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CentralMaizeGuard: Enhanced deep learning model for maize disease detection and management

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The detection of maize plant leaf diseases is a critical aspect of agricultural management, necessitating accurate and efficient methodologies. The field of maize plant leaf disease detection encounters several challenges that hinder the development of robust and effective solutions. One prominent challenge is the diversity of disease indicators, wherein various pathogens can cause similar symptoms, making it challenging to differentiate between diseases accurately. Additionally, limited annotated datasets pose a constraint, hindering the training of deep learning models and potentially leading to suboptimal generalization. The dynamic nature of plant growth and environmental conditions further complicates disease detection, as the appearance of symptoms may vary at different stages of plant development. Another challenge lies in achieving a balance between accuracy and computational efficiency, especially in real-time applications, as many existing models struggle to provide rapid and precise results simultaneously. This paper addresses prevailing challenges in disease detection by introducing a customized CenterNet approach, incorporating DenseNet-65 as its foundational architecture. Common issues encountered in traditional disease detection models are addressed through our proposed approach, which demonstrates superior performance in both disease classification and precise localization of affected regions. A comparative analysis is conducted against conventional and contemporary methodologies, emphasizing the innovation and competitiveness of our model in advancing maize plant leaf disease detection. We evaluated our approach on a standard dataset CD&S and attained a classification accuracy of 98.62%. This contribution not only expands the current understanding of disease detection in agriculture but also offers a practical and efficient solution for improved maize crop management.

Key words: CenterNet, classification, deep learning, DenseNet, maize plant

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1. Introduction

Maize or corn is an important agricultural plant grown worldwide. In comparison to other crop types, maize has the highest worldwide yield and is crucial for supplying raw material, energy, and nutrition to an increasing number of humans worldwide [1]. Maize is a significant contributor of various ingredients for numerous commercial products. Maize has a substantial value because it is widely used as the main source of nourishment for humans as well as livestock. The maize plant is susceptible to several diseases that can cause a yearly decline of 7% to 10% [2, 3], regardless of its great productivity capabilities. Most maize illnesses are brought on by different molds, bacteria, infections, and viroid. Fading leaf shades, rot, scab, plague, necrotic tissue, brownish color, and malformations are common signs of illness that can be used to discover and identify foliar illnesses in corn plants. The three main fungi illnesses found in the production of maize plants are categorized as i) The Northern corn leaf blight (NLB), ii) southern corn leaf blight (SLB), and iii) grey leaf spot (GLS) [4]. At present, reliable recognition of corn leaf ailments is a crucial precaution for the yield of maize for growers without expertise. The in-person screening of leaves used in the conventional approach for identifying maize diseases relies on the expertise of farming professionals as well as an understanding of crop pathogens. Such methods result in incorrect understanding of the illness frequently leading to inadequate insecticide applications, which not only harm the ecosystem but also worsen corn's toxicity. Consequently, systems that can track the growth of maize plants and diagnose illnesses quickly and precisely are needed.

The surveillance and prediction of crop illnesses have recently gained significant importance because of the evolution of technological innovations like satellite imaging, GPS, and global data systems [5, 6]. Classical crop infection diagnosis approaches are gradually being replaced by computerized techniques that employ machine learning (ML), and deep learning (DL) methods as a result of the rapid advancement in the area of computer vision [7]. Recently, as a potential substitute for physical examination, various automatic plant illness detection approaches centered on digital images have been developed [8]. At first, hand-engineered characteristics derived from ML techniques were used in farming to boost the capacity for making decisions. Different methods have been used in the past as key point descriptors for describing the characteristics of the employed visuals, including the grey level co-occurrence matrix (GLCM) [9], structural patterns [10, 11], and color spaces [12], among others. These methods consider appearance, color, organization, and other analytical factors to obtain sample appearance characteristics, which results in a streamlined illustration of plant pathogens [13]. To execute the classification process of leaf abnormalities, these collected characteristics are passed as input to tune various ML predictors like Random Forest (RF) [13], support vector machine (SVM) [15, 16], or neural network (NN) [17] approaches. Although hand-engineered key points calculation techniques are simple to implement and only need a few samples, these techs involve human knowledge and demand a lot of computing time.

Because of its improved capacity for recognizing patterns and distributing them into related groups, DL networks, a category of ML approaches, have recently grown in importance. DL techniques involving convolution NNs (CNN) [14], recurrent NNs (RNN) [15], and deep belief networks (DBN) have been extensively applied for a variety of jobs, containing agriculture-related activities like production volume prediction, plant type classification, and crop diagnostics for diseases (CBD) [20]. CNNs have been one of the most widely used DL approaches because of their capacity to derive semantic descriptions from the given visual images and then acquire organizational structures in an adaptable manner [16]. CNN architecture is equipped with the ability to retrieve key image attributes from the training set regardless of the involvement of human subject-matter specialists, enabling better decisions to be made. Because of the robustness of DL frameworks, these are heavily investigated in the farming industry including maize crop analysis. Various works have utilized the idea of transfer learning by employing pre-tuned DL approaches like VGG, residual networks [17], GoogleNet [18], and Dense frameworks [19, 20]. While others propose custom DL approaches to accomplish the recognition of different plant disorders [21–25]. These methods can produce precise findings with little data preparation or computational expense. In addition, DL strategies surpass previous approaches by using geometric data from the provided visuals and are resistant to changes like angle, resizing, and rotation. Additionally, these methods exhibit outstanding precision in determining the existence of maize diseases when used with pre-trained architectures [17, 20, 26]. Most of the currently used techniques categorize maize illness at the image level, which is recorded in confined experimental environments and has a significant chance of false-positive results.

Since the dataset is created under controlled conditions, it embodies ideal scenarios characterized by consistent background surroundings and the absence of imperfections like clutter and blurriness in the samples. Consequently, models trained on such data tend to exhibit misclassification when applied to images taken in more realistic environments, often yielding a higher rate of false positives. It is of utmost importance to accurately identify instances of maize abnormalities in field samples to achieve an enhanced recognition power (recall rate). Accomplishing both the precise identification and associated categorization of these disease spots within the maize can be invaluable for agricultural experts or users, as it provides additional vital information such as the size and location of the infected areas. This supplementary data further facilitates the assessment of disease severity on a larger scale and aids in devising appropriate treatment strategies. Currently, there is an ongoing and continuous development of deep learning frameworks for identifying objects. Cutting-edge frameworks like SSD [27], YOLO [28], and Faster-RCNN [29] exhibit strong capabilities in promptly localizing and cataloging objects in real-world scenarios. However, there has been limited research addressing the intricate agricultural task of simultaneously localizing and finely categorizing plant diseases [43–45]. In a related work [30], a Region-based CNN is employed to precisely determine the location and category of maize illness, yielding reasonable outcomes. Despite the efficacy demonstrated by deep learning methods, achieving reliable classification and recognition of maize disease from field samples remains a tough challenge. During the process of creating a robust model, researchers encounter several noteworthy challenges. These encompass tasks like preparing the data, managing variations both within samples and between classes, and addressing unfavorable lighting conditions, which encompass distortions and occlusions [31]. The existence of sophisticated background interference further hinders the precise recognition of plant diseases in real-world situations. Given that backgrounds can be complicated and obscure elements of interest, discerning the subtle attributes of multi-class plant diseases could prove to be effective. Additionally, there is a strong demand for models that are efficient in terms of computational requirements and can provide faster inference speeds, especially for applications in real-time agriculture.

