Disease Detection & Severity Prediction of Pomegranate Fruit

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***Abstract*—This paper presents an integrated framework for the comprehensive analysis of diseases affecting pomegranate fruit. The suggested system, which makes use of deep learning techniques, includes semantic segmentation for diseased region localization, multiclass illness classification, and image processing-based severity assessment. Initially, four common diseases—Alternaria, Anthracnose, Bacterial Blight, and Cercospora—are successfully identified through the use of a Convolutional Neural Network (CNN) for multiclass classification. Then, annotated photos are used as training data for Semantic Segmentation, which uses the UNet architecture to identify the unhealthy spots within the fruit. The area and percentage of the segmented region are determined, and thresholds for high, medium, and low severity levels are then defined. The segmentation results are then used as inputs for severity estimate. Early identification and intervention tactics are made easier by the severity level prediction, which is based on the proportion of the segmented region. In order to improve pomegranate fruit management methods, the suggested framework provides a thorough method of disease analysis by combining categorization, semantic segmentation, and severity prediction.**

***Index Terms*—Convolutional Neural Networks, Deep learning, Unet, Semantic segmentation, Annotation.**

I. INTRODUCTION

One important fruit that is grown in India is the pomegranate. The International Trade Center states that when it comes to pomegranate production, India leads the world. Every year, about 5On the other hand, not much research has been done on pomegranate fruit quality classification. Because of its high antioxidant content and many health advantages, the pomegranate (Punica granatum L.) is an important crop and food for humans. Pomegranates, like many other fruits, are prone to a number of illnesses, which can have a substantial effect on fruit supply and quality. Accurate evaluation and early identification of these illnesses essential vital to maintaining the sustainability of pomegranate farming and efficient disease control. This research provides a thorough approach for the analysis and treatment of pomegranate fruit-related disorders in this context. In order to provide a comprehensive method for disease diagnosis and prediction, the suggested framework incorporates cutting-edge deep learning techniques, such as multiclass disease classification, semantic segmentation, and severity estimate. Our first framework component employs Convolutional Neural Networks (CNNs) to classify diseases into many classes. We discuss the categorization of four common pomegranate fruit diseases: Cercospora, Alternaria, Anthracnose, and Bacterial Blight. Our methodology enables focused disease management techniques and early intervention efforts by precisely identifying and classifying various disorders. We next perform fine-grained segmentation of sick spots within pomegranate fruit using Semantic Segmentation approaches, namely the UNet architecture. This stage makes it possible to pinpoint the location of afflicted areas precisely, which helps to quantify and visualize the severity of the illness. Annotated images with matching masks or ground truth annotations are supplied as a dataset to train the semantic segmentation model, guaranteeing precise segmentation performance. Additionally, we present a module for estimating the severity of pomegranate fruit diseases using segmented photos as a basis. This module defines severity thresholds for high, medium, and low severity levels after calculating the area and percentage of the segmented regions. The severity estimation module, which makes use of image processing techniques, allows for the real-time assessment of illness severity, which facilitates prompt decision-making and the development of disease management strategies. This finding is important because it has the potential to completely change how pomegranate cultivation handles illness. Our system provides a holistic solution for illness diagnosis and management by merging categorization, semantic segmentation, and severity prediction. This ultimately leads to improved fruit quality, higher produc-

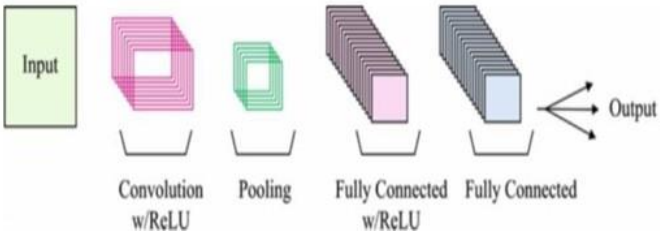


Fig. 1. Architecture of CNN.

tion, and sustainable agriculture practices.

