

```

In [4]: import tensorflow as tf

# Define constants
IMAGE_SIZE = 256
BATCH_SIZE = 64

# Load the dataset
test_ds = tf.keras.preprocessing.image_dataset_from_directory(
    "PlantVillage", # Change this path if needed
    shuffle=False,
    image_size=(IMAGE_SIZE, IMAGE_SIZE),
    batch_size=BATCH_SIZE
)

# Get class names
class_names = test_ds.class_names

# Import required libraries
import numpy as np
import tensorflow as tf
from tensorflow.keras.models import load_model
from sklearn.metrics import classification_report, confusion_matrix, roc_curve
import seaborn as sns
import matplotlib.pyplot as plt

# Load the trained model
model_version = 2 # Change if using a different saved version
model_path = f"../models/{model_version}"
model = load_model(model_path)

# Load test dataset
# Ensure 'test_ds' is available in the same format as used during training
y_true = []
y_pred = []
y_pred_prob = []

for images, labels in test_ds:
    preds = model.predict(images)
    y_true.extend(labels.numpy()) # Actual labels
    y_pred.extend(np.argmax(preds, axis=1))
    y_pred_prob.extend(preds) # Predicted labels

# Convert lists to NumPy arrays
y_true = np.array(y_true)
y_pred = np.array(y_pred)
y_pred_prob = np.array(y_pred_prob)

# Get class names
class_names = ['Tomato_Bacterial_spot',
    'Tomato_Early_blight',
    'Tomato_Late_blight',
    'Tomato_Leaf_Mold',
    'Tomato_Septoria_leaf_spot',
    'Tomato_Spider_mites_Two_spotted_spider_mite',

```

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'Tomato__Target_Spot',
'Tomato__Tomato_YellowLeaf__Curl_Virus',
'Tomato__Tomato_mosaic_virus',
'Tomato_healthy']

# -----
# 1[] Precision and F1 Score
# -----
precision = precision_score(y_true, y_pred, average='weighted')
recall = recall_score(y_true, y_pred, average='weighted')
f1 = f1_score(y_true, y_pred, average='weighted')

print(f"[] Precision: {precision:.4f}")
print(f"[] Recall: {recall:.4f}")
print(f"[] F1 Score: {f1:.4f}")

# -----
# 2[] Confusion Matrix
# -----
cm = confusion_matrix(y_true, y_pred)

plt.figure(figsize=(10,7))
sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=class_names,
plt.xlabel("Predicted Label")
plt.ylabel("Actual Label")
plt.title("Confusion Matrix")
plt.show()

# -----
# 3[] ROC Curve & AUC
# -----
# Convert labels to one-hot encoding for multi-class ROC curve
y_true_one_hot = tf.keras.utils.to_categorical(y_true, num_classes=len(class_names))
y_pred_prob = model.predict(test_ds) # Get probability outputs

plt.figure(figsize=(10, 7))

for i in range(len(class_names)):
    fpr, tpr, _ = roc_curve(y_true_one_hot[:, i], y_pred_prob[:, i])
    auc_score = auc(fpr, tpr)
    plt.plot(fpr, tpr, label=f'{class_names[i]} (AUC = {auc_score:.2f})')

plt.plot([0, 1], [0, 1], 'k--') # Diagonal line (random model)
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.title("ROC Curve")
plt.legend()
plt.show()

