

ORIGINAL ARTICLE

A novel approach for crop disease detection using transfer-learning-based deep convolutional neural networks

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Abstract

Crop production quality can be enhanced through effective early stage monitoring of crops. In contemporary agriculture, precision farming systems that incorporate advanced technologies, such as drones, are employed for monitoring. Nevertheless, current models lack the ability to be applied broadly across various agricultural settings, leading to the suboptimal detection of crop diseases. Therefore, this study proposes a novel method for monitoring crop diseases using the Transfer-Learning-based Deep Convolutional Neural Network technique. The process commenced with the collection of a multi-crop multi-disease dataset, followed by data preprocessing through the application of Bilateral Filtering and Partial Dynamic Range Adjustment with Histogram Equalization. Subsequently, the dimensionality of the images was reduced using the Multi-Weighted Covariance Matrix Component Analysis method, and the data were organized using the K-Means Clustering algorithm. In addition, various features were extracted, with the most relevant features selected using the Mountain Gazelle Pareto Front Optimizer algorithm. To identify distinct disease characteristics, a Multidimensional Feature Distribution plot was created using the chosen features. Ultimately, the assessed spectral index of the clustered color bands, optimal features, and Multidimensional Feature Distribution plot were used to detect multi-crop diseases using the proposed Transfer Learning based Dynamic Contextual Feature Pooled Convolutional Neural Network model. The effectiveness of the proposed method was evaluated through an experimental analysis using a publicly accessible dataset. The proposed method demonstrated accuracy, precision, recall, and F1 score values of 98.09%, 97.24%, 97.58%, and 97.99%, respectively, which is higher than those of existing methods.

Keywords Transfer learning based dynamic contextual feature pooled convolutional neural network (TL-DCFP-CNN) · Crops · Multi-weighted covariance matrix component analysis (MWCMCA) · Multi-diseases · K-means clustering (KMC) · Smart farming and mountain Gazelle pareto front optimizer (MGPFO)



1 Introduction

The escalating global demand for food, coupled with the multifaceted challenges posed by climate change, necessitates robust solutions for agricultural sustainability, with plant disease management emerging as a critical determinant of crop productivity [41].

Therefore, early and effective monitoring methods for crop diseases are used to enhance food productivity [43].

Traditional methods of disease detection, often reliant on manual inspection, can be useful for monitoring small-scale crops but they often struggle to cover larger areas and can be labor-intensive and time-consuming for the identification of diseases in extensive crops, highlighting the urgent need for more efficient and accurate diagnostic tools [29, 37].

To address these challenges, smart farming enhances precision agriculture through advanced sensing, robotics, and Information and Communication Technology (ICT) to optimize yields and resource use [1, 48]. Various types of data are collected from red–green–blue (RGB) and thermal images using advanced drone and UAVs technologies. These technologies help obtain high spatial information from multiple onboard sensors, increase efficiency, and enable the rapid detection of crop diseases over large areas [46].

Moreover, the integration of advanced technological solutions, particularly those leveraging machine learning (ML) and deep learning, has improved crop disease detection and management [11, 23] and has emerged as a critical pathway to bolster agricultural resilience against pervasive plant pathogens [20]. This technological advancement is particularly crucial for addressing food security challenges, especially in regions heavily reliant on agriculture, where early and accurate detection of these diseases is paramount to implementing timely interventions and mitigating widespread crop failure, thereby safeguarding food production and economic stability [8, 39].

Most existing research methodologies that use ML techniques, such as RF, SVM, Artificial Neural Networks (ANN), are effective in high-dimensional spaces and minimize overfitting issues while training various data subsets. They are also beneficial for pattern generation and decision-making abilities [15, 30].

In this context, Conventional deep learning models, such as convolutional neural networks (CNN) [9], ResNet, and VGG, have gained prominence as robust tools for agricultural visualizations of crop classification, monitoring, automatic extraction of relevant features [4, 35, 42] and precise disease identification via image analysis, offering a significant leap forward in precision agriculture [20].

These advanced techniques can analyze visual cues from plant leaves, stems, and fruits, enabling rapid and accurate identification of various pathogens and physiological disorders [21]. This proactive approach not only minimizes crop losses but also supports sustainable agricultural practices by enabling targeted interventions [8].