II. DEEP LEARNING MODELS IN POMEGRANATE FRUIT DISEASE DETECTION

A. Multi-class classification using Convolutional neural networks

Convolutional neural networks (CNNs) are a potent tool for recognizing and categorizing a variety of pomegranate fruit diseases, including as Bacterial Blight, Alternaria, Anthracnose, and Cercospora. The way this multi-class classification method operates is by examining the fruit's digital photos. By automatically recognizing patterns and variations in color, texture, and shape within the images, the CNN functions as a multi-layered feature extractor. Then, these patterns are applied to distinguish between fruit that is disease-free and fruit that is contaminated.The CNN gains the ability to identify the distinctive visual traits connected to every disease by being trained on an extensive collection of labeled photos that include instances of each ailment. After being trained, the CNN can identify the most likely ailment present, if any, by analyzing fresh, unviewed photos. With the ability to swiftly and precisely detect problems in their pomegranate crops, farmers and other agricultural experts may find this technology to be a useful tool that promotes early intervention and higher-quality fruit.

A class of deep learning architectures known as convolutional neural networks (CNNs) is motivated by the way neurons in the brain are connected and the structure of the visual cortex. CNNs are made especially for image analysis jobs; they are skilled at using specialized filters to capture different elements and objects in images. Convolutional layers are the brains behind CNNs; they are in charge of feature detection. Convolutional neural networks (CNNs) are a family of deep learning architectures inspired by the architecture of the visual cortex and the connections between neurons in the brain. CNNs are adept at utilizing customized filters to capture various components and objects in images because they were designed specifically for image analysis tasks. CNNs are powered by convolutional layers, which are in charge of feature detection.

Pooling layers, which downsample the feature maps and reduce their spatial dimensions while keeping significant features, usually come after the convolutional layers. The network can learn intricate patterns and relationships within the data by introducing non-linearity through the use of ReLU (Rectified Linear Unit) activation layers. Feature extraction and classification are then carried out by fully connected layers, which combine the characteristics that were collected from the convolutional layers and map them to distinct output classes. CNNs are able to perform accurate classification and recognition tasks by learning to assign learnable weights and biases to objects within the images through the iterative process of forward and backward propagation.

The dimension of the output of a convolutional layer in a Convolutional Neural Network (CNN) can be calculated using the following equation:

$conv(n,k) = ([\ ((iw-fw)/s)+1],[((ih-fh)/s)+1],fc)$

'iw' - input width, 'ih' - input height, 'fw' - filter width, 'fh' - filter height, 'fc' - number of channels or the number of filters in the previous layer, and 's' - the stride value, which determines the number of pixel shifts over the input matrix.

The pooling layer is used to calculate the average or maximum values within each pooling zone, thereby reducing the dimensions of the input data. After going through this procedure, the photos are sharper than they were in the beginning, and they are sent to further layers for more processing. Conversely, the Rectified Linear Unit (ReLU) activation layer makes it easier to compute for the layers that come after by converting input values into non-negative values.

III. SEMANTIC SEGMENTATION USING UNET

Convolutional neural network (CNN) architecture U-Net was created specifically for semantic segmentation tasks in medical picture analysis. In 2015, Olaf Ronneberger, Philipp Fischer and Thomas Brox presented it in their paper "U-Net: Convolutional Networks for Biomedical Image Segmentation." The U-shaped structure of the U-Net architecture, which includes a contracting path, a bottleneck, and an expanded way,is what distinguishes it. The design is commonly used in medical image segmentation, such as recognizing organs or tumors in images, because it is especially well-suited for jobs where detailed localization is required.

A. Unet Architecture

1. Contracting path(Encoder); The contracting path is the left side of the U-shaped network, and it is responsible for capturing context and reducing the spatial dimensions. It is made up of several convolutional layers with tiny receptive fields, each of which has an activation function called a Rectified Linear Unit (ReLU).Maxpooling is used for downsampling, reducing the spatial resolution while increasing the receptive field.

2. Bottleneck: The bottleneck connects the contracting path to the expansive path. It is a bottleneck layer with a high number of convolutional filters, allowing the network to capture high level features and context.

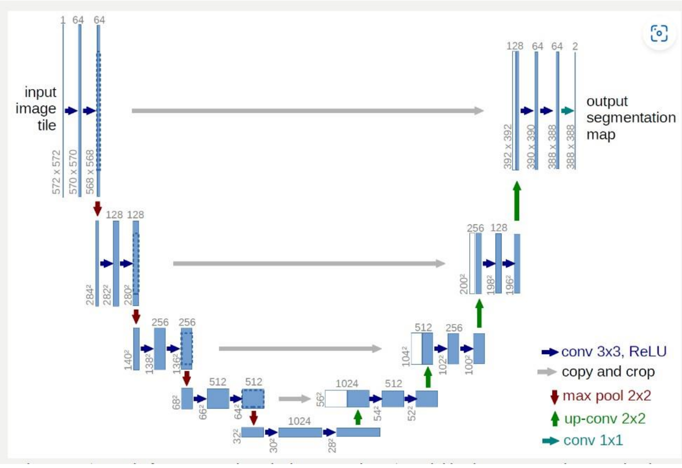


Fig. 2. Architecture of UNET.

3. Expansive Path(Decoder): The expansive path is the right side of the U-shaped network, responsible for precise localization and segmentation. It involves upsampling the feature maps using transposed convolutions to increase spatial resolution. Skip connections are introduced, connecting the corresponding layers from the contracting path to the expansive path. These skip connections help in preserving high-resolution details during upsampling. Each layer in the expansive path consists of a transposed convolution followed by a ReLU activation.

4. Skip Connections: Skip connections are a key feature of the U-Net architecture. They connect the corresponding layers between the contracting and expansive paths. These connections enable the network to use both low-level and high-level features during segmentation. High-level features capture the global context, while low-level features capture specific local information.

5. Final Layer: The last layer maps the high-dimensional feature representation to the required number of output channels using a 1x1 convolution. A suitable activation function is applied, often softmax for multi-class segmentation or sigmoid for binary segmentation, to produce pixel-wise probability maps.

6. Loss Function: The choice of loss function depends on the nature of the segmentation task. Common choices include cross-entropy loss for multi-class segmentation or binary cross-entropy for binary segmentation.

IV. Severity Estimation Of Segmented images

For severity estimation of segmented images, we follow a systematic approach consisting of several key steps. First, we retrieve the segmented images by providing their file paths. Then, we proceed to preprocess these images. This involves converting them to grayscale to simplify further analysis. Subsequently, we employ a thresholding technique to convert the grayscale image into a binary one, where pixels are classified as either foreground or background based on their intensity values. Once we have the binary representation, we move on to quantify the severity of the segmented region. To achieve this, we calculate the total number of pixels in the image, which serves as the denominator for our subsequent computations. Then, we determine the area of the segmented region by counting the white pixels, which represent the segmented portion of interest. With these metrics in hand, we compute the percentage of the segmented region relative to the entire images. Following the quantification of the segmented region, we establish thresholds for defining severity levels. These thresholds delineate what constitutes high, medium, and low severity levels based on the percentage of the segmented region. These predefined thresholds allow us to categorize the severity of each segmented image into distinct levels.

Fig. 3. Samples of Pomegranate fruit diseases dataset: Cercospora, Bacterial Blight, Anthracnose, Alternaria, and Healthy images respectively.

Finally, leveraging these calculated percentages and the predefined severity thresholds, we predict the severity level of each segmented image. By comparing the percentage of the segmented region against the established thresholds, our system autonomously assigns a severity level to each image.

V. Findings and Analysis

This part explains the dataset used, what was done in the experiments, and discusses the outcomes in depth.

A. *Dataset*

We obtained our dataset from Kaggle, a platform for hosting datasets and machine learning competitions. The dataset is called ”Pomegranate Fruit Diseases Dataset for Deep Learning Models”. It contains a total of 5098 images. These images are categorized into five classes representing different diseases and the healthy state of the pomegranate fruit. The classes include ”Alternaria”, ”Anthracnose”, ”Bacterial Blight”, ”Cercospora”, and ”Healthy”.