The current strategy is focused on overwhelming the problems of existing works by presenting an effective DL approach called CentralMaizeGuard. Clearly, an improved CenterNet approach is suggested by presenting a more robust key points extractor to recognize the various groups of maize leaves in field samples. We have altered the conventional CenterNet approach by using the DenseNet-65 network to estimate a more relevant set of sample attributes. Improvements made to the conventional CenterNet approach enhance its capacity to capture prominent features even for samples with challenging backgrounds and dynamic environmental scenarios. By employing an end-to-end training approach, the model adeptly conducts both detection and classification tasks, showcasing commendable efficacy within real-world conditions. The unique attributes of our framework are delineated below:

1. An improved DL strategy called the CentralMaizeGuard is proposed with effective visual information capabilities to robustly recognize the various types of maize leaf abnormalities.
2. We employed DenseNet as the base network which ensures that the information from earlier layers is readily available and contributes to the learning

process in later layers, allowing the network to estimate both low-level and high-level features, ultimately enhancing the model's ability to represent complex patterns in images.

3. Enhanced identification and categorization of infected regions on maize plant leaves are achieved through the improved recall empowerment of the introduced method, attributed to the inclusion of an effective feature extractor.
4. Through extensive experimentation conducted on an openly available database, we showcase the effectiveness of our methodology. The outcomes underscore the commendable performance of our approach even in tough scenarios encompassing factors like complex backgrounds, fluctuating illumination conditions, and diseased region size variations.

The subsequent sections of the paper are organized as follows: Section 2 investigates prior research pertaining to disease identification in plants, with a specific focus on diseases affecting maize crops. In Section 3, we explain the employed methodology and provide a comprehensive breakdown of the model's architecture. Section 4 provides insights into the employed dataset, implementation process, and experimental configuration, as well as the resultant findings and subsequent discussion. Ultimately, our conclusions and potential directions for future exploration are presented in Section 5.

2. Related work

This article [32] outlines a methodology for detecting maize leaf disease in IoT nodes. Initially, IoT nodes were modeled to gather visual characteristics of plant samples, and the obtained data was transferred via optimized routes nominated by employing the Competitive Shuffled Shepherd Optimization approach. This phase was devised by integrating CSO and Shuffled Shepherd Optimization to determine the most efficient path. In this research work, the procedure of leaf abnormality recognition involved several steps. Pre-processing was conducted through ROI extraction, and numerous features such as CNN, and energy texture key points were extracted. Ultimately, the maize leaf illness was identified from the calculated key points using a Deep Quantum Neural Network (Deep QNN). The weights of this method were tuned employing the proposed CSSO network. In summary, the paper proposes a comprehensive approach that includes IoT node simulation, optimal route selection, and a multi-step detection process using advanced algorithms for efficient maize leaf disease detection. In [33], the author addressed the issue of disease detection and classification in maize crops by leveraging DL models. The developed application not only identified and classified diseases but also segmented infected portions of input samples. This segmentation capability permitted the tracking of disease spots on individual leaves. To achieve this, a data sample comprising 3 classes of maize plant abnormalities was taken from the University Research Farm Koont, PMAS-AAUR, across various growing phases and with varying environmental settings. The gathered dataset was utilized to tune several prediction frameworks, comprising various versions of YOLO. The application's focus is on delivering accurate recognition of viruses in maize crops while providing valuable insights through segmented images, enhancing the monitoring of disease progression on individual leaves, however, unable to recognize small-sized infected areas. The paper in [34] introduced a dense CNN framework called NPNet-19 designed for identifying infections in maize crops. The approach's performance and resilience were evaluated by utilizing an expanded data sample comprising 15 960 samples, enabling classification across 7 groups with 6 as infected categories and 1 as non-infected class. The main testing sample was sourced from maize fields in Telangana. The training phase involved samples from the PlantVillage and open-source datasets. The approach exhibited an accuracy of 97.51% at train time and a testing dataset accuracy of 88.72%. However, the model needs performance improvement. A maize disease recognition method based on the two main models i.e., DenseNet121 and CBAM was presented in [35]. This paper presented the comparative analysis with five models and the results were presented. The proprietary dataset was utilized for experimentation and used the synthetic data generation method for optimization. This method can resolve the issue of small-size datasets along with complicated backgrounds, However, unable to perform well in some cases like size and color variations.

To detect maize disease, severity, and crop loss estimation, a DL-based model was proposed in [36]. For this purpose, they collected real-time data and applied preprocessing steps. The model outcomes were presented using the Grad-Cam approach which showed that it performed well for disease recognition. Additionally, the authors presented the web application with a user-friendly interface. The approach performed well on small datasets, however, needs further improvements in the case of larger datasets. Early detection of corn leaf disease is essential for the food industry, which can be possible using the automated methodology. For this purpose, a method [37] was proposed based on enhanced K-nearest neighbor, evaluation was accomplished on the PlantVillage data sample. To tackle the issue of maize leaf disease recognition, the author presented a lightweight model [38] which is based on YOLOv5s. In this methodology, Faster-C3 was utilized instead of the traditional CSP phase to decrease the number of parameters. Another customization is the addition of improved CARAFE and CoordConv which was employed for refinement of location and semantic information. After that, the model is trained using channel-wise knowledge distillation which improves accuracy. The model performed well along with lightweight methodology on the PlantVillage dataset, however, performance degrades on illumination and light changes in real-world scenarios. Another approach was proposed in [39] for recognizing abnormalities of maize plants based on YOLOv5s. This method was proposed with CNN and a fusion of multiscale features in which a coordinate attention unit was introduced with a weight feature. To improve and reduce feature loss, spatial pyramid pooling is optimized and achieves good results under complex conditions. However, we need to train the model on larger datasets. In [40], authors proposed a method to identify the diseases of maize leaves. The method was based on a wavelet threshold-guided bilateral filter, and Resnet which was used to reduce the issues of different alterations, noise, etc. An average down-sampling approach was used to overcome the overfitting issue and then optimization was done using the attenuation module. The method performed well for the small dataset which needs to be trained on the larger and challenging dataset.

In [41], a CNN approach for detecting maize leaf blight was proposed, featuring multi-scale key points fusion for infected portion recognition. The technique comprised three key stages: preprocessing, model tuning, and implementing the recognition unit. Initially, an improved model was functional to address detection issues triggered by huge light variations. The second phase involved using an enhanced RPN to regulate the bounding box of infected samples, identifying and eliminating negative anchors to refine the search space for the classifier. A transmission unit was introduced to join the network tuning part with the recognition phase, facilitating feature fusion between low and high-level key points to enhance the results of recognizing small-sized infected portions. Simultaneously, the transmission module enables feature sharing between the fine-tuning network and the detection module. In the final step, the identification unit, using the optimized anchor, concentrated on locating affected samples. By eliminating the redundant detection using candidate regions and leveraging feature sharing, the model achieves efficiency comparable to a one-stage model. In this study [42], the author utilized images obtained from UAVs, a mobile phone, and the Maize Tassel Counting (MTC) data sample to evaluate the recognition results of the Faster R-CNN with two different feature extraction networks: ResNet and VGGNet. The findings revealed that with the ResNet key points computation model, the Faster-RCNN approach performed effectively as compared to VGGNet in identifying maize tassels from the samples investigated. The study in [2] introduced a CNN enhanced with a Multi-Activation Function (MAF) for the detection of maize plant illness, to enhance the recognition results achieved by traditional AI approaches. Addressing the challenge of limited disease datasets, the paper employed a pre-processing phase to enlarge the available data sample by accomplishing a data augmentation step. The approach utilized the idea of transfer learning to expedite the model tuning process, causing the optimized and reliable recognition of 3 groups of maize plant illness: maculopathy, rust, and blight. To test the efficacy of this work, baseline tests were conducted by selecting 5 CNNs with optimal performance. Subsequent ablation experiments on five CNNs demonstrated that the incorporation of the MAF unit enhances the overall results of CNNs. In [43], the authors investigated the application of the AlexNet for swift and reliable detection of maize plant viruses. The PlantVillage data sample was employed for result validation, encompassing 2 groups of maize abnormalities: LeafSpot and CommonRust viruses with total samples of 1363 and 929 respectively. Modified Faster R-CNN was introduced in [44] to detect the maize leaf disease from images. The improvements encompass several key modifications. First, a batch normalization layer was added into the conv layer to optimize the network's tuning performance and enhance its recall capability. In the next phase, a central cost method was utilized to design a hybrid loss method, aiming to elevate the recognition results of lesions with huge similarity. Subsequently, 4 types of CNN models were chosen as the fundamental key points learner for the Faster R-CNN approach. The random gradient descent technique was employed to fasten the network training, determining the computation of the key features. Lastly, the learned approach was applied to test samples with varying environmental settings and attained good results. In [45], the author utilized a DL method designed for the recognition of diseased images of maize crops within field conditions. The samples were gathered from fields at ICAR IIMR in Ludhiana, India, focusing on 3 significant plant illnesses: Maydis, Turcicum, and Banded Leaf and Sheath Blight. The data collection involved non-destructive image capture employing digital cameras and cellphones, resulting in diverse backgrounds. To address the issue of class imbalance, artificial samples were produced through several image transformation techniques like sample rotation at various angles, and light variation approaches. The method employed 3 varying structures of the 'Inception v3' model, training them with the gathered samples of maize diseases using a baseline training approach. The work performed well, however, unable to locate the exact location of the diseased portion.

The performed analysis of the existing techniques in the literature review reveals that these methods exhibit noteworthy advancements in the field of disease identification in maize crops. However, a critical examination reveals certain challenges that underscore the need for a more effective approach. Some prevalent issues include limited adaptability to complicated backgrounds, sensitivity to variations in lighting conditions, and difficulties in handling distortions within field images. Additionally, the existing methods may struggle with accurate identification when faced with cluttered backgrounds or intricate inter-class variations.

These challenges collectively emphasize the necessity for a novel and robust approach that can address these limitations, providing improved accuracy and reliability in maize disease identification under diverse and challenging environmental conditions.

3. Technique: CentralMaizeGuard

This section presents the proposed methodology which is a single-stage detector approach for recognizing numerous maize leaf diseases from images. The main idea of our model is an alteration of CenterNet along with DenseNet-65 features extraction to enhance the performance of disease detection. Figure 1 shows the whole methodological steps in terms of architecture and model alteration. This consists of two major components: the first focuses on the generation of annotations while the second involves an enhanced CenterNet network tailored for identifying maize leaf diseases. Initially, the image with its annotated sample (bbox) is fed into DenseNet-65. The bbox identifies the area of interest through key points. The improved model is then tuned to categorize the regions that have been identified.

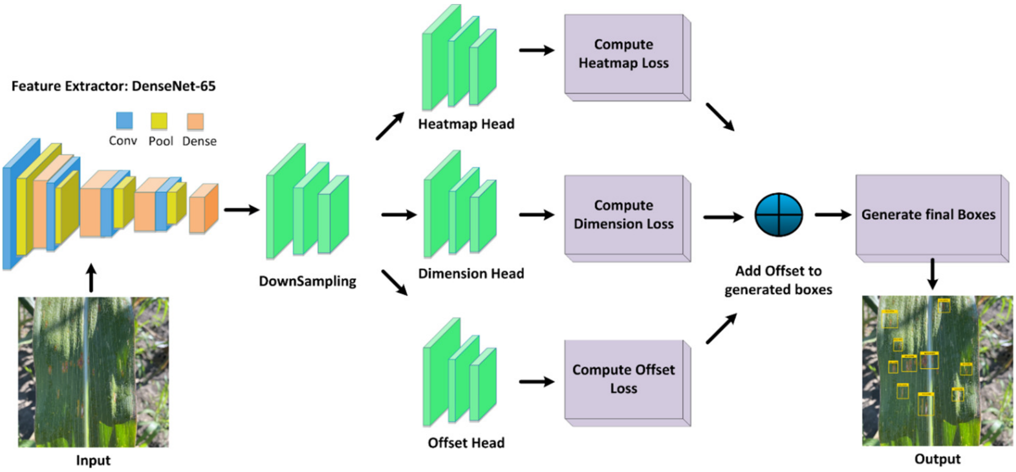


Figure 1: Flow of CentralMaizeGuard model

3.1. Generation process of annotations

Accurately locating the damaged region in the input samples is essential for a successful training process. Annotations perform a crucial part in the development and training of DL models because of ground truth development, supervised learning, model evaluation, object localization, etc. To achieve this, we employed LabelImg [27] to create annotations. These annotations are then saved in the file, including crucial information: i) the class linked to every affected part, and ii) bbox scores specifying the coordinates for producing a rectangular area around the identified portions.

3.2. Traditional CenterNet model

Accurate categorization of maize leaf diseases into multiple classes requires the effective computation of key points. Nevertheless, generating a discerning feature vector poses a challenge due to the following factors: i) The use of large-size key point vectors in models may lead to overfitting. ii) Employing a small key point set might cause the technique to overlook crucial object behaviors, such as texture and color changes, making it difficult to distinguish diseased portions from the normal regions of samples. To obtain a robust and discriminating set of visual characteristics, an automated feature computation method must be used. Because there are large differences in size, location, texture, and color, models that rely on manually created key points frequently do not perform well when it comes to correctly diagnosing and recognizing illnesses of maize leaves. To tackle these issues, we implemented an Improved CenterNet DL-based framework, which was selected due to its ability to calculate effective features straight from input. To determine important details, the CenterNet convolution filters examine the suspected image's structure. For maize leaf disease recognition, this model was chosen above RCNN, Fast-RCNN [28], and Faster-RCNN [15, 29], due to the latter systems' dependence on a two-stage object detection process. An RPN is first used in [29] to locate ROIs around putative objects. The identification heads in the framework then use the collective key points linked to each ROI to determine the category of the object and create a rectangle box. These techniques fall short of real-time object detection criteria due to their computational inefficiency. By concurrently setting characteristics and position boxes for objects in input samples, CenterNet successfully overcomes the drawbacks of the models. Because of its one-stage object detection capacity, CenterNet is more suitable for real-time object detection scenarios and is computationally efficient.

The following aspects cause difficult to identify exact locations for the classification of maize leaf diseases: i) locating the exact affected region during extensive light and hue fluctuations, and ii) assigning an output label to each object. These problems are skillfully handled by the CenterNet approach, which quickly and accurately identifies and categorizes impacted areas into various classifications. It does this by switching from a 2-step object identification technique to a one-stage recognition one and by making use of heat maps. By focusing on important details, the Heat-map module increases recall rates. Consequently, this lowers the computational expense of feature calculation in the suggested framework.

3.3. Improved CenterNet (CentralMaizeGuard)

ResNet was applied in the conventional CenterNet architecture [30] to calculate image key points for medical image analysis. To evade non-linear transformations, the ResNet architecture uses identity techniques and skip connections, which permit gradients to flow directly from the back to the front layers via the identity method. Because of its large number of parameters, the ResNet-101 model runs into the vanishing gradient issue. We offer a densely linked CNN, called DenseNet, as the key points extractor for the original CenterNet approach to address this problem in the ResNet-101 framework. DenseNet-65 is used in place of ResNet-101. Featured DenseNet-65 is more cost-effective than ResNet-101 since it features a smaller layer network and fewer parameters. Multiple dense blocks (DBs) connected progressively by further convolutional and pooling layers make up DenseNet. Complex transformations are demonstrated by this framework, which helps to mitigate the lack of location data in the final top-level features. Additionally, DenseNet facilitates feature propagation, which improves reusability and makes it ideal for identifying illnesses in maize leaves, speeding up the training process. DenseNet-65 functions as CenterNet's key points calculator in our suggested approach. The proposed approach operates through the following steps:

3.3.1. DenseNet-65

Each of the four tightly connected modules that make up DenseNet-65 has the minimum layers as compared to ResNet-101. Further, the DenseNet-65 approach has a computing benefit in comparison to the ResNet-101 CNN network because of its reduced parameter count. The DB is a crucial component of DenseNet-65, illustrated in Figure 2, where $f \times f \times m_0$ represents the feature maps (FMs) of the $(N-1)$-th layer. Here, f signifies the dimension of the FMs, and m_0 denotes the channel count. The non-linear transformation H(.) for reducing total channels

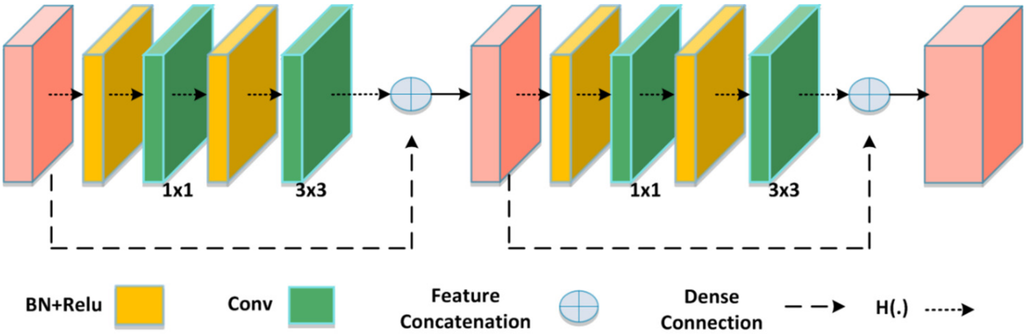


Figure 2: DenseNet-65 architecture

along with a 3×3 ConvL for rearranging computed features is applied. Long-dashed arrows denote the dense links, utilized to connect the $(N-1)$-th layer to the N-th layer, achieving concatenation through the output of H(.). Finally, the outcome of the $(N+1)$-th layer is $f \times f \times (m_0 + 2m)$.

The abundant dense links result in an increased number of FMs. To address this, a transition layer is added to decrease the dimension of key points from the preceding DB, as explained in [32, 33]. The visual information calculated by this network undergoes down sampling with a stride rate (R) of 4. Subsequently, these down sampled features are utilized to compute three kinds of heads.

3.3.2. Heat map Head

This is responsible for estimating key points over the down sampled deep features from DenseNet-65. This aids in locating the affected regions of the disease along with their corresponding classes. In the context of object detection, key points represent the box center, and they are calculated using the subsequent expression:

$$\hat{O}_{i,j,c} = \exp\left(-\frac{(i - \hat{p}_1)^2 + \left(j - \hat{p}_j\right)^2}{2\sigma_p^2}\right). \tag{1}$$

Here, the predicted down-sampled key point locations are displayed by $\hat{p}_1$ and $\hat{p}_j$, whereas the actual ground truth key point coordinates are presented by i and j. Additionally, the object size-adaptive standard deviation is displayed by σ_p, and the total output labels are indicated by c. If the $\hat{O}_{i,j,c}$ has a value of one, it presents the center for a potentially key point; if not, designated as background.

3.3.3. Dimension head

This is tasked with estimating the directions of the bbox. The L1 norm, defined as $(u_2 - u_1, v_2 - v_1)$, is utilized for this reason against a located object "e" with output label "c", and dimensions (u_1, u_2, v_1, v_2).

3.3.4. Offset head

This value is calculated to mitigate the discretization error that arises from down sampling the given image. Once the center scores are computed, these values are successively plotted back to a high-resolution image.

3.3.5. Multitask loss

Multi-task loss techniques are included in CenterNet, an end-to-end learning method, to boost its detection results and precisely locate the infected portions with the relevant class. The suggested approach utilized a multi-task loss $L_{\text{centernet}}$

on all above discussed heads, which is given as:

$$L_{\text{centernet}} = L_{\text{map}} + \lambda_{\text{dim}} L_{\text{dim}} + \lambda_{\text{off}} L_{\text{off}} \,. \tag{2}$$

Here, $L_{\text{centernet}}$ represents the overall loss calculated by CenterNet, while L_{map}, L_{dim}, L_{off} denoting the losses associated with the Heat map, dimension, and Offset heads, respectively. Additionally, λ_{dim} and λ_{off} are constants with 0.1 and 1 scores, respectively.

The L_{map} is calculated as:

$$L_{\text{map}} = \frac{-1}{n} \sum_{i,j,c} \begin{cases} (1 - \hat{O}_{i,j,c})^{\alpha} & \text{if } \hat{O}_{i,j,c} = 1, \\ (1 - O_{i,j,c})^{\beta} & \text{otherwise.} \end{cases} \tag{3}$$

In this context, n represents the total features, $O_{i,j,c}$ signifies the actual center of the key features, and $\hat{O}_{i,j,c}$ represents the center of detected features. Additionally, α and β are the hyperparameters of the L_{map}, with 2 and 4 scores for all our experiments, respectively. While the L_{dim} is determined by the following formula:

$$L_{\text{dim}} = \frac{1}{n} \sum_{k=1}^{n} \left| \hat{b}_k - b_k \right| . \tag{4}$$

In this expression, $\hat{b}_k$ represents the estimated dimensions of bbox, while b_k denotes the real values of bboxes. The variable n represents the total images. Finally, the L_{off} is computed as:

$$L_{\text{off}} = \frac{1}{n} \sum_{p} \left| \hat{F}_{\hat{p}} - \left(\frac{p}{R} - \hat{p} \right) \right| . \tag{5}$$

Here, $\hat{F}$ is presenting the computed offset sore, while p is the real and $\hat{p}$ is the down-sampled key point. While R is presenting the output stride.

3.4. Test phase

The presented CentralMaizeGuard is different from other methods i.e., proposal generation and selective search. So, in the test phase, we input the image with bbox to the trained model, then the proposed method generates the center points of disease areas on leaves. As a result, it gives the diseased area with location, size, and class of that detected area.

4. Results

In this part of the manuscript, we have provided vast details of the data sample used for model tuning and testing. Moreover, we have described the details of metrics employed to estimate the maize plant leaf disease performance of the proposed approach. Further, a huge experimental analysis showing both the visual and quantitative results is provided to clarify the model's effectiveness.

4.1. Evaluation parameters

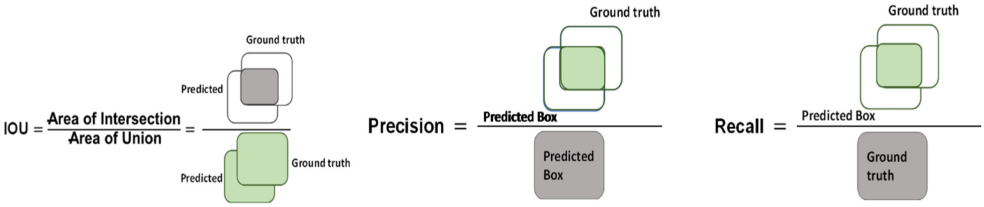
To analyze the identification, and classification results of the CentralMaize-Guard framework, several evaluators like precision value, recall measure, accuracy metric, F1-measure, intersection over union (IoU), mean Average Precision (mAP) are used. The mathematical elaboration of the accuracy metric is provided in Equation (6).

$$\text{Accuracy} = \frac{TrP + TrN}{TrP + FaP + TrN + FaN}\,. \tag{6}$$

Further, the mathematical description of the mAP is given in Equation (7), where s designates the analyzed sample, while S shows the total data samples.

$$\text{mAP} := \sum_{j=1}^{S} AP(s_j)/S. \tag{7}$$

The pictorial representation of the precision, IOU, and recall is given in Figure 3.



(a) (b) (c)

Figure 3: Pictorial illustration of (a) IOU evaluators, (b) Precision, and (c) Recall

4.2. Dataset

In this study, for model tuning and evaluation, an online available data sample named Corn Disease and Severity (CD&S) [46] is utilized. The CD&S data sample was generated by the Agronomy Center for Research and Education at Purdue University. The samples in this repository were taken employing cell phones with diverse and complicated background settings from real-world scenarios. There are 2112 visual samples in this dataset with a dimension ratio of 3000 × 3000. Further, the images are categorized into three types NLB, Northern leaf spot (NLS), and GLS groups. In the NLB group, there are a total of 511 images, which are 562, and 524 for the NLS, and GLS categories. The CS&D data sample is complex in nature and contains images with huge sample distortions like cluttered backgrounds, dead leaves, and varying intensity variation conditions. Such complicated data sample nature makes it effective for our model tuning and evaluation to prove its robustness for maize plant leaf diseases. A few examples from all three groups of the used data sample are given in Figure 4 from where it is quite evident that the infected regions on plant leaves are quite different in structure, mass, and looks and have huge similarities with background as well. Further, for model tuning and testing we have employed a distribution of 70%, and 30%, respectively.

Figure 4: Dataset samples

4.3. CentralMaizeGuard performance analysis

The proficiency of the suggested maize plant leaf disease localization and classification technique, denoted as "CentralMaizeGuard," is assessed through a comprehensive evaluation, employing key measures like precision, recall, F1 score, and error rates on both class-wise and entire dataset basis. These parameters deliver a thorough analysis of the model's performance across distinct disease categories, shedding light on its aptitude to accurately identify and classify specific pathologies.

Initially, attained results values are discussed in the form of precision, and recall on a class-wise basis, as examining these metrics on a class-wise basis is paramount in evaluating the effectiveness of the CentralMaizeGuard approach for maize plant leaf illnesses recognition. Precision, which estimates the measure of positive estimates, and recall, measuring the framework's ability to recognize all instances of disease, provides a better understanding of the model's performance for each specific disease class. This detailed analysis allows for targeted identification of areas requiring improvement, whether it be addressing false positives for a particular disease (low precision) or improving the model's sensitivity to instances of a specific pathology (low recall). Such insights facilitate the formulation of customized optimization strategies tailored to the unique characteristics of each disease class, contributing to an informed decision-making process for disease management and intervention strategies. Furthermore, this class-wise precision and recall assessment enhances the transparency and communicative efficacy of the results, enabling the scientific community to grasp the specific strengths and limitations of CentralMaizeGuard in handling various maize plant leaf diseases. The scores in Figure 5 are clear stating that our proposed approach shows effective results against three groups of maize plant leaf illnesses. Clearly, for precision measure, the CentralMaizeGuard acquires values of 98.96%, 97.71%,

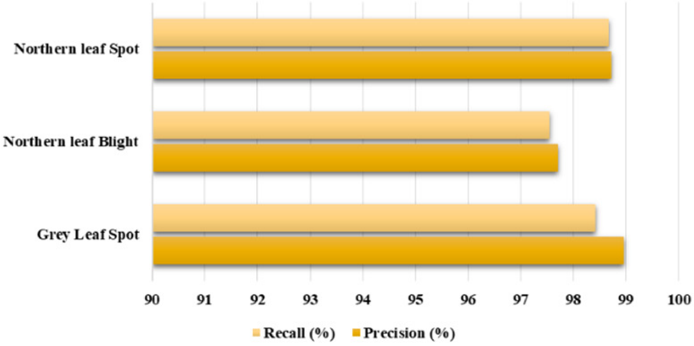


Figure 5: Attained precision, and recall results on class-basis

and 98.72% for GLS, NLB, and NLS groups, which are 98.42%, 97.55%, and 98.68% for recall metric respectively.

Evaluating the performance of the CentralMaizeGuard technique extends beyond precision and recall, encompassing the crucial metrics of F1 score and error rate for a comprehensive class-wise model assessment. The F1 score, which strikes a stability among precision and recall scores, delivers a combined estimate of the framework's ability to achieve both high positive prediction accuracy and comprehensive capture of true positive instances for each disease class. This metric is particularly valuable in scenarios where an equal emphasis is placed on minimizing false positives and false negatives. Simultaneously, examining the error rate on a class basis affords insights into the overall performance of the approach by quantifying misclassifications. The attained scores for the F1 metric along with error rates for all three anomalies of maize plant leaves are given in Figure 6. The numbers in Figure 6 clearly deliver the insight that the presented methodology exhibited very small values of error for all three groups of maize plant leaf diseases by attaining effective F1-scores which clearly proves the better generalization capability of the CentralMaizeGuard approach.

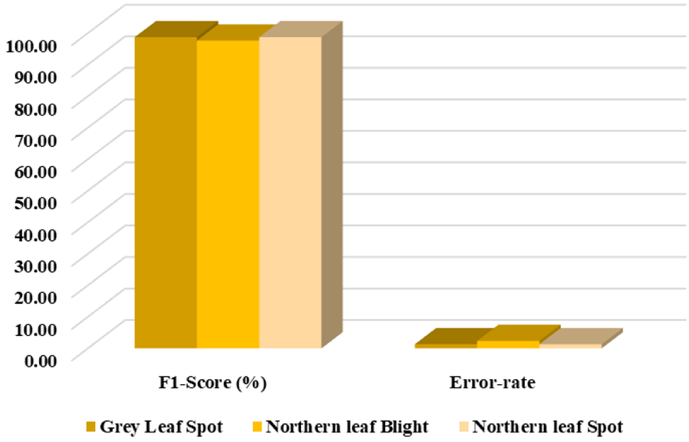


Figure 6: Attained precision, and recall results on class-basis

Next, the results of the CentralMaizeGuard are discussed in terms of class-wise accuracy score, as this metric provides an intricate perspective on how well the model performs across distinct disease categories, shedding light on its capabilities and limitations for each class. Moreover, presenting accuracy values on a per-class basis enhances transparency, empowering stakeholders in agriculture or healthcare to grasp the model's reliability for individual diseases. This approach not only aids in diagnostic and intervention decisions but also facilitates benchmarking against other models, delivering a valued understanding of the comparative effectiveness of the model across diverse infection classes. For the CentralMaizeGuard technique, the attained class-wise accuracy values are provided in Figure 7. The values in Figure 7 clarify that our proposed technique shows improved results in recognizing all classes of maize plant leaf diseases with scores of 98.95%, 98.64%, and 98.28% for GLS, NLB, and NLS groups respectively clearly proving the effectiveness of the model.

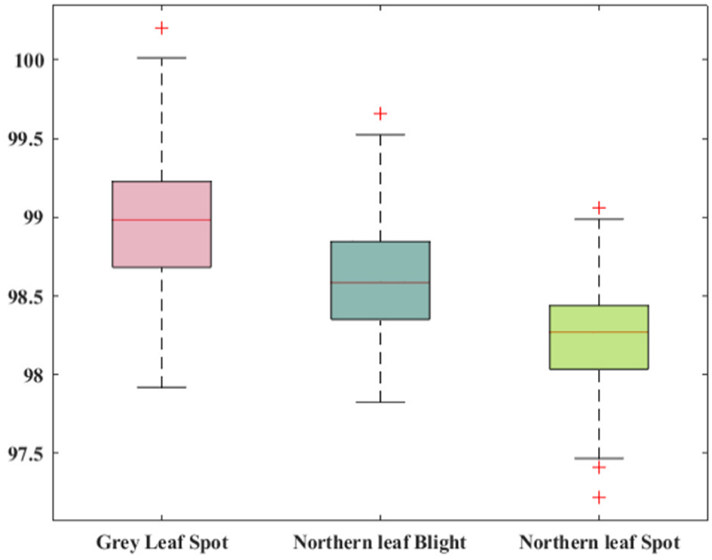
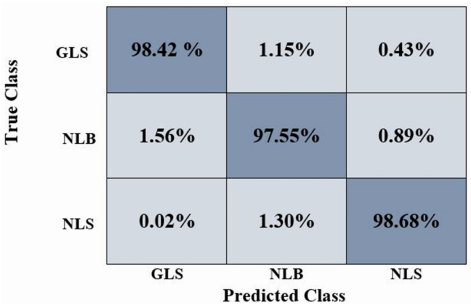


Figure 7: Class-based accuracy results from the CentralMaizeGuard technique

Next, the results of the approach are discussed in the form of a confusion matrix, as reporting a confusion matrix is crucial as it provides a comprehensive snapshot of a framework's results, showcasing the division of true positives, negatives, and false positives, negative estimations against various groups. Figure 8



True Class	GLS	NLB	NLS
GLS	98.42 %	1.15%	0.43%
NLB	1.56%	97.55%	0.89%
NLS	0.02%	1.30%	98.68%

Predicted Class

Figure 8: Obtained confusion matrix for the CentralMaizeGuard technique

presents the confusion matrix attained for the CentralMaizeGuard technique. The values in Figure 8 show that the proposed approach performs well for all three classes due to its high recall power. Further, the highest misclassification value is reported among the NLB, and NLS with a score of 1.56% due to the structural resemblance among classes, however, still both are recognizable.

At last, we have provided results of the CentralMaizeGuard technique in locating the various categories of maize plant leaf illnesses in terms of the entire dataset by using numerous metrics like accuracy, recall, precision, and F1-score. The attained result is shown in Figure 9 from where it is quite visible that our approach performs effectively for locating and classifying maizeplant leaf diseases. Descriptively, we attained the accuracy score of 98.62% along with the precision, recall, and F1 measure of 98.46%, 98.22%, and 98.34% which prove the efficacy of our approach due to its high recall and generalizability power.

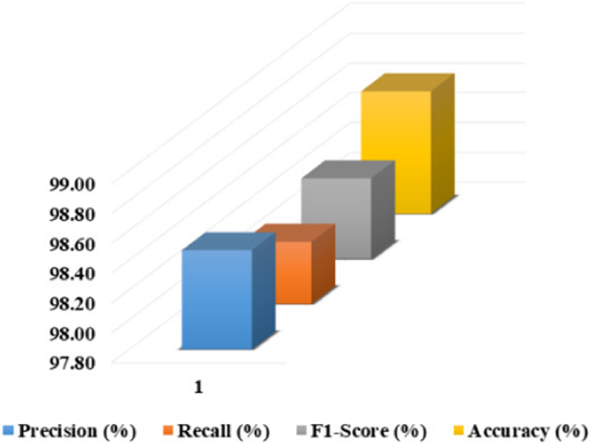


Figure 9: CentralMaizeGuard technique results on the entire dataset

4.4. Localization results

In this part, we have discussed the localization results of the CentralMaizeGuard technique as computing localization results is pivotal for effective detection of maize plant leaf diseases, as it provides crucial insights into the precision and accuracy of disease localization. For this reason, we have both provided the evaluation in terms of pictorial presentation and numeric scores. The attained visual outputs are provided in Figure 10, clearly indicating that the proposed framework is skillful in locating the various maize plant leaf diseases under complex background settings due to its effective feature engineering capability and high generalization power. To discuss the localization results in terms of numeric scores, we have utilized standard evaluation measures like mAP and IOU.

The use of metrics such as these parameters plays a key role in this evaluation. MAP quantifies the average precision across different disease classes, offering a comprehensive measure of the model's ability to precisely locate diseases on maize plant leaves. Meanwhile, IOU assesses the overlap between estimated and actual bounding boxes, indicating the spatial accuracy of disease localization. These metrics are essential for understanding the reliability of the model in pinpointing disease regions accurately. The higher the mAP and IOU values, the more confident we can be in the reliable localization of maize plant leaf illnesses. This information is invaluable for agricultural decision-making, enabling farmers and researchers to identify and address diseases promptly, and assisting in improving crop management and yield. For the CentralMaizeGuard technique, we have attained the mAP, and IOU scores of 0.952 and 98.12%, respectively which indicates the high recognition power of the suggested approach.

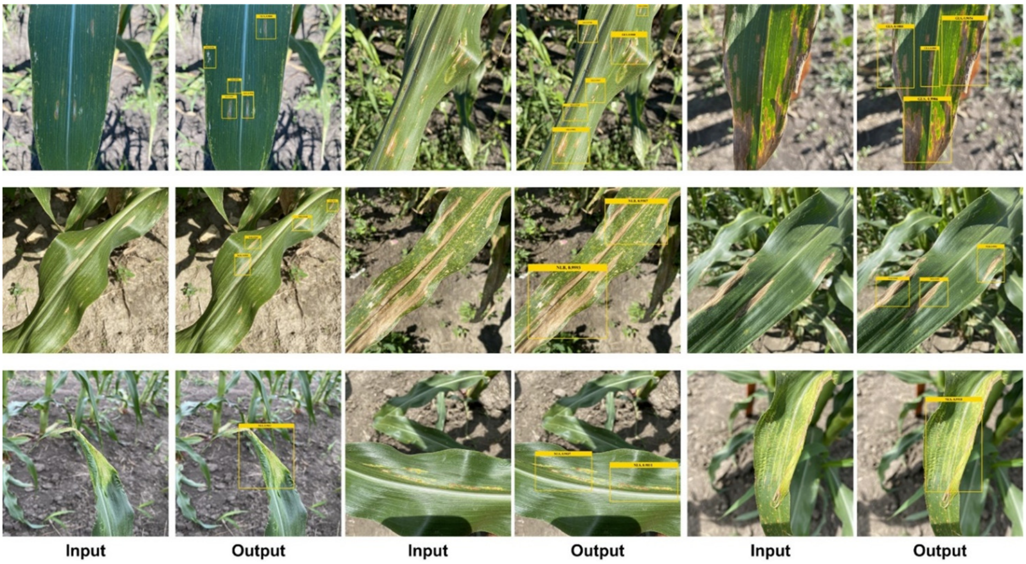


Figure 10: Localization results of our method

4.5. Heatmaps analysis

In this section, we employ the GradCAM approach to compute heatmaps, offering a visual understanding of the decision-making procedure of our proposed maize plant leaf disease detection system. GradCAM generates visualizations that highlight the regions within an image that contribute most to the model's prediction, offering a transparent and interpretable representation of where the model focuses its attention. These heatmaps not only provide insights into the specific features or patterns influencing disease detection but also enhance the model's explainability. This interpretability is crucial in gaining the trust of end-users, researchers, and stakeholders in agriculture, as it facilitates a clear understanding of the model's reasoning behind disease predictions. The attained visual results have been depicted in Figure 11 in which the red color shows the most significant regions that contributed to making the decision. It is obvious from the reported results that our CentralMaizeGuard technique is taking the correct regions of the plant leaves to accomplish the outcome that is clearly proving the explainability of the suggested model.