Deep learning models can overcome the challenge of limited disease-specific data through transfer learning, adapting knowledge from large existing image datasets to new, smaller agricultural datasets [47]. Moreover, recent studies have demonstrated that transfer-learning-augmented deep convolutional neural networks can effectively recognize diverse crop diseases, even under limited training data conditions [10, 40]. Furthermore, combining data-augmentation techniques with pretrained CNNs such as AlexNet has been reported to substantially improve few-shot classification performance on PlantVillage leaf images [12, 21, 27]. Moreover, employing depthwise separable convolutions in architectures such as InceptionV3 and InceptionResNetV2 can markedly decrease the number of trainable parameters without sacrificing diagnostic accuracy [17].

Hu et al. [18] demonstrated that using a Generative Adversarial Network (GAN) for data augmentation, combined with ImageNet-pretrained models, improved few-shot leaf disease classification accuracy by up to 25%. Similarly, Deng et al. [14] successfully applied transfer learning, migrating Inception V3 to fruit leaf datasets. This shows that GAN-based data augmentation and transfer learning are effective strategies for improving plant disease classification, especially with limited training data.

Kim et al. [24] developed a deep learning model for the early and automatic detection of Rice Bakanae disease (RBD) using drone imagery. The ResNet50 and You Only Look Once Version 3 (YOLOV3) deep learning models were used to detect the infected bunches and classify the infected areas affected by RBD. According to the experimental analysis, the YOLOV3 model achieved a higher precision accuracy of 90.49% compared to the other models. In addition, it reduces confusion and improves the efficiency of rice field inspections. However, training a limited dataset requires more time.

Wang et al. [45] developed machine learning models for the automatic detection of cotton root rot disease based on Unmanned Aerial Vehicle (UAV) imagery. The k-means segmentation algorithm was used to effectively detect cotton crop disease. According to the experimental analysis, the proposed model outperformed conventional classification techniques, achieving an improvement in the overall accuracy. However, a high omission error leaves untreated infected area, which harms crop health and lowers overall agricultural productivity.

Amarasingam et al. [5] developed a deep learning model for detecting white leaf disease in sugarcane crops using UAV imagery. YOLOV5 and a Recurrent-Convolutional Neural Network (R-CNN) were used to detect white leaf disease in sugarcane crops. The results revealed that YOLOV5 was the best architecture for detecting white leaf disease using UAV because of its good performance and compact size compared to other models; however, inaccurate detection occurred owing to interference caused by the background color.

Nguyen et al. [33] developed machine-learning models for the early detection of wheat Yellow Rust disease using UAV imagery. Random Forest (RF) and Support Vector Machine (SVM) were used to detect Yellow Rust in wheat crops. The experimental analysis shows that the proposed method outperforms conventional techniques. In addition, the effective early detection of crop diseases has not only advanced our understanding but has also helped farmers by indicating a prevention period. However, the limited sample size affects the reliability of the model.

Abdulridha et al. [2] developed machine-learning models for the detection of stem rust disease in wheat crops based on drone images. RFC, SVM, Decision Tree classifiers were used to evaluate the wavelength extraction and severity of stem rust disease in wheat crops. The results revealed that the RFC achieved higher accuracy and performance detection compared with other classifiers; however, accurate detection remained challenging, particularly before the appearance of visible symptoms.

Lan et al. [25] developed deep learning models for rice spike detection based on drone images. The R-CNN and YOLO approaches were used to effectively detect diseases in rice plants. The results revealed that YOLO achieved superior performance in terms of accuracy and efficiency compared to other conventional methods. In addition, it provides technical support for the effective management of the rice growth process through accurate disease detection. However, complex field conditions can lead to false, duplicate, and missed detection.

Ishengoma et al. [22] developed deep learning models for the identification of fall armyworm diseases in maize leaves based on UAV images. The CNN models Visual Geometry Group and MobileNetV2 were used to examine the infected disease in maize leaves using drone images. According to the experimental results, MobileNetV2 achieved better accuracy, sensitivity, specificity, and precision compared with other existing models; however, it had lower classification accuracy, which required additional hyperparameters to tune the model size.