Classes	Number of images
Cercospora	631
Bacterial_Blight	966
Anthracnose	1166
Alternaria	885
Healthy	1450

Fig. 4. Details of dataset

```
        shuffle=True,
        seed=42
    )
    test_images = test_generator.flow_from_dataframe(
        dataframe=test_df,
        x_col='Filepath',
        y_col='Label',
        target_size=TARGET_SIZE,
        color_mode='rgb',
        class_mode='categorical',
        batch_size=BATCH_SIZE,
        shuffle=False
    )
```

```
Found 3569 validated image filenames belonging to 5 classes.
Found 1530 validated image filenames belonging to 5 classes.
Found 5099 validated image filenames belonging to 5 classes.
```

Fig. 5. Code part of spitting of dataset (classification stage)

Spitting of dataset for training and testing in classification stage and semantic segmentation stage is mentioned using the screenshots.

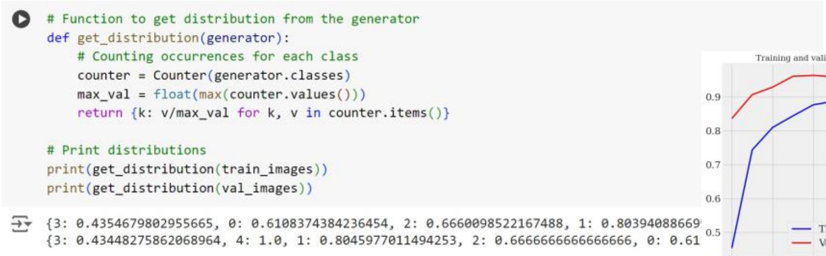
B. Performance Evaluation of CNN model

The current Classification Model based on CNN, hyperparameter values are shown below Table 2. The confusion matrix, also known as the error matrix, is a specific table used to evaluate the performance of a model. It provides a summary of the model’s predictions, particularly in multiway classification tasks like ours. In our case, we are classifying 4 types of diseases ‘Alternaria’,’Anthracnose’,’Bacterial$_{B}$*light′,′ Cercospora′*.

The confusion matrix, as depicted below,

Sensitivity, also known as true positive rate or recall, is a metric that measures the proportion of actual positive cases that are correctly identified as positive by the model.

Sensitivity =TP/(TP+FN)



```
# Function to get distribution from the generator
def get_distribution(generator):
    # Counting occurrences for each class
    counter = Counter(generator.classes)
    max_val = float(max(counter.values()))
    return {k: v/max_val for k, v in counter.items()}

# Print distributions
print(get_distribution(train_images))
print(get_distribution(val_images))
```

```
{3: 0.4354679802955665, 0: 0.6108374384236454, 2: 0.6660098522167488, 1: 0.80394088669
{3: 0.43448275862068964, 4: 1.0, 1: 0.8045977011494253, 2: 0.6666666666666666, 0: 0.61
```

Fig. 6. Classification- Distributions

```
        CSVLogger(csv_path),
        EarlyStopping(monitor='val_loss', patience=20, restore_best_weights=False),
    ]

    model.fit(
        train_dataset,
        epochs=num_epochs,
        validation_data=valid_dataset,
        callbacks=callbacks
    )
```

```
Train: 600 - 600
Valid: 200 - 200
Test : 200 - 200
Epoch 1/50
38/38 [==============================] - ETA: 0s - loss: 0.5549 - dice_coef: 0.4480
Epoch 1: val_loss improved from inf to 0.78549, saving model to files/model.h5
/usr/local/lib/python3.10/dist-packages/keras/src/engine/training.py:3103: UserWarning: You are saving your model a
  saving_api.save_model(
38/38 [==============================] - 409s 10s/step - loss: 0.5549 - dice_coef: 0.4480 - val_loss: 0.7855 - val_
Epoch 2/50
```

