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Automated Detection of Wheat Powdery Mildew Using YOLACT Instance Segmentation

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***Abstract*:There is a 5% annual decline in wheat results worldwide due to Blumeria graminis f. sp. tritici (Bgt), which makes an accurate identification methodology important. This study addressed the challenges encountered in early wheat powdery mildew detection through the development of an innovative technique that makes use of the YOLACT model, a real-time object recognition system. The review of the literature covers a variety of approaches, such as deep learning and hyperspectral imaging, with an emphasis on YOLACT incorporation for improved early detection. The study describes dataset collection, YOLACT integration, and preparation methods. Having a 95.6% recognition rate, a mean Intersection over Union (MIoU) of 0.85, a precision of 0.81, and a mean average precision (mAP) of 0.56, the results illustrate the efficiency of the YOLACT model. Comparative assessments illustrate how much stronger the suggested YOLACT methodology is. The study concludes by highlighting the accuracy of the YOLACT model in detecting wheat powdery mildew and stressing the value of texture analysis and the best possible combination of vegetative indices (VIs) for early diagnosis. By fusing technology with realistic farming situations, the YOLACT model not only increases disease identification but also can entirely reinvent agriculture and increase crop cultivation's sustainability and efficiency practices**

Keywords:Wheat diseases, Segmentation, Deep learning, pretrained modelsPowdery Mildew, YOLACT

I. INTRODUCTION

Triticum aestivum L., or bread wheat, is an important staple grain that provides 20% of the world's daily caloric intake [1]. However, there is a serious threat to the world's wheat supply in the form of wheat powdery mildew, which is mostly caused by Blumeria graminis f. sp. tritici (Bgt) and results in a 5% yearly loss [2]. Conventional identification techniques, which require laborious laboratory testing and visual inspections, are unreliable and time-consuming. While accurate, traditional methods including polymerase chain reaction (PCR), immunofluorescence, enzyme-linked immunosorbent assay (ELISA) [3], and fluorescence in situ hybridization (FISH) have significant execution times. Due to the time-consuming nature of collecting field samples, district-level machine learning (ML) techniques like Bayes splitting, decision trees, and support vector machines have restrictions that prevent real-time use [4]. Although disease-resistant cultivars and pesticides are frequently used, their disadvantages—such as increased costs and environmental impact—lead to the quest for substitute alternatives [5]. Early disease severity evaluation and identification are necessary for the timely use of fungicides (DS). RGB (color, shape, and texture) photography provides useful disease distinction, while it has drawbacks such as difficult background removal and changing illumination. In this work, we steer clear of the complications related to hyperspectral imaging and instead concentrate on cutting-edge deep learning techniques, especially employing the novel YOLACT model [6], [7]. The objective of this research is to apply new insights obtained from texture and spectral data to overcome challenges, improve early detection, and quantitatively evaluate wheat powdery mildew.

Organization of this paper:

This paper is organized into the following sections. The methods for gathering datasets, integrating the YOLACT model, and detecting wheat powdery mildew are briefly described in Section 2. A thorough summary of the YOLACT model integration and wheat powdery mildew detection results is provided in Section 3. In Section 4, the results are analyzed in detail, the study's shortcomings are acknowledged, and suggestions for improvement are made. Section 5 concludes by summarizing the main findings and drawing conclusions.

II. RELATED WORK

Several researchers [1] use Genetic host resistance characterized by either race-specific (qualitative), race-non-specific (quantitative), or both types of resistance. Sophisticated techniques in breeding and selection are employed to transfer resistance from diverse genetic resources to superior cultivars—methods for molecular breeding, such as high-throughput genotyping using sequencing or chip arrays. The use of marker-assisted selection (MAS) in molecular breeding techniques is highlighted.

Feng et al. [2] discuss the canopy spectral reflectance measured during wheat's flowering and filling phases using a ground feature type spectrometer. Data Preprocessing, Special

Transformation, Feature Extraction, and Modelling Techniques were used. The model with the highest overall performance was the Random Forest Regression (RFR), whose coefficient of determination (R2) varied between 0.741 and 0.852. With R2 ranging from 0.849 to 0.852, the mean centralization (MC) method paired with the RFR model (MC-RFR) yielded the maximum estimation accuracy of spectral data processing.