Notably, MobileNetV2 has emerged as a lightweight yet accurate alternative for on-device disease diagnosis, achieving comparable classification performance to heavier architectures while drastically reducing computational overhead [16]. This efficiency enables deployment on resource-constrained mobile platforms, facilitating real-time field diagnostics [38]. Recent hybrid Vision-Transformer architectures, exemplified by MobilePlantViT, have demonstrated comparable accuracy to conventional CNNs while preserving low-latency inference on edge hardware [44]. Empirical evaluations further reveal that integrating CNNs with Vision Transformers within a unified hybrid framework can yield higher classification accuracy across multiple plant disease datasets compared with standalone models [3].

While machine learning and deep learning have significantly advanced crop disease detection, several limitations persist regarding the accuracy and applicability of these models, particularly when considering diverse crop types, environmental conditions, and the visual complexities of plant disease symptoms.

- **Limited model generalizability:** Current models often perform well on specific datasets but struggle to accurately predict diseases across different crops and under varying environmental conditions, as they may not be trained on a wide range of scenarios.
- **Shadowing and Lighting Issues:** Inconsistent lighting, particularly shadows cast by leaves or foliage, can obscure important disease indicators on plants, leading to misinterpretations by AI systems. This can result in misreading the data, with the shaded areas possibly being incorrectly identified as unhealthy.
- **Data Complexity:** High-dimensional data generated by drones using RGB, near-infrared (NIR), and thermal imaging can be complex to process and analyze, requiring advanced computational techniques and specialized expertise.
- **Disease Symptom Overlap:** Many crop diseases share similar visual symptoms like discoloration or wilting, making accurate visual differentiation and disease classification challenging for both human experts and AI models.

Despite the success of existing transfer learning approaches, they largely rely on fixed pooling operations and lack explicit modeling of contextual feature dependencies, which limits their ability to capture subtle disease patterns in complex agricultural environments. This paper presents an innovative crop disease monitoring system that integrates Transfer-Learning-based Deep Convolutional Neural Networks and Multi-Faceted Data Processing approaches to provide highly accurate and efficient detection of plant diseases. The major contributions of the proposed work are summarized as follows:

- To accurately classify the crop disease across a wide range of agricultural conditions using the proposed Transfer Learning based Dynamic Contextual Feature Pooled Convolutional Neural Network (TL-DCFP-CNN) approach
- To avoid inconsistent lighting conditions and improve image contrast through preprocessing strategy using Partial Dynamic Range Adjustment with Histogram Equalization (PDRAHE) approach
- To reduce the dimensionality of the high dimensional data captured from the RGB and thermal images from the drone system were captured using the Multi-Weighted Covariance Matrix Component Analysis (MWC-MCA) approach
- To obtain optimal and discriminative features for disease classification using the Mountain Gazelle Pareto Front Optimizer (MGPFO) based feature selection approach.
- To enhance feature representation in transfer-learning-based CNN models by introducing a Dynamic Contextual Feature Pooling (DCFP) mechanism that replaces conventional fixed pooling operations with context-aware adaptive weighting, enabling improved extraction of subtle disease-related spatial patterns.

Although CNN models based on transfer learning have been used extensively for crop disease detection, the most of the existing methods mainly rely on fine-tuning pretrained architectures in combined with common pooling operations like max-pooling or average-pooling. These pooling strategies perform fixed spatial aggregation and often fail to capture contextual dependencies between neighboring feature regions, leading to the loss of subtle disease-specific patterns. In contrast, a Dynamic Contextual Feature Pooling (DCFP) mechanism is introduced in the proposed TL-DCFP-CNN architecture. This mechanism adaptively assigns weights to feature activations based on the contextual information surrounding them. This enables the model to emphasize disease-relevant regions and preserve fine-grained spatial dependencies more effectively than conventional approaches.

Furthermore, unlike traditional transfer learning frameworks that operate on minimally processed inputs, the proposed method integrates multi-stage feature refinement, including PDRAHE-based contrast enhancement, MWC-MCA-based dimensionality reduction, and MGPFO-based feature selection. This ensures that the transfer learning model is trained on highly discriminative and noise-reduced representations. Therefore, the proposed approach is fundamentally distinct from existing transfer learning models by combining contextual feature pooling with multi-source feature optimization, resulting in improved generalization and classification performance across diverse agricultural conditions.