Fig. 7. Semantic segmentation- Distributions

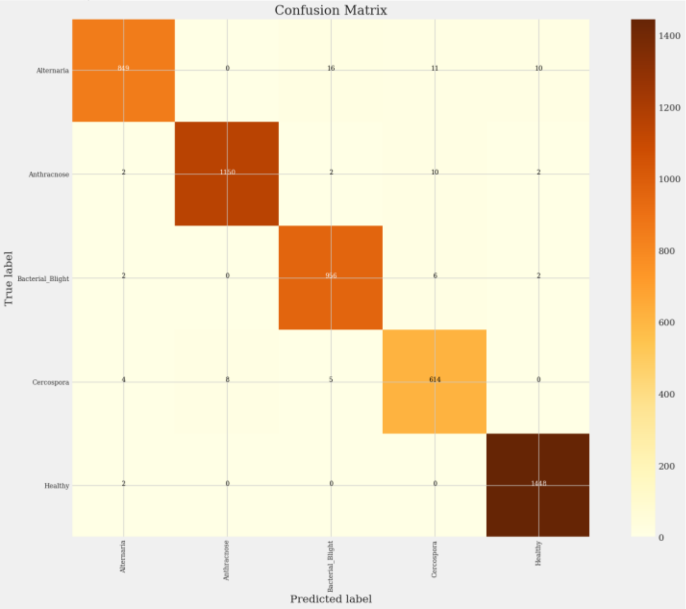


Fig. 8. Confusion matrix

Specificity refers to the ratio of true negatives to the total number of actual negatives, indicating the accuracy in identifying instances that are truly negative.

Specificity= TN/(TN+FP)

Recall represents the percentage of true positives correctly identified.

Recall = TP/(TP+FN)

F-score: It’s a metric that gauges how accurate a model is on the given dataset.

F-score = 2*((precision*recall)/(precision + recall))

Precision: It refers to the fraction of predicted positive

Fig. 9. Performance Parameter graph

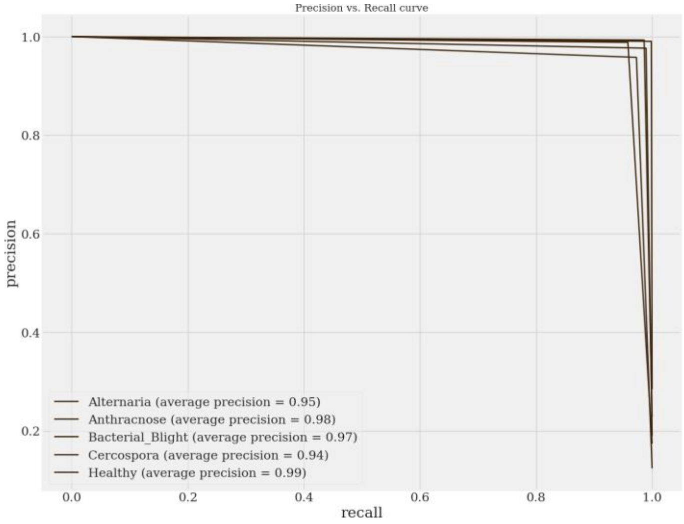


Fig. 10. Precision vs Recall curve

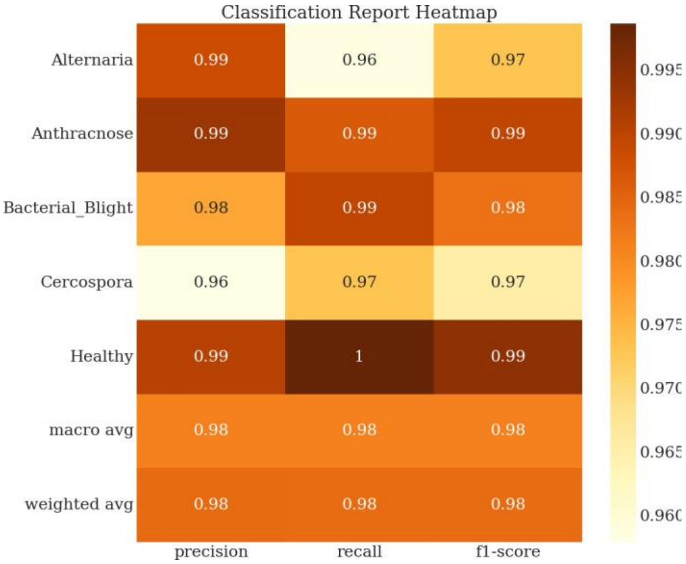


Fig. 11. Classification report

instances that are genuinely true positives.