The authors [3] use Hyperspectral images of wheat crops, with an emphasis on both healthy and powdery mildew-affected samples, to make up the dataset utilized in this work. The approach uses hyperspectral pictures and machine learning to detect early artifacts in multiple steps: Characteristic Extraction by taking vegetation indices (VIs) and normalized difference texture indices (NDTIs) out of hyperspectral photos, Improvement using NDTIs and VIs to intensify the difference between wheat damaged by powdery mildew and healthy wheat, Classification of Powdery mildew is detected by using partial least-squares linear discrimination analysis. To increase identification accuracy, optimum features (VIs & NDTIs) are combined. To evaluate the severity of an illness, a regression model based on partial least-squares regression is developed (DS). Achieving a Kappa coefficient of 0.56 and an overall accuracy rating of more than 82.35%. These indicators demonstrate the model's ability to detect unhealthy leaves at early stages, even in circumstances where symptoms are invisible and hard to detect with standard methods. With a coefficient of determination (R2) beyond 0.748 and 0.722 for calibration and validation, respectively, the calibrated and validated DS determine model functions well.

Kusch, et al. 2023[7] made Developments in proteomics and genomics, especially in the case of wheat powdery mildews (genus Blumeria)—insights about these fungi's genetic adaptability methods. The determination of how transposable elements influence the genomes of powdery mildews. Identification of the adaptable genome architecture in the absence of clear conserved gene space areas. Transposons are neo-functionalized to produce new virulence factors, especially putative secreted effector proteins. Investigation of effector identification by plant immune receptors expressed by several allelic variations of resistance genes. Effectors rapidly evolve due to copy number variation and sequence diversification.

Mapuranga, et al.2022[8] used More than 100 powdery mildew resistance genes or alleles that have been found in common wheat and its wild relatives, aligning to 63 distinct loci (Pm1–Pm68). Combining temperature conditions with the genetics of host-pathogen interactions. Investigation of relationships in the wheat genome between resistance genes and other resistance genes or a virulence gene that relate to them in pathogens. The pathogenic mechanisms of Blumeria graminis f. sp. tritici (Bgt) are becoming clearer.

Sosa-Zuniga, et al.2022[9] were able to achieve identification of grapevine cultivars resistant to powdery mildew. Pay attention to the Run (Resistance to Uncinulanecator) and Ren (Resistance to Erysiphe necatar) gene families, which are the two primary gene families in the Vitaceae that give resistance to powdery mildew. These resistance genes are used in grapevine breeding initiatives to create novel cultivars that are genetically resistant to powdery mildew.

Liang and Wang [10] used wheat Powdery mildew spore image dataset. Deep learning technique applied to picture segmentation with particular attention to photos of wheat powdery mildew spores. Introduction of a better U-Net-based framework- Following the 1024-channel feature map in the down-sampling phase, a pyramid pooling module is added to extract various-sized pooling features and merge them into a global feature map. Several skip connections in the original U-Net were adjusted to get more features that were useful for segmenting spore images. The dataset of wheat powdery mildew spore images showed a segmentation mean intersection over union of 91.4%.

With a focus on Powdery Wheat (PW) disease, the study [11] uses deep learning (DL) and machine learning (ML) techniques to classify wheat diseases. - For the classification task, a convolutional neural network, or CNN, is employed. The CGIAR pictures dataset is used to apply transfer learning, which uses a pre-trained model. The CNN classifies PW wheat illness with an accuracy of 89.9% when tested using photos. Using transfer learning, the pre-trained model achieves an 86.5% classification accuracy on photos from the CGIAR dataset. The dataset used in the study is made up of 450 photos of wheat that were gathered from primary and secondary sources. The CNN is trained and tested using this dataset. A different dataset, the CGIAR pictures dataset, is mentioned where transfer learning is used to apply the pre-trained model.

III. MATERIALS AND METHODS

The materials and methods which are performed for experimentation are briefly explained in this section.

A. Dataset collection:

To recognize the powdery mildew disease recognition, a total number of 2000 images were collected from secondary sources. As, the number of collected images is too short for training purposes in the YOLACT model, which is further increased by data augmentation cropping, flipping, and rotation techniques. With the usage of data augmentation techniques, a total number of 5500 wheat images have been generated. The augmentation images generated by image augmentation techniques are shown in Figure 1.

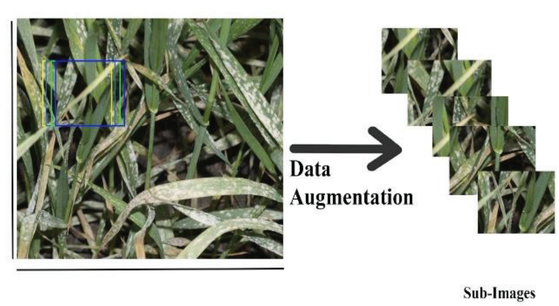

Fig. 1. Sample of augmented images

B. Architecture of YOLACT model:

A 101-layer residual network (ResNet-101) is used by the YOLACT model in this paper's analysis. ResNet-101 [13], a feature extraction network with superior performance and lower processing power requirements, is employed. Furthermore, Deformable Convolutional Neural Networks (DCNs) are used every three stages (C3 to C5) on the ResNet-101 [14]. This indicates that for every 3 x 3 convolutional layer in the ResNet module, the network replaces it with 3 × 3 deformable convolutional layers. The DCNS structure has been introduced to this network since YOLACT is a one-shot sampling technique that does not require a resampling step. . DCNs can also increase the network's ability to accommodate different aspect ratios, rotations, and scaling [15]. The sampling approach of the ResNet network was modified. The overflow of the YOLACT model is shown in Figure2.

YOLACT is a one-shot sampling method that does not require resampling by adding CNN structure to improve the network ability to handle different scales, rotations, and aspect ratios. The ResNet sampling method has been changed to free sampling. This function remaps the mask based on the excess intersection (IoU) of the expected leaf mask and the original leaf mask.

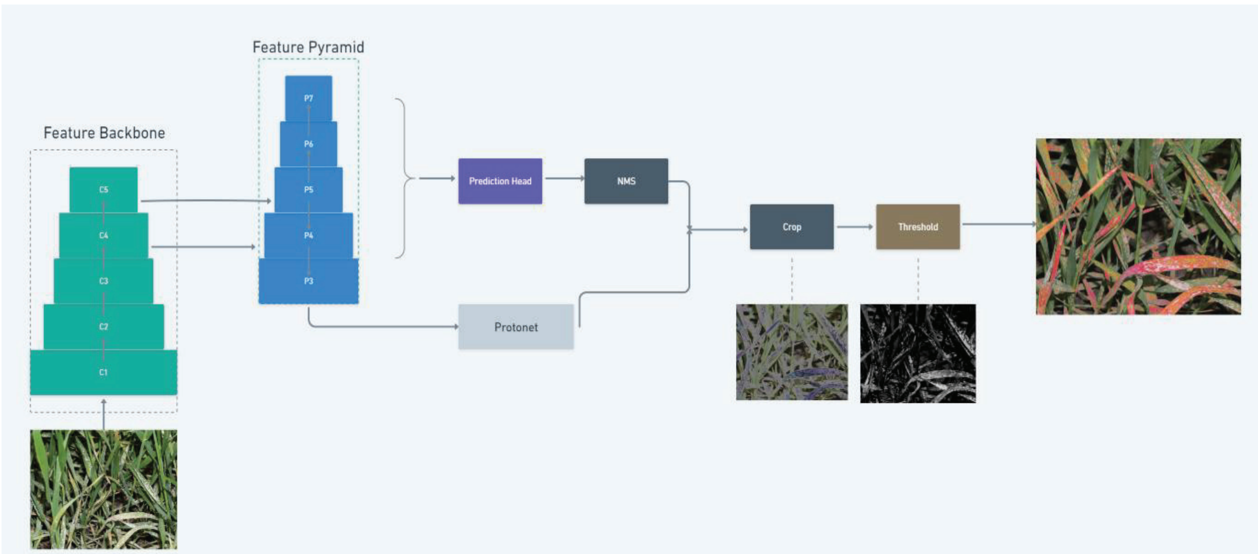

Fig. 2. Overview of YOLACT model

IV. EXPERIMENTAL RESULTS AND DISCUSSIONS

A laptop with an AMD Ryzen 5 5600H processor with 3.30 GHz Radeon Graphics and 16.0 GB of installed RAM (15.4 GB useable), was used in the experimental setting up. The programming language used on the system was Python version 3.7, and it ran on a 64-bit Windows 11 environment. The goal of this setup was to achieve the greatest computational efficiency for efficient network model testing and training. The IoU threshold quantifies the overlap between true and predicted values. In the experiment, only IoU values greater than 0.5 were considered correctly predicted. Figure 3 shows the segmentation results at different IoU thresholds.

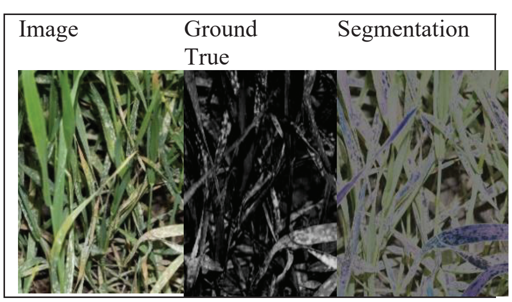

Fig. 3. Segmentation results achieved by YOLACT model

A. Prediction results:

The accuracy of the YOLACT model was the main performance variable applied to assess the model's effectiveness. When evaluating the model's ability to locate and characterize wheat powdery mildew, accuracy is crucial.Table 1 illustrates the accuracy, mIoU, and total segmentation rate (mAP) of the network for Powdery mildew disease segmentation.

TABLE I. EVALUATION PARAMETERS OF THE YOLACT MODEL

Performance parameters	**Recognition rate**
Accuracy	95.6%
Mean Intersection over Union (MIoU)s	0.85
Precision	0.81
Mean average precision (mAP)	0.56

B. Prediction results comparison:

To validate the performance of the proposed method in this study, we compared it to state-of-the-art instancesegmentation models, as shown in Table 2.

TABLE II. PERFORMANCE COMPARISON OF THE YOLACT MODEL WITH THE PREVIOUS STATE OF ART MODELS

References	Techniques	Dataset Samples (images)	Achieved Accuracy (%)
Wang et al. [1]	CNN	450	85.6
Khan et al. [4]	Canopy Spectral Reflectance	1526	90.3
Kumar & Kukreja [11]	CNN	450	89.9
Our study	YOLACT	450	95.6

V. CONCLUSION AND FUTURE SCOPE:

The study indicates that the YOLACT model and advanced deep learning techniques perform together effectively to precisely recognize wheat powdery mildew. Using a particular emphasis on temporal spectrum analysis and feature selection, the model demonstrates high sensitivity and offers a solid foundation for disease identification. Texture analysis tackles issues with hyperspectral pictures, primarily through Normalized Difference Texture Indices (NDTIs). The ability to differentiate between healthy and ill leaves has been enhanced by using a mix of vegetative indices (VIs) and non-destructive examination indicators (NDTIs), specifically the Partial Least-Squares Discriminant Analysis (PLS-LDA). With detectable alterations occurring three to six days post-vaccination, the approach offers a quick diagnosis of the illness. With the use of connected features, ranging this new Partial Least Square Regression (PLSR) model correctly evaluates disease severity throughout the various phases of development. This study offers significant improvements to the field of agricultural disease detection by providing useful methods for precisely and rapidly identifying wheat powdery mildew. At the crossroads of agriculture and technology, these findings are critical to better crop management and sustainable farming methods. The integration of additional data sources, such as thermal imaging, may be studied in future research to ensure continued relevance through agricultural technology optimization. Field tests conducted in a variety of circumstances will evaluate the model's viability in actual farming.

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