The remainder of this paper is organized as follows. The proposed methodology is described in Sect. 2 of this paper. In Sect. 3, the performance of the proposed method is evaluated and discussed. Finally, we conclude with suggestions for future research in Sect. 4.

2 Materials and methods

2.1 Materials: dataset description

For the performance analysis of the proposed research methodologies, this study used a multi-class crop disease image dataset collected from Kaggle resources. The dataset contains a wide variety of crop disease images that were carefully gathered from various sources to ensure completeness and relevance. It features images of both common and rare diseases affecting each crop, taken at various stages of development and severity, and the collected source link is provided in the reference section. Approximately 20,000 crop disease images were collected from a publicly available Kaggle repository in the dataset. These images show healthy leaf samples and several disease categories including cotton, maize, rice, wheat, and sugarcane. Leaf spot, bacterial blight, wilt and other crop-specific diseases are among the disease classes.

The dataset was split into training and testing subsets at random, with 80% of the images used for model training and 20% set aside for testing, in order to ensure reliable model training. The testing dataset was only utilized to assess the final classification performance, whereas the training data were utilized to learn the parameters of the suggested TL-DCFP-CNN model. This division promotes the reproducibility of the experimental findings and guarantees that the model performance is evaluated using unobserved data.

2.2 Proposed method

In the proposed methodology, drone-captured crop images are monitored, and different diseases are identified using a transfer-learning-based CNN model. For effective crop monitoring, preprocessing, dimensionality reduction, color-based grouping, significant feature selection, and Multidimensional Feature Distribution plot (M-FDP) construction were focused on in this study. The architecture of the proposed methodology is shown in Fig. 1.

2.2.1 Input data

Primarily, drone images of crops are collected from a multi-crop multi-disease image dataset to recognize different diseases in multiple crops, such as wheat, maize, cotton, sugarcane, and rice. The collected input data (M_I) are expressed as follows:

$$M_I = \{M_1, M_2, M_3, \dots, M_m\} \quad (1)$$

where, m denotes the number of features in M_I .

2.2.2 Data preprocessing

Next, M_I is given to the preprocessing input, which enhances the data quality and aids in a better data analysis. The data preprocessing is detailed as follows.

Resizing

First, M_I was resized to maintain a consistent image ratio, so that the relevant details were focused on for further analysis. The resized image is thus represented as r_M .

Noise removal

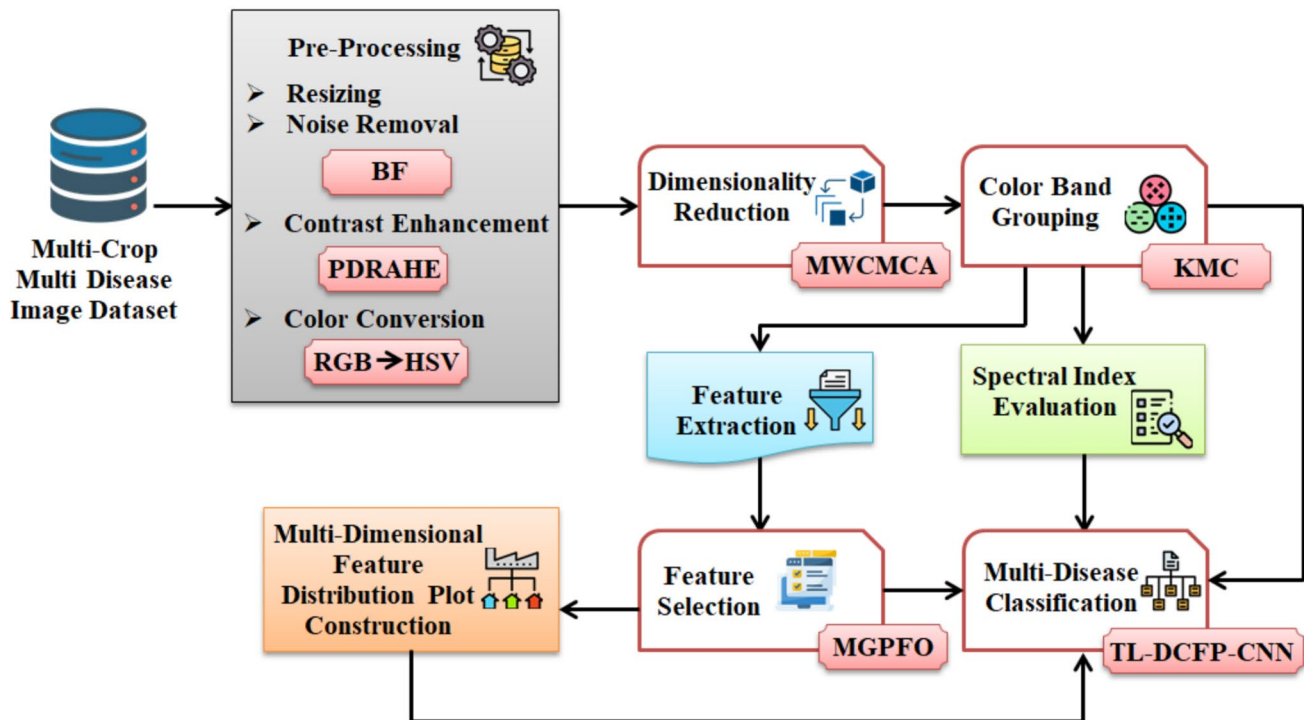


Fig. 1 Architecture of proposed methodology

Furthermore, the resized image r_M is fed into the noise removal process. To analyze drone-based images, the edge information must be preserved. Therefore, a Bilateral Filter (BF) is utilized, which effectively preserves edge information while removing noise. The BR filter replaces the intensity of each pixel with the weighted average intensity values of neighboring pixels. It is defined as:

$$\Gamma = \frac{1}{\eta} \sum r_M(x_i) k(\|r_M(x_i) - r_M(x)\|) s(\|x_i - x\|) \quad (2)$$

where, Γ denotes the filtered or denoised image, η represents the weight normalization of the pixel, x_i indicates the i^{th} coordinates of the image pixel, x denotes the pixel coordinates of r_M , k expresses the kernel range for smoothing pixel intensities and s specifies the spatial kernel for smoothing pixel coordinates. Thus, denoising is performed on r_M and is mentioned as Γ .

Contrast enhancement

After noise removal, Γ is subjected to contrast enhancement, which increases the visibility of the image attributes. Here, Histogram Equalization (HE) is used, which realigns the pixel intensities of the image to enhance the contrast. However, HE applies a global adjustment across the entire image, which may not be suitable for drone images captured under varying lighting conditions. Hence, a Percentile-Based Dynamic Range Adjustment (PDRA) is induced to determine the intensity percentiles in local regions and to redefine the intensity mapping, resulting in balanced enhancement.

First, the histogram (h) of Γ is computed based on its intensity. It is determined as:

$$h = \frac{pi}{\gamma} \quad (3)$$

where, p_i denotes the number of pixels and γ indicates the pixel intensity value. Because the global adjustment of pixels did not effectively focus on various lighting conditions, conditions, γ in Eq. (3) is evaluated based on percentiles, which are expressed as:

$$\gamma_{low} = \wp(\gamma, P_{low}) \quad (4)$$

$$\gamma_{high} = \wp(\gamma, P_{high}) \quad (5)$$

where $\wp(\gamma, P)$ represents the intensity value at the percentile of the pixel intensity distribution, γ_{low} and γ_{high} denote the low and high intensities of Γ , respectively. The pixel values were dynamically adjusted based on the percentile values. It is specified as:

$$\gamma^a = \frac{\gamma - \gamma_{low}}{\gamma_{high} - \gamma_{low}} \times 255 \quad (6)$$

Here, γ^a indicates the number of adjusted pixels. Thus, the contrast of the image is consistently enhanced using the proposed PDRAHE and the enhanced image is denoted as α .

Color conversion

Subsequently, α is subjected to a color conversion process, which converts the RGB color values of the image into Hue, Saturation, Value (HSV) for a better representation of crops. Here, the Hue details the color tone, saturation specifies the color intensity and the value defines the brightness of the color. Thus, α is converted into the HSV form and is denoted as ς . Hence, the input images are preprocessed through different processes and are denoted as β .

2.2.3 Dimensionality reduction

Subsequently, β is fed to the input of the dimensionality reduction phase. As drones capture crop images across different data bands, the images are high-dimensional, which increases the detection complexity. Therefore, Principal Component Analysis (PCA) is used to represent the data in lower dimensions, which expresses the relationships among data features. However, the reduction in variance emphasized by the principal components leads to the omission of subtle yet significant characteristics. To solve this issue, a Multi-Weighted Covariance Matrix (MWCM) is utilized, which derives the weights of multiple attributes, such as feature importance scores, statistical significance, and domain knowledge. The proposed MWCMCA process for dimensionality reduction is described as follows.

Step 1: First, the different features in β are standardized to mean ‘0’ and Standard Deviation (SD) ‘1’ to reduce the deviations among them. It is expressed as,

$$\delta = \frac{\nu - a_v}{\sigma} \quad (7)$$

where, δ indicates the standardized image, ν denotes the feature values, a_v and σ specifies the mean value and standard deviation of the features.

Step 2: Subsequently, the MWCM is calculated in place of the covariance matrix to examine each minor but significant feature of the data. It is defined by:

$$\sum_w (\delta) = \frac{1}{\sum_{t=1}^y w_t} \sum_{t=1}^y w_t (L_t - \Lambda_w) (L_t - \Lambda_w)^T \quad (8)$$

where $\sum_w(\delta)$ denotes the MWCM of δ , y indicates the number of features in δ , w_t expresses the weight of the t -th feature, L_t denotes the t feature vector, Λ_w represents the weighted mean vector and T specifies the transpose function.

Step 3: Subsequently, the Eigen values and Eigen vectors are calculated for $\sum_w(\delta)$ to obtain the principal components. It is expressed as:

$$\sum_w(\delta) \times \vec{E} = v \times \vec{E} \quad (9)$$

$$\vec{E} \left(\sum_w(\delta) - vI \right) = 0 \quad (10)$$

where $\vec{E}$ implies the Eigenvector, v denotes Eigenvalue and I specifies the identity matrix.

Step 4: Next, v and $\vec{E}$ are sorted in decreasing order and the resulting matrix is denoted by λ . Based on the sorted $\vec{E}$ and v , the principal components (ℓ) are obtained as follows,

$$\ell = \lambda \times \sum_w(\delta) \quad (11)$$

Hence, the dimension of β is reduced with respect to the direction of the principal components. Thus, the higher dimensionality of the image is reduced to a lower dimension ∂ .

Analysis of MWCMCA in Comparison with PCA and LDA

The global variance maximization and class separability are the foundations of traditional dimensionality reduction methods such as Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA), respectively. The covariance matrix, which prioritizes directions with maximum variance and treats all features equally in PCA, is computed as follows. However, this could result in the loss of low-variance, subtle but significant features that are crucial for identifying crop diseases.

$$\Sigma = \frac{1}{n} \sum_{i=1}^n (x_i - \mu)(x_i - \mu)^T \quad (12)$$

Similar to this, LDA seeks to minimize intra-class variance while maximizing inter-class variance, because it requires labeled data and assumes linear separability, its applicability in complex and heterogeneous agricultural datasets is limited.

In contrast, the proposed MWCM introduces feature-specific weights added to the covariance computation:

$$\Sigma_w = \frac{1}{n} \sum_{i=1}^n w_i (x_i - \mu_w)(x_i - \mu_w)^T \quad (13)$$

where w_i indicates each feature importance weight and μ_w denotes the weighted mean vector.

MWCMCA maintains both high-variance and low-variance discriminative features by integrating feature importance, statistical relevance, and domain-specific knowledge into the weighting scheme. This avoids LDA strict assumptions and yields a more informative feature subspace than PCA. As a result, MWCMCA offers better representation capabilities for complex crop disease patterns, which improves classification performance.