# -----
# 4[] Classification Report
# -----
print("[] Classification Report:\n")
print(classification_report(y_true, y_pred, target_names=class_names))

```

Found 16011 files belonging to 10 classes.

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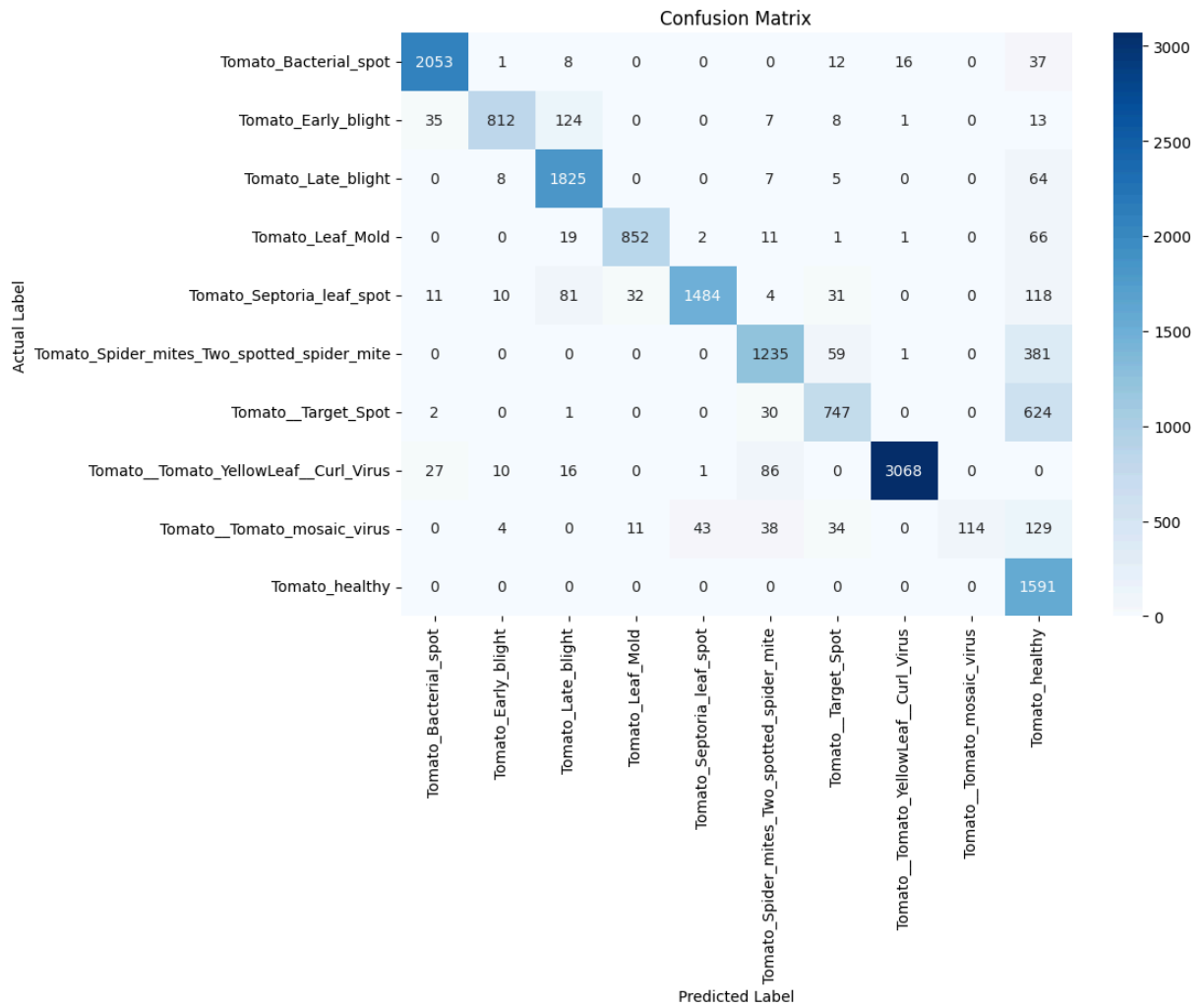
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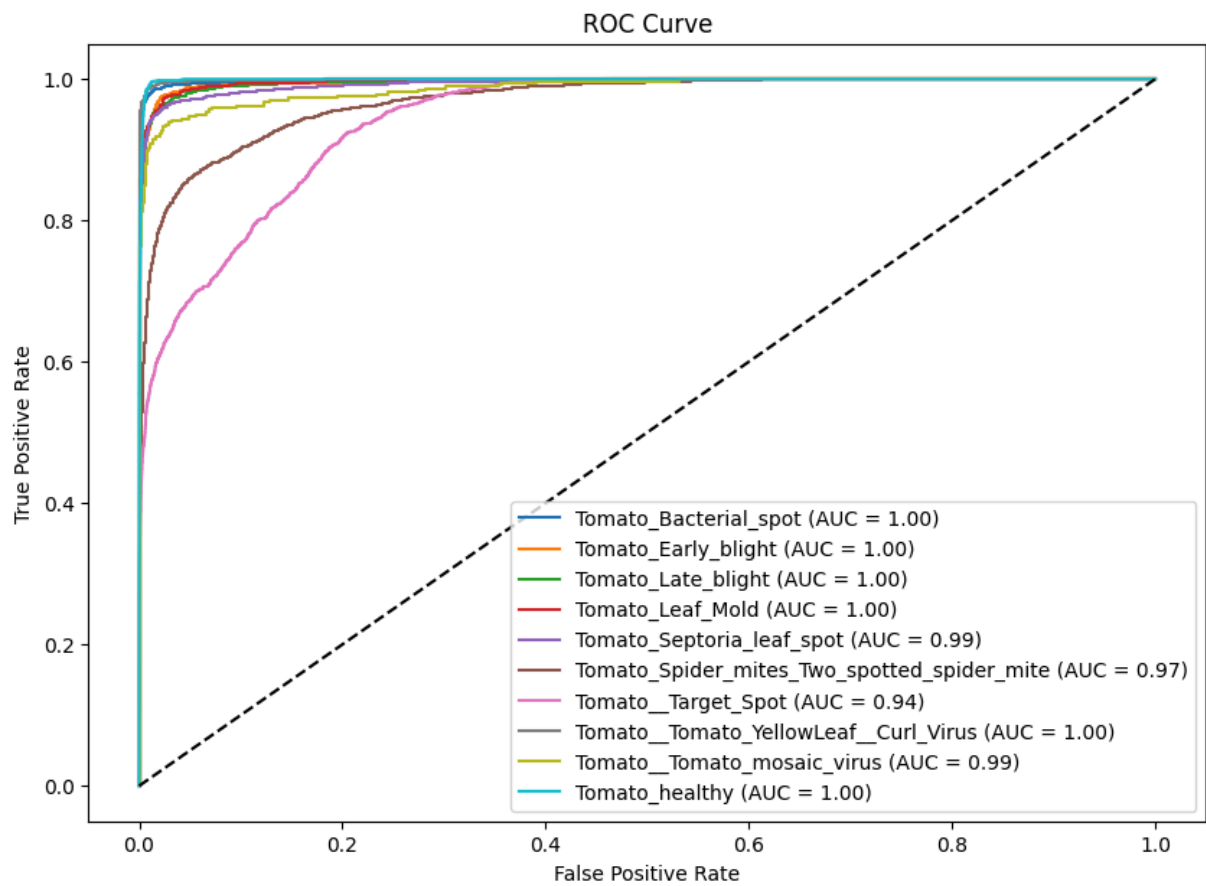
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□ Precision: 0.8959
□ Recall: 0.8607
□ F1 Score: 0.8620



251/251 [=====] - 13s 47ms/step



Classification Report:

support		precision	recall	f1-score
2127	Tomato_Bacterial_spot	0.96	0.97	0.96
1000	Tomato_Early_blight	0.96	0.81	0.88
1909	Tomato_Late_blight	0.88	0.96	0.92
952	Tomato_Leaf_Mold	0.95	0.89	0.92
1771	Tomato_Septoria_leaf_spot	0.97	0.84	0.90
1676	Tomato_Spider_mites_Two_spotted_spider_mite	0.87	0.74	0.80
1404	Tomato__Target_Spot	0.83	0.53	0.65
3208	Tomato__Tomato_YellowLeaf__Curl_Virus	0.99	0.96	0.97
373	Tomato__Tomato_mosaic_virus	1.00	0.31	0.47
1591	Tomato_healthy	0.53	1.00	0.69
16011	accuracy			0.86
16011	macro avg	0.90	0.80	0.82
16011	weighted avg	0.90	0.86	0.86

In []: