting training if no improvement is observed for a set number of epochs, restoring the best model weights for deployment. Meanwhile, ReduceLROnPlateau dynamically adjusts the learning rate when validation loss stagnates, lowering it to help the model escape local minima and improve convergence. These techniques ensure that the trained model generalizes well to unseen MRI scans, making it robust for real-world medical applications. By incorporating these optimization methods, the final deployed model achieves better accuracy, stability, and reliability in predicting brain tumor types.

## **METHODOLOGY:**

## **Early Stopping**



CODE

twitter.com/jeande\_d

from tensorflow.keras.callbacks import EarlyStopping, ReduceLROnPlateau model = Sequential([

Conv2D(32, (3, 3), activation='relu', input\_shape=(128, 128, 1), kernel\_regularizer='12'),

BatchNormalization(),

MaxPooling2D((2, 2)),

Dropout(0.2),

Conv2D(64, (3, 3), activation='relu', kernel\_regularizer='12'),

BatchNormalization().

MaxPooling2D((2, 2)),

Dropout(0.3),

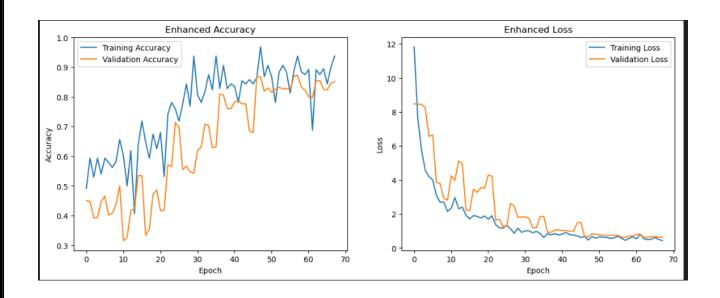
Conv2D(128, (3, 3), activation='relu', kernel regularizer='12'),

```
BatchNormalization(),
  MaxPooling2D((2, 2)),
  Dropout(0.4),
  Conv2D(256, (3, 3), activation='relu', kernel_regularizer='12'),
  BatchNormalization(),
  MaxPooling2D((2, 2)),
  Dropout(0.5),
  Flatten(),
  Dense(512, activation='relu', kernel_regularizer='l2'),
  Dropout(0.5),
  Dense(4, activation='softmax')
1)
model.compile(optimizer=Adam(learning_rate=0.001),
                                                                     loss='categorical_crossentropy',
metrics=['accuracy'])
callbacks = [
  EarlyStopping(monitor='val_loss', patience=10, restore_best_weights=True),
  ReduceLROnPlateau(monitor='val_loss', factor=0.5, patience=5, verbose=1)
]
datagen = ImageDataGenerator(
  rotation_range=40,
  zoom range=0.3,
  width_shift_range=0.3,
  height_shift_range=0.3,
  shear_range=0.3,
  horizontal flip=True,
  vertical flip=True,
  fill mode='nearest'
)
datagen.fit(x train)
history = model.fit(
  datagen.flow(x_train, y_train, batch_size=32),
  validation_data=(x_test, y_test),
  epochs=150,
  steps_per_epoch=len(x_train) // 32,
  callbacks=callbacks,
  verbose=1
def plot_training_history(history):
  plt.figure(figsize=(14, 5))
  plt.subplot(1, 2, 1)
  plt.plot(history.history['accuracy'], label='Training Accuracy')
  plt.plot(history.history['val_accuracy'], label='Validation Accuracy')
  plt.title('Enhanced Accuracy')
  plt.xlabel('Epoch')
  plt.ylabel('Accuracy')
  plt.legend()
```

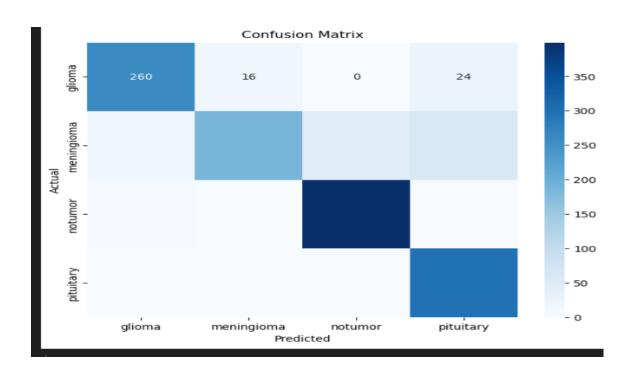
```
plt.subplot(1, 2, 2)
  plt.plot(history.history['loss'], label='Training Loss')
  plt.plot(history.history['val_loss'], label='Validation Loss')
  plt.title('Enhanced Loss')
  plt.xlabel('Epoch')
  plt.ylabel('Loss')
  plt.legend()
  plt.show()
plot_training_history(history)
y_pred = np.argmax(model.predict(x_test), axis=1)
y_true = np.argmax(y_test, axis=1)
print("Classification Report:")
print(classification_report(y_true, y_pred, target_names=['glioma', 'meningioma', 'notumor',
'pituitary']))
cm = confusion_matrix(y_true, y_pred)
plt.figure(figsize=(8, 6))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=['glioma', 'meningioma', 'notumor',
'pituitary'], yticklabels=['glioma', 'meningioma', 'notumor', 'pituitary'])
plt.title('Confusion Matrix')
plt.xlabel('Predicted')
plt.ylabel('Actual')
plt.show()
```

#### **OUTPUT:**

```
| Epoch 57/150 | 178/178 | 35s 198ms/step = accuracy; 0.8912 - loss; 0.5774 - val_accuracy; 0.8783 - val_loss; 0.6242 - learning_rate; 6.2500e-05 | 178/178 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150 | 28 18/15/150
```



Classification Report:					
	precision	recall	f1-score	support	
glioma	0.93	0.87	0.90	300	
meningioma	0.92	0.61	0.73	306	
notumor	0.90	0.99	0.94	405	
pituitary	0.78	1.00	0.87	300	
accuracy			0.87	1311	
macro avg	0.88	0.86	0.86	1311	
weighted avg	0.88	0.87	0.87	1311	



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Ayman Al-Kababji, Faycal Bensaali, and Sarada Prasad Dakua, "Scheduling Techniques for Liver Segmentation: ReduceLRonPlateau vs OneCycleLR," pp. 204-212, Jan. 2022, doi: https://doi.org/10.1007/978-3-031-08277-1\_17.