Plant Disease Detection

importing Depedencies

```
import json
from zipfile import ZipFile
from PIL import Image

import numpy as np
import matplotlib.pyplot as plt
import matplotlib.image as mpimg

import tensorflow as tf
from tensorflow.keras.preprocessing.image import ImageDataGenerator
from tensorflow.keras import layers, models


gpus = tf.config.experimental.list_physical_devices('GPU')
for gpu in gpus:
    tf.config.experimental.set_memory_growth(gpu, True)
```

Uploading Dataset

Data set link:https://www.kaggle.com/datasets/abdallahalidev/plantvillage-dataset

```
# Mounting Google Drive
from google.colab import drive
drive.mount('/content/drive')
```

```
Mounted at /content/drive
```

```
# Unzipping the uploaded archive.zip file
zip_path = '/content/drive/My Drive/archive.zip'
with ZipFile(zip_path, 'r') as zip_ref:
    zip_ref.extractall('/content/plantvillage-dataset')


import os
print("Contents of '/content/plantvillage-dataset/New Plant Diseases Dataset(Augmented)':")
print(os.listdir('/content/plantvillage-dataset/New Plant Diseases Dataset(Augmented)'))
print("\nContents of '/content/plantvillage-dataset/new plant diseases dataset(augmented)':")
print(os.listdir('/content/plantvillage-dataset/new plant diseases dataset(augmented)'))
# Check contents of 'test'
print("\nContents of '/content/plantvillage-dataset/test':")
print(os.listdir('/content/plantvillage-dataset/test'))
```

```
Contents of '/content/plantvillage-dataset/New Plant Diseases Dataset(Augmented)':
['New Plant Diseases Dataset(Augmented)']

Contents of '/content/plantvillage-dataset/new plant diseases dataset(augmented)':
['New Plant Diseases Dataset(Augmented)']

Contents of '/content/plantvillage-dataset/test':
['test']
```

```
import os

def find_image_folders(base_dir):
    image_extensions = ('.png', '.jpg', '.jpeg')
    folders_with_images = []

    for root, _, files in os.walk(base_dir):
        if any(file.lower().endswith(image_extensions) for file in files):
            folders_with_images.append(root)

    return folders_with_images

base_dir = '/content/plantvillage-dataset'
image_folders = find_image_folders(base_dir)

print("Folders containing image files:")
for folder in image_folders:
    print(folder)
```

```
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Corn_(maize)___Ce
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Strawberry___Leaf
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Tomato___Early_bl
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Tomato___Tomato_m
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Peach___Bacterial
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Tomato___Tomato_Y
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Grape___Esca_(Bla
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Blueberry___healt
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Apple___healthy
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Orange___Haunglon
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Tomato___Leaf_Mol
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Tomato___Bacteria
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Tomato___Spider_m
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Tomato___Late_bli
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Potato___healthy
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Raspberry___healt
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Cherry_(including
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Apple___Black_rot
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/valid/Cherry_(including
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Corn_(maize)___Co
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Peach___healthy
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Pepper,_bell___he
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Strawberry___heal
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Apple___Cedar_app
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Apple___Apple_sca
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Squash___Powdery_
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Soybean___healthy
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Grape___Leaf_blig
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___Target_S
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Corn_(maize)___he
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___healthy
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___Septoria
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Potato___Early_bl
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Grape___healthy
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Corn_(maize)___No
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Pepper,_bell___Ba
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Grape___Black_rot
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Potato___Late_bli
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Corn_(maize)___Ce
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Strawberry___Leaf
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___Early_bl
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___Tomato_m
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Peach___Bacterial
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___Tomato_Y
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Grape___Esca_(Bla
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Blueberry___healt
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Apple___healthy
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Orange___Haunglon
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___Leaf_Mol
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___Bacteria
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___Spider_m
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Tomato___Late_bli
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Potato___healthy
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Raspberry___healt
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Cherry_(including
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Apple___Black_rot
/content/plantvillage-dataset/new plant diseases dataset(augmented)/New Plant Diseases Dataset(Augmented)/train/Cherry_(including
```

```
import json
class_indices = train_gen.class_indices
with open('class_indices.json', 'w') as f:
    json.dump(class_indices, f)

print("Class indices saved to class_indices.json")
```

```
Class indices saved to class_indices.json
```

```
import json
with open('class_indices.json', 'r') as f:
    class_indices = json.load(f)
class_labels = list(class_indices.keys())
print("Class Labels:", class_labels)
```

```
Class Labels: ['Apple___Apple_scab', 'Apple___Black_rot', 'Apple___Cedar_apple_rust', 'Apple___healthy', 'Blueberry___healthy', 'Che
```

```
df = '/content/plantvillage-dataset/New Plant Diseases Dataset(Augmented)/images'
```

```
df = '/content/plantvillage-dataset/New Plant Diseases Dataset(Augmented)/New Plant Diseases Dataset(Augmented)/train'
```

Displaying Random 9 images

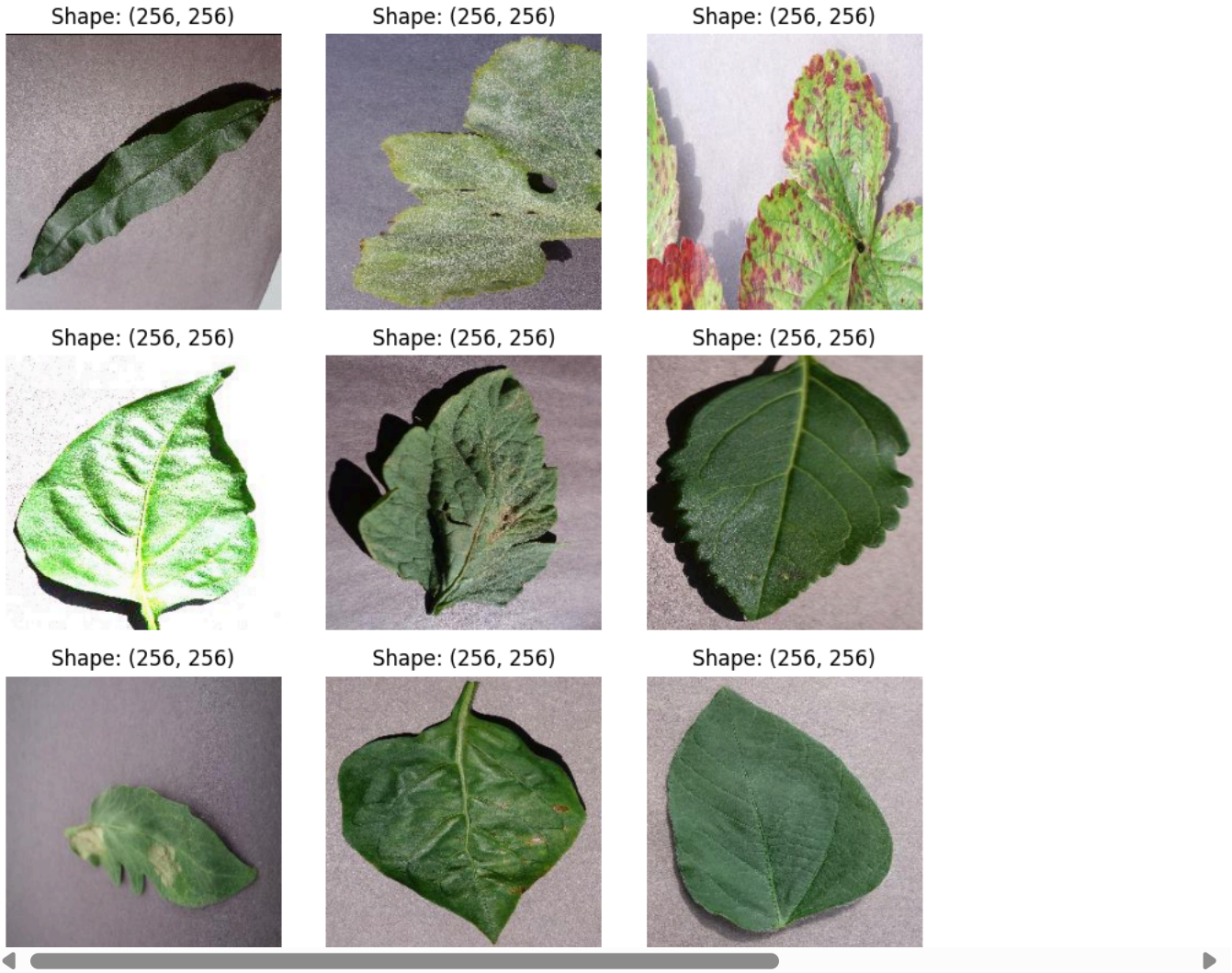
```
image_paths = [os.path.join(dp, f) for dp, dn, filenames in os.walk(df) for f in filenames if f.lower().endswith(('png', 'jpg', 'jpeg'))]

print(f"Number of images found: {len(image_paths)}")

if len(image_paths) < 9:
    print("Not enough images for sampling. Showing all available images instead.")
    selected_paths = image_paths
else:
    selected_paths = random.sample(image_paths, 9)

plt.figure(figsize=(8, 8))
for i, path in enumerate(selected_paths):
    img = Image.open(path)
    plt.subplot(3, 3, i + 1)
    plt.imshow(img)
    plt.title(f'Shape: {img.size}')
    plt.axis('off')
plt.tight_layout()
plt.show()
```

```
Number of images found: 70295
```




```
img_size = 224
batch_size = 32
```

```
from tensorflow.keras.preprocessing.image import ImageDataGenerator
```