Precision= TN/(TN+FP)

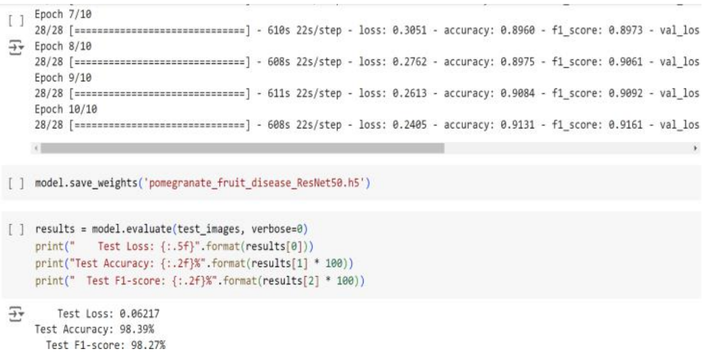
Accuracy: It refers to the primary measure of performance, indicating the proportion of correctly predicted observations out of the total observations. It represents the capability to differentiate between normal and abnormal cases.

Accuracy = (TP+TN) / (TP+TN+FP+FN)

False positives and false negatives are type-I and type II error respectively.

C. Semantic segmentation using UNET

In this study, we utilized the Label Studio online tool to annotate images within the ”Pomegranate Fruit Diseases Dataset for Deep Learning Models.” These annotations were then employed for segmentation tasks, specifically using the UNet model.500 epocs are used for this result. Images of diseases,Annotations,Segmentation masks are given below respectively.



```
Epoch 7/10
28/28 [==============================] - 610s 22s/step - loss: 0.3051 - accuracy: 0.8960 - f1_score: 0.8973 - val_los
Epoch 8/10
28/28 [==============================] - 608s 22s/step - loss: 0.2762 - accuracy: 0.8975 - f1_score: 0.9061 - val_los
Epoch 9/10
28/28 [==============================] - 611s 22s/step - loss: 0.2613 - accuracy: 0.9084 - f1_score: 0.9092 - val_los
Epoch 10/10
28/28 [==============================] - 608s 22s/step - loss: 0.2405 - accuracy: 0.9131 - f1_score: 0.9161 - val_los
```

```
model.save_weights('pomegranate_fruit_disease_ResNet50.h5')
```

```
results = model.evaluate(test_images, verbose=0)
print("    Test Loss: {:.5f}".format(results[0]))
print("Test Accuracy: {:.2f}%".format(results[1] * 100))
print("  Test F1-score: {:.2f}%".format(results[2] * 100))
```

```
    Test Loss: 0.06217
Test Accuracy: 98.39%
  Test F1-score: 98.27%
```

Fig. 12. Classification output

```
        recall_value = recall_score(mask, y_pred, labels=[0, 1], average="binary", zero_division=0)
        precision_value = precision_score(mask, y_pred, labels=[0, 1], average="binary", zero_division=0)
        SCORE.append([name, f1_value, jac_value, recall_value, precision_value])

    """ Metrics values """
    score = [s[1:] for s in SCORE]
    score = np.mean(score, axis=0)
    print(f"F1: {score[0]:0.5f}")
    print(f"Jaccard: {score[1]:0.5f}")
    print(f"Recall: {score[2]:0.5f}")
    print(f"Precision: {score[3]:0.5f}")

    df = pd.DataFrame(SCORE, columns=["Image", "F1", "Jaccard", "Recall", "Precision"])
    df.to_csv("files/score.csv", index=False)
```

```
100%|██████████| 200/200 [02:22<00:00,  1.40it/s]F1: 0.67088
Jaccard: 0.54698
Recall: 0.73715
Precision: 0.66353
```

Fig. 13. Segmentation output

D. Severity estimation of segmented images

This module assesses the area and proportion of segmented regions, establishing thresholds for high, medium, and low severity levels. By utilizing image processing methods, our