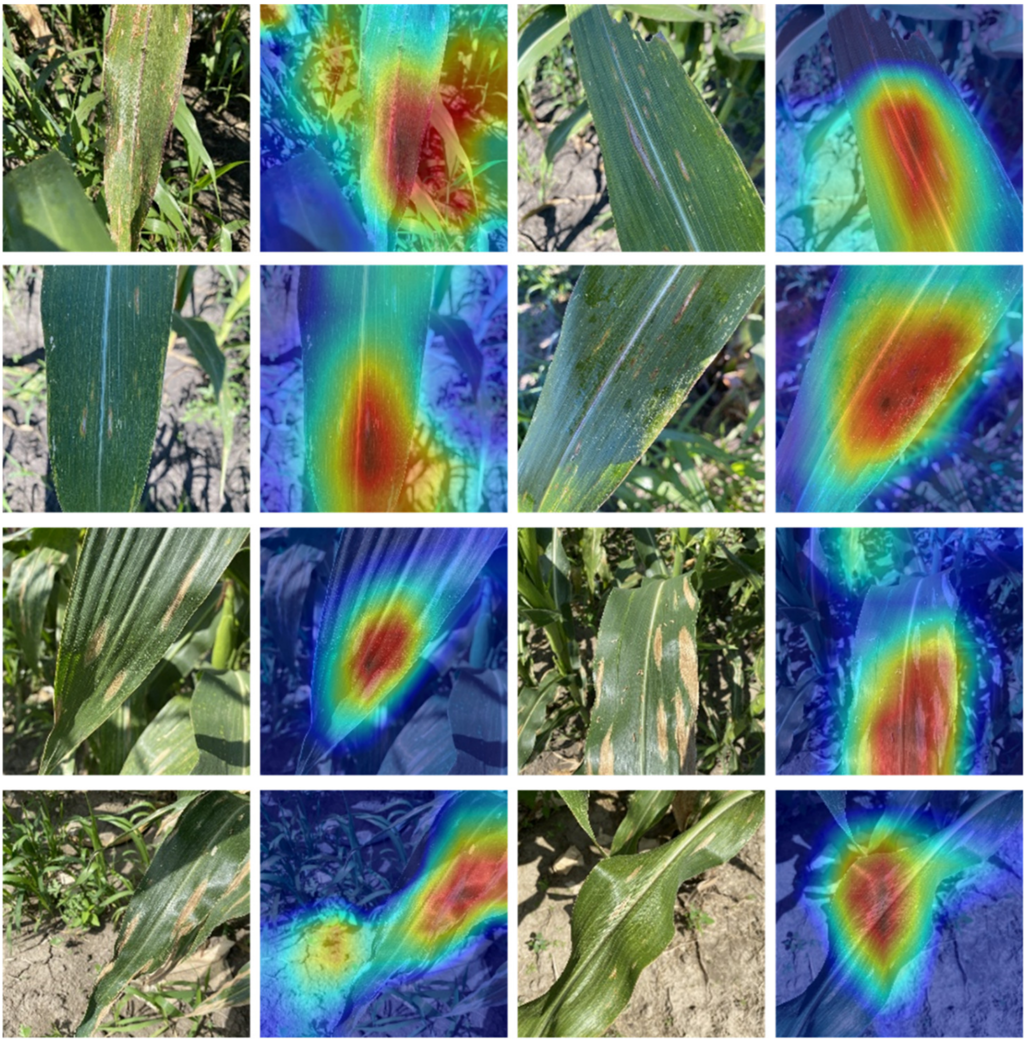


Figure 11: Heatmaps of our proposed model

4.6. CentralMaizeGuard performance analysis with DL methods

Computing relevant features is paramount for effective maize plant leaf disease recognition as it directly influences the framework's ability to discern distinctive configurations linked with diverse diseases. Extracting meaningful features enhances the model's discriminative power, allowing it to capture key characteristics specific to each pathology. Well-chosen key points not only boost classification results but also contribute to the model's robustness in handling diverse instances of disease presentation. In essence, the selection and computation of relevant features serve as a critical foundation for achieving accurate and reliable recognition of maize plant leaf diseases, enabling informed decision-making in agriculture and crop management. For this reason, we have performed a comparison of the employed feature extractor with several other DL models to indicate the significance of our framework against them both in the aspect of results and computational complexity. To perform this, several state-of-the-art models like ResNet [47], InceptionResNetV2 [48], Alexnet [49], GoogleNet [50], VGGNet [51], EffcientNet-B0 [52], and ConvNeXt [53] have been chosen as discussed in [54] to compare the performance comparison of our approach against them and gained values are presented in Table 1. The classification accuracy of both the train and test data samples indicates the significance of our approach in comparison to other base approaches. The major cause for this improved result is that the mentioned CNN architectures, including ResNet, InceptionResNetV2, AlexNet, GoogleNet, VGGNet, EfficientNet-B0, and ConvNeXt, have

Table 1: CentralMaizeGuard technique comparative analysis with deep learning approaches

Frameworks	Accuracy (%) Train set	Accuracy (%) Test set	Trainable parameters (M)
GoogleNet	86.82	73.12	7.8
AlexNet	91.26	82.11	62.3
VGG-19	92.51	81.33	143
ResNet18	84.91	75.04	11
ResNet34	88.11	82.35	21.5
ResNet50	95.78	91.58	23.72
ResNet101	93.51	86.42	44.5
EffcientNet-B0	96.74	93.43	40.09
InceptionResNet	92.05	83.62	54.3
ConvNeXt	93.45	89.97	25.5
Proposed	**99.01**	**98.62**	**6.9**

been influential in various computer vision tasks including in recognizing the maize plant leaf diseases. However, each approach faces specific challenges. For instance, deeper networks like ResNet and InceptionResNetV2 encounter vanishing gradient issues during training, potentially hindering convergence. AlexNet and VGGNet, while pioneering, are prone to increased computational demands due to their depth. GoogleNet's inception modules, while efficient, may pose challenges in terms of interpretability. EfficientNet-B0 aims to balance model size and accuracy but tuning its hyperparameters can be complex. ConvNeXt introduces inter-group connections but scaling it to larger architectures may lead to increased computational costs. DenseNet-65 addresses some of these challenges by introducing dense connectivity patterns, ensuring efficient information flow, and reducing vanishing gradient issues. DenseNet's densely connected blocks facilitate feature reuse and alleviate the computational burden associated with training very deep networks, making it a promising solution to overcome the limitations of the architectures and shows improved results in recognizing various maize plant leaf ailments. Descriptively, for the train time accuracy results, the peer models have shown an average accuracy score of 91.51%, which is 99.01% for our case. So, for the train time accuracy results, our framework has delivered a performance gain of 7.50%. Further, for the test time accuracy, the base models have presented an average score of 83.90%, which is 98.12% for our case, with a performance improvement of 14.72%. Moreover, we have compared the model size with the base models as well in Table 1, from where it is quite evident that in terms of framework depth the suggested approach comprises fewer tuning parameters with a value of 6.9 million in comparison to all other approaches, which provided a computational advantage to the CentralMaizeGuard technique as well.