Normalization

```
data_gen = ImageDataGenerator(
    rescale=1./255,
```

```
    validation_split=0.2
)

train_gen = data_gen.flow_from_directory(
    df,
    target_size=(img_size, img_size),
    batch_size=batch_size,
    subset='training',
    class_mode='categorical'
)
```

```
Found 56251 images belonging to 38 classes.
```

```
validation_gen = data_gen.flow_from_directory(
    df,
    target_size=(img_size, img_size),
    batch_size=batch_size,
    subset='validation',
    class_mode='categorical'
)
```

```
Found 14044 images belonging to 38 classes.
```

```
print(f"Training data batches: {len(train_gen)}")
print(f"Validation data batches: {len(validation_gen)}")
```

```
Training data batches: 1758
Validation data batches: 439
```

Model building

```
from tensorflow.keras import layers, models

model = models.Sequential([
    layers.Conv2D(16, (3, 3), activation='relu', input_shape=(img_size, img_size, 3)),
    layers.MaxPooling2D(2, 2),

    layers.Conv2D(32, (3, 3), activation='relu'),
    layers.MaxPooling2D(2, 2),

    layers.Flatten(),
    layers.Dense(128, activation='relu'),
    layers.Dense(train_gen.num_classes, activation='softmax')  # Output layer with number of classes
])
```

```
/usr/local/lib/python3.11/dist-packages/keras/src/layers/convolutional/base_conv.py:107: UserWarning: Do not pass an `input_shape`/`
  super().__init__(activity_regularizer=activity_regularizer, **kwargs)
```

```
model.summary()
```

Model: "sequential"

Layer (type)	Output Shape	Param #
conv2d (Conv2D)	(None, 222, 222, 16)	448
max_pooling2d (MaxPooling2D)	(None, 111, 111, 16)	0
conv2d_1 (Conv2D)	(None, 109, 109, 32)	4,640
max_pooling2d_1 (MaxPooling2D)	(None, 54, 54, 32)	0
flatten (Flatten)	(None, 93312)	0
dense (Dense)	(None, 128)	11,944,064
dense_1 (Dense)	(None, 38)	4,902

Total params: 11,954,054 (45.60 MB)

Training Model

```
model.compile(
```

```
    optimizer='adam',
    loss='categorical_crossentropy',
    metrics=['accuracy']
)
```

```
history = model.fit(
    train_gen,
    epochs=5,
    validation_data=validation_gen
)
```

```
Epoch 1/5
/usr/local/lib/python3.11/dist-packages/keras/src/trainers/data_adapters/py_dataset_adapter.py:122: UserWarning: Your `PyDataset` cl
  self._warn_if_super_not_called()
1758/1758 ━━━━━━━━━━━━━━━━━━━━ 3048s 2s/step - accuracy: 0.5614 - loss: 1.7136 - val_accuracy: 0.8589 - val_loss: 0.4723
Epoch 2/5
1758/1758 ━━━━━━━━━━━━━━━━━━━━ 3083s 2s/step - accuracy: 0.8978 - loss: 0.3194 - val_accuracy: 0.8559 - val_loss: 0.4815
Epoch 3/5
1758/1758 ━━━━━━━━━━━━━━━━━━━━ 3087s 2s/step - accuracy: 0.9559 - loss: 0.1373 - val_accuracy: 0.8604 - val_loss: 0.5246
Epoch 4/5
1758/1758 ━━━━━━━━━━━━━━━━━━━━ 3146s 2s/step - accuracy: 0.9747 - loss: 0.0810 - val_accuracy: 0.8671 - val_loss: 0.5566
Epoch 5/5
1758/1758 ━━━━━━━━━━━━━━━━━━━━ 3138s 2s/step - accuracy: 0.9784 - loss: 0.0659 - val_accuracy: 0.8656 - val_loss: 0.5975
```

```
# Evaluate model performance
val_loss, val_accuracy = model.evaluate(validation_gen)
print(f"Validation Accuracy: {val_accuracy * 100:.2f}%")
```

```
439/439 ━━━━━━━━━━━━━━━━━━━━ 226s 512ms/step - accuracy: 0.8660 - loss: 0.5997
Validation Accuracy: 86.56%
```