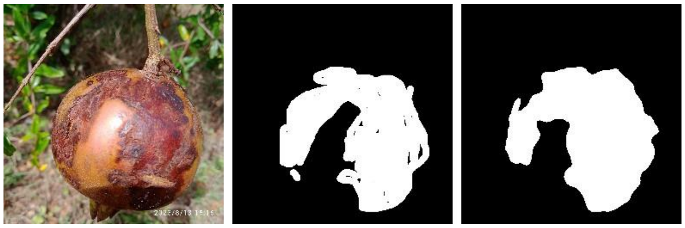


Fig. 14. Cercospora-input image,annotation,segmentation mask respectively

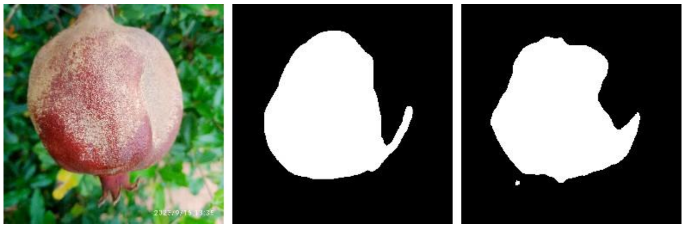


Fig. 15. Alternaria-input image,annotation,segmentation mask respectively

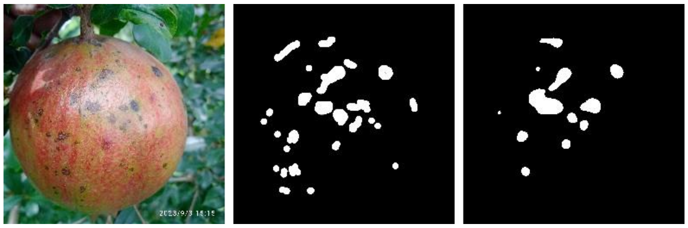


Fig. 16. Anthracnose-input image,annotation,segmentation mask respectively

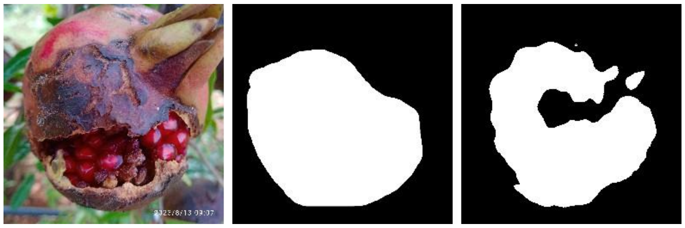
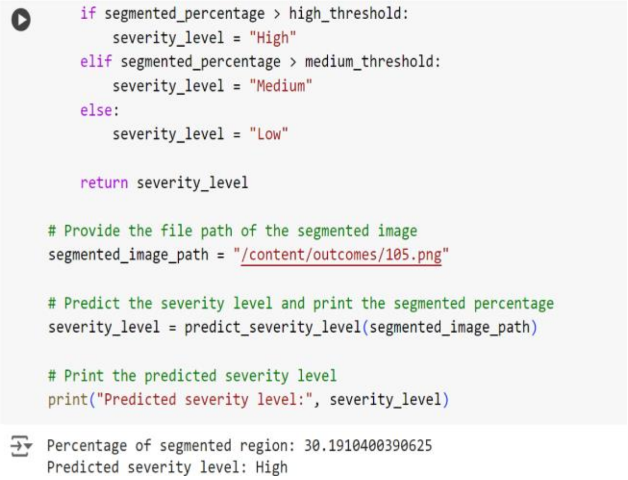


Fig. 17. Bacterial Blight-input image,annotation,segmentation mask respectively

module enables rapid evaluation of disease severity, aiding in timely decision-making and the implementation of disease management strategies.

VI. CONCLUSION AND FUTURE SCOPE

The project undertakes a multi-faceted approach to address the diagnosis and severity assessment of pomegranate fruit diseases, employing advanced deep learning methodologies. Initially, the project focuses on the classification of prevalent diseases including Alternaria, Anthracnose, Cercospora, and Bacterial Blight, utilizing Convolutional Neural Networks (CNN). Subsequently, semantic segmentation techniques are employed using UNet architecture to accurately delineate diseased regions within pomegranate fruit images. This segmentation process provides detailed insights into the spatial extent



```
    if segmented_percentage > high_threshold:
        severity_level = "High"
    elif segmented_percentage > medium_threshold:
        severity_level = "Medium"
    else:
        severity_level = "Low"

    return severity_level

# Provide the file path of the segmented image
segmented_image_path = "/content/outcomes/105.png"

# Predict the severity level and print the segmented percentage
severity_level = predict_severity_level(segmented_image_path)

# Print the predicted severity level
print("Predicted severity level:", severity_level)
```

```
Percentage of segmented region: 30.1910400390625
Predicted severity level: High
```

Fig. 18. Severity Prediction


Fig. 19. Alternaria-Severity levels: High, Medium, Low respectively.