4.7. CentralMaizeGuard performance analysis with other object identification methods

In this experiment, we conduct a comprehensive comparison of our proposed maize plant leaf disease detection model with well-established object detection approaches. Specifically, we benchmark our model against the widely utilized Faster R-CNN algorithm [54], along with other prominent one-stage object detection algorithms like the Single Shot Detector (SSD) [27] and YOLO [28]. This comparative analysis serves a crucial purpose in evaluating the efficacy and efficiency of our approach against established benchmarks in the field. Faster R-CNN, known for its accuracy, and the real-time capabilities of SSD and YOLO represent diverse paradigms in object detection. By systematically comparing our model with these methodologies, we aim to discern the strengths and weaknesses of each approach, providing valuable insights for optimizing disease detection in maize plants. The evaluation criteria centered on two key aspects: mAP as an estimate of identification accuracy and test time to gauge computational efficiency. mAP provides a comprehensive overview of precision-recall trade-offs, offering insights into the model's ability to precisely locate diseases. Simultaneously, the consideration of test time is crucial for real-world applications, especially in agriculture, where rapid and efficient disease detection is paramount. This dual evaluation strategy allows us to not only gauge the accuracy of our approach compared to benchmarks but also assess its computational efficiency, ensuring practical viability in real-time scenarios. The attained comparison is listed in Table 2 which clearly indicates the proficiency of the CentralMaizeGuard framework in comparison to other models. Comparatively, the lowest MAP value is attained by the SSD model with a number of 0.71, while the second lowest value is attained by the YOLO model with a score of 0.87. The Resnet50-based Faster-RCNN approach shows comparative results with a mAP score of 0.94, however, with a huge test time of 0.26 seconds. Comparatively, the proposed approach shows effective and efficient performance with a mAP value of 0.952 along with a test time of 0.19 seconds indicating the robustness of our approach as compared to other models. The superior results achieved by the adapted CenterNet, attributed to DenseNet-65's dense connectivity patterns, fostering effective feature reuse and information flow critical for capturing intricate disease-related patterns. Notably, Faster R-CNN, while accurate, tends to be computationally demanding due to its multi-stage architecture. SSD, although efficient, may struggle with accuracy for smaller objects. YOLO, optimized for real-time processing, sacrifices precision under complex background conditions. The customized CenterNet overcomes these drawbacks by leveraging DenseNet-65's strengths, achieving a balance between accuracy and computational efficiency. Its key point-based approach aids precise disease localization, addressing limitations seen in other models. This comparative analysis underscores the efficacy of our approach in overcoming drawbacks associated with traditional object detection models, positioning the customized CenterNet as a robust solution for accurate and efficient maize plant leaf disease detection.

Table 2: CentralMaizeGuard technique comparative analysis with base models

Model	MAP	Time (s)
YOLO	0.87	0.19
SSD	0.71	0.34
VGG-16-based Faster-RCNN	0.89	0.23
Resnet50- based Faster-RCNN	0.94	0.26
Proposed	**0.952**	**0.19**

4.8. CentralMaizeGuard performance analysis with SOTA methods

In this phase of our investigation, we turn our attention to a comparison with the latest and state-of-the-art approaches in maize plant leaf disease detection. Our aim is to benchmark the results of our customized CenterNet, incorporating DenseNet-65, against the most recent methodologies dedicated to the same task. By evaluating our approach alongside the latest advancements in the field, we seek to ascertain not only the relative effectiveness but also the competitiveness of our model in the current landscape of disease detection methodologies for maize plants. For comparison, the selected SOTA approaches along with comparative analysis are provided in Table 3. Ahmad et al. [55] suggested an approach for recognizing maize plant leaf diseases by evaluating numerous DL frameworks and reported the highest classification accuracy for the DenseNet-169 model with an accuracy score of 81.60%. Chen et al. [56] proposed an approach called DFCANet to classify various categories of maize plant leaf ailments and obtained an accuracy score of 98.47%. While in [57], initially a clustering step was performed to identify the area of interest, afterward various DL approaches were applied to perform the categorization job of grouping the maize samples into various types of diseases. The approach reported the highest classification score of 97.77% for the DenseNet-121 approach. Divyanth et al. [58] suggested a 2-phase clustering approach via using numerous DL-based segmentation approaches like DeepLabv3+, UNet, and SegNet to identify the infected portions of the maize plant leaves. Initially, the complete plant leaf was presented to the network to locate the focused regions which were classified into different groups in the next phase. The approach has reported an accuracy score of 92.37%. In [21], a DL approach called ClGan is suggested for maize plant leaf illness cataloging and reported an accuracy value of 98.53%. Comparatively, the CentralMaizeGuard technique attains the highest classification accuracy of 98.62%. The approaches proposed in [21, 55, 56] only accomplish the sample level classification tasks

Table 3: CentralMaizeGuard technique comparative analysis with SOTA methods

Study	Approach	Accuracy score (%)
[55]	Transfer learning using DenseNet169	81.60
[57]	SLIC method with DenseNet121 CNN	97.77
[56]	DFCANet CNN	98.47
[58]	UNet and DeepLabv3+	92.37
[21]	ClGan	98.53
Proposed		**98.62**

and unable to identify the exact location of infected regions. While the methods discussed in [57–59] employ a 2-phase recognition task by initially segmenting the regions and then performing the classification task which increases the computing burden. Unlike approaches solely focused on sample-level classification tasks, our model excels in both classification and precise localization of infected regions on maize plant leaves. By leveraging a key point-based approach, it efficiently identifies the exact location of diseases, a capability lacking in certain SOTA methods. Additionally, our approach streamlines the process by avoiding a two-phase recognition task, as seen in methods employing initial segmentation. This strategic design choice reduces computational complexity, enhancing the efficiency of our model while maintaining robust performance in maize plant leaf disease detection. These advancements position our model as a competitive and innovative contribution to the evolving landscape of maize plant leaf abnormality identification, indicating its proficiency for practical implementation in agriculture and crop management.

5. Conclusions

Our proposed maize plant leaf disease detection technique builds upon the customized CenterNet architecture, with DenseNet-65 serving as the foundational network. The key innovation lies in the strategic integration of DenseNet-65, which leverages dense connectivity patterns to enhance feature reuse and information flow. This modification contributes to superior disease classification and precise localization of infected regions. The approach not only addresses existing challenges in traditional and state-of-the-art methodologies but also positions itself as an innovative solution for efficient and accurate disease detection in maize plants. Through a comprehensive comparative analysis, we have shown superior results in both disease classification and precise localization of affected regions when benchmarked against traditional and state-of-the-art methodologies. Our model not only addresses existing challenges in accuracy, computational efficiency, and disease diversity but also establishes itself as a competitive and innovative solution for practical implementation in agriculture. Future work could delve into expanding the dataset to enhance model generalization, exploring transfer learning techniques, and investigating real-time deployment strategies for on-field disease monitoring. Additionally, further research could focus on the interpretability of the model's decisions and the incorporation of multi-modal data sources to strengthen disease detection capabilities in varied environmental conditions. These avenues of exploration aim to contribute to the ongoing evolution of effective and reliable maize plant leaf disease detection systems.

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