Visualization

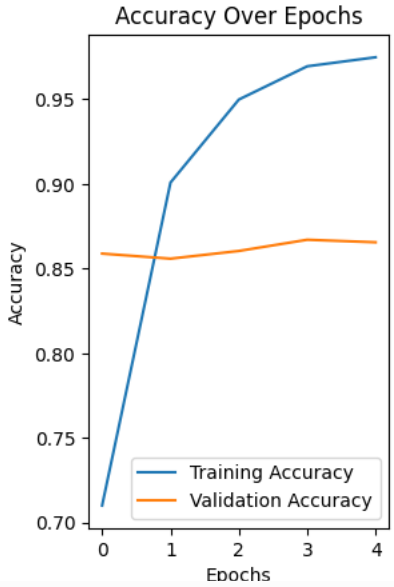
```
import matplotlib.pyplot as plt
```

```
plt.figure(figsize=(12, 5))
```

```
<Figure size 1200x500 with 0 Axes>
```

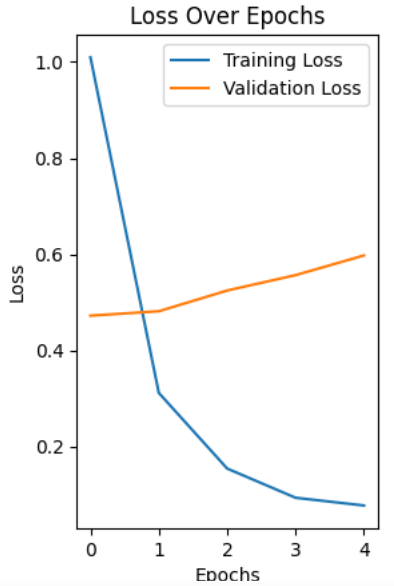
```
# Plotting accuracy
plt.subplot(1, 2, 1)
plt.plot(history.history['accuracy'], label='Training Accuracy')
plt.plot(history.history['val_accuracy'], label='Validation Accuracy')
plt.title('Accuracy Over Epochs')
plt.xlabel('Epochs')
plt.ylabel('Accuracy')
plt.legend()
```

```
<matplotlib.legend.Legend at 0x7bbab5109b90>
```




```
# Plotting loss
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 Over Epochs')
plt.xlabel('Epochs')
plt.ylabel('Loss')
plt.legend()
```

```
<matplotlib.legend.Legend at 0x7bbab54719d0>
```




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

```
predictions = model.predict(validation_gen, batch_size=batch_size)
predicted_labels = np.argmax(predictions, axis=1)
true_labels = validation_gen.classes
```

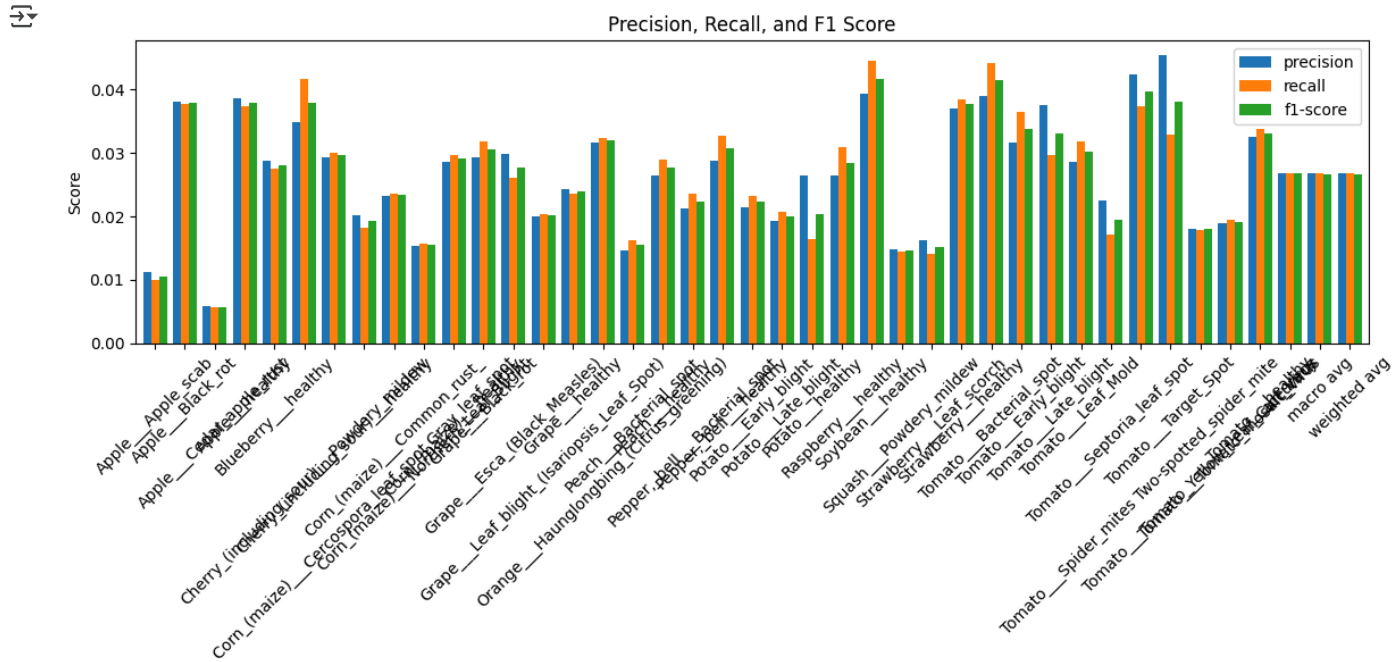
```
439/439 ━━━━━━━━━━━━━━━━━━━━ 232s 527ms/step
```

```
from sklearn.metrics import confusion_matrix, classification_report
report = classification_report(true_labels, predicted_labels, target_names=validation_gen.class_indices.keys())
print("Classification Report:\n", report)
```

```
Classification Report:
                                                    precision    recall  f1-score   support
```

Apple___Apple_scab	0.01	0.01	0.01	403
Apple___Black_rot	0.04	0.04	0.04	397
Apple___Cedar_apple_rust	0.01	0.01	0.01	352
Apple___healthy	0.04	0.04	0.04	401
Blueberry___healthy	0.03	0.03	0.03	363
Cherry_(including_sour)___Powdery_mildew	0.03	0.04	0.04	336
Cherry_(including_sour)___healthy	0.03	0.03	0.03	365
Corn_(maize)___Cercospora_leaf_spot Gray_leaf_spot	0.02	0.02	0.02	328
Corn_(maize)___Common_rust_	0.02	0.02	0.02	381
Corn_(maize)___Northern_Leaf_Blight	0.02	0.02	0.02	381
Corn_(maize)___healthy	0.03	0.03	0.03	371
Grape___Black_rot	0.03	0.03	0.03	377
Grape___Esca_(Black_Measles)	0.03	0.03	0.03	384
Grape___Leaf_blight_(Isariopsis_Leaf_Spot)	0.02	0.02	0.02	344
Grape___healthy	0.02	0.02	0.02	338
Orange___Haunglongbing_(Citrus_greening)	0.03	0.03	0.03	402
Peach___Bacterial_spot	0.01	0.02	0.02	367
Peach___healthy	0.03	0.03	0.03	345
Pepper,_bell___Bacterial_spot	0.02	0.02	0.02	382
Pepper,_bell___healthy	0.03	0.03	0.03	397
Potato___Early_blight	0.02	0.02	0.02	387
Potato___Late_blight	0.02	0.02	0.02	387
Potato___healthy	0.03	0.02	0.02	364
Raspberry___healthy	0.03	0.03	0.03	356
Soybean___healthy	0.04	0.04	0.04	404
Squash___Powdery_mildew	0.01	0.01	0.01	347
Strawberry___Leaf_scorch	0.02	0.01	0.02	354
Strawberry___healthy	0.04	0.04	0.04	364
Tomato___Bacterial_spot	0.04	0.04	0.04	340
Tomato___Early_blight	0.03	0.04	0.03	384
Tomato___Late_blight	0.04	0.03	0.03	370
Tomato___Leaf_Mold	0.03	0.03	0.03	376
Tomato___Septoria_leaf_spot	0.02	0.02	0.02	349
Tomato___Spider_mites Two-spotted_spider_mite	0.04	0.04	0.04	348
Tomato___Target_Spot	0.05	0.03	0.04	365
Tomato___Tomato_Yellow_Leaf_Curl_Virus	0.02	0.02	0.02	392
Tomato___Tomato_mosaic_virus	0.02	0.02	0.02	358
Tomato___healthy	0.03	0.03	0.03	385
accuracy			0.03	14044
macro avg	0.03	0.03	0.03	14044
weighted avg	0.03	0.03	0.03	14044

```
df_report[['precision', 'recall', 'f1-score']].plot(kind='bar', figsize=(12, 6), width=0.8)
plt.title('Precision, Recall, and F1 Score')
plt.ylabel('Score')
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```




```
import pickle
```

```
with open('plant_disease_prediction_model.pkl', 'wb') as model_file:
    pickle.dump(model, model_file)
```