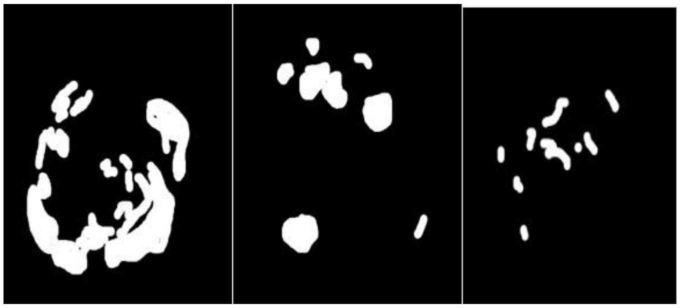


Fig. 20. Anthracnose-Severity levels: High, Medium, Low respectively.

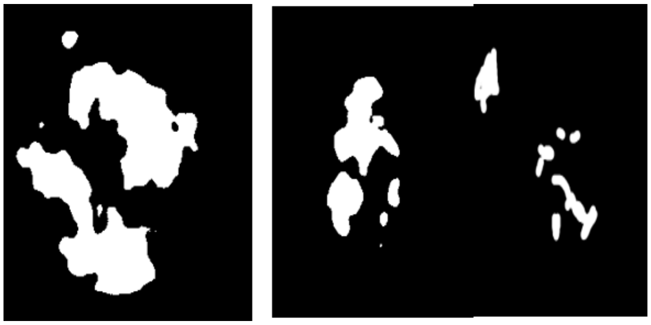


Fig. 21. Cercospora-Severity levels: High, Medium, Low respectively.

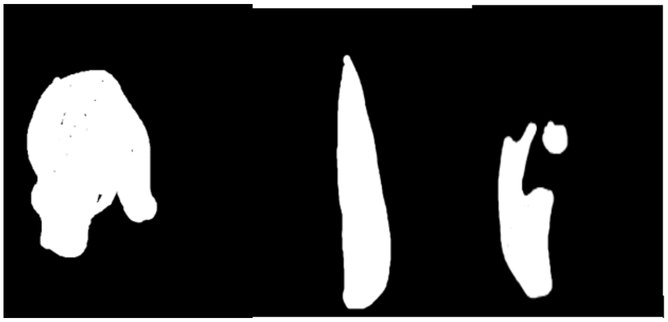


Fig. 22. Bacterial Blight-Severity levels: High, Medium, Low respectively.

of each disease, enabling precise localization and analysis. Building upon the segmented diseased regions, the project further extends its capabilities by predicting the severity of each disease instance, categorizing them into high, medium, or low severity levels. However, the project identifies certain limitations and outlines future research directions. Notably, while severity prediction based solely on the affected area is a significant advancement, the depth of the disease within the fruit is acknowledged as an important factor that requires further investigation. Research endeavors are warranted to develop methodologies capable of capturing the three- dimensional aspects of fruit diseases, thereby enhancing the accuracy of severity assessment. Moreover, the project recognizes the challenge posed by the presence of multiple diseases within a single image, which may lead to inaccuracies in the system's output. Addressing this complexity requires innovative approaches to discern and characterize multiple diseases simultaneously, thereby improving the system's diagnostic capabilities. Furthermore, the scarcity of datasets containing corresponding masks for image segmentation presents a significant hurdle. The manual creation of masks using tools like Label Studio Online is labor-intensive and time-consuming. Hence, there is a pressing need to develop automated methods or algorithms for efficiently generating masks, facilitating dataset expansion and system scalability. In conclusion, the project represents a significant contribution to the field of agricultural disease management, leveraging deep learning techniques for the accurate diagnosis and severity assessment of pomegranate fruit diseases. By identifying key areas for future research and development, the project lays the foundation for enhanced disease management strategies and contributes to the body of knowledge in this domain.

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