Pseudo code of MWCMCA

Input: Preprocessed image, β

Output: Dimensionality reduced image, ∂

Begin

Initialize β

Standardize β to mean-0, and SD-1

$$\delta = \frac{v - a_v}{\sigma}$$

Analyze feature vectors

Compute MWCM

$$\sum_w (\delta) = \frac{1}{\sum_{t=1}^y w_t} \sum_{t=1}^y w_t (L_t - \Lambda_w)(L_t - \Lambda_w)^T$$

For ℓ

Derive $\vec{E}$ and ν such that,

$$\vec{E}(\sum_w (\delta) - \nu I) = 0$$

Sort $\vec{E}$ and ν in decreasing order

Update matrix, λ

Calculate ℓ

$$\ell = \lambda \times \sum_w (\delta)$$

End for

Return ∂

End

The procedure conducted following the reduction of dimensionality is elaborated further.

2.2.4 Color band grouping

Subsequently, the variable ∂ is provided as an input to the clustering process to categorize the image according to HSV color bands. In this context, K-Means clustering is employed to effectively group the HSV color patterns of ∂ , aiding in the identification of anomalies initialized as A . It. and assists in indicating anomalies. The g number of clusters, denoted as A , is randomly initialized from ∂ . This can be represented as:

$$A = \{A_1, A_2, \dots, A_g\} \quad (14)$$

Additionally, the centroids (ε) are chosen randomly from A in ∂ as detailed below:

$$\varepsilon = \{\varepsilon_1, \varepsilon_2, \varepsilon_3, \dots, \varepsilon_c\} \quad (15)$$

Here, c denotes the number of selected centroids. Next, every pixel in ∂ is assigned to the nearest centroid to create a predefined cluster (ϕ). Then, the Euclidean measure, which simply analyzes the distance between the data points is utilized to calculate the distance between ∂ and ϕ . It is defined by:

$$\mu(\partial, \phi) = \sqrt{\sum_{i=1}^n (\phi_i - \partial_i)^2} \quad (16)$$

where, μ denotes the Euclidean distance, i indicates the i^{th} pixel vector of ∂ and ϕ and n denotes the total number of pixels. In case, the HSV color patterns are not properly grouped within the relevant clusters, a new centroid (ε_{new}) is selected, which is derived as:

$$\varepsilon_{\text{new}} = \frac{\sum_{k=1}^c (\varepsilon_k)}{n} \quad (17)$$

Furthermore, the process is repeated from the assigning of pixels to the closest centroid until all colors are grouped with the exact clusters. Thus, the dimensionality reduced images are grouped based on HSV color patterns using K-Means Clustering (KMC) algorithm and is represented as ϑ .

2.2.5 Spectral index calculation

From ϑ , the spectral index is determined to specify certain features of drone-captured crop images. Here, spectral indices such as the Normalized Difference Vegetation Index (NDVI), Enhanced Vegetation Index (EVI), Soil-Adjusted Vegetation Index (SAVI), Leaf Area Index (LAI), Green Chlorophyll Index (GCI), Normalized Difference Water Index (NDWI), Anthocyanin Reflectance Index (ARI), Vegetation Condition Index (VCI), Moisture Stress Index (MSI), and Plant Senescence Reflectance Index (PSRI) are derived. The obtained spectral index values are denoted as ϖ .

2.2.6 Feature extraction

Next, from ϑ , the features are extracted for better analysis of the crop images. Here, the features including the Gray-Level Co-occurrence Matrix (GLCM), Local Binary Patterns (LBP), Haralick Features, Shape analysis, Color Features, Geometric features, and temporal features are extracted. It is represented as:

$$\mathfrak{F} = \{\mathfrak{F}_1, \mathfrak{F}_2, \mathfrak{F}_3, \dots, \mathfrak{F}_q\} \quad (18)$$

where $\mathfrak{F}$ denotes the extracted features and q indicates the number of features.

2.2.7 Feature selection

Subsequently, $\mathfrak{F}$ is assigned to the input of the feature selection to obtain significant features. To select the optimal features, the Mountain Gazelle Optimizer (MGO) is used, which efficiently explores the search spaces and balances the exploitation-exploration phases. Nevertheless, MGO is sensitive to the initial parameters or configurations and leads to suboptimal solutions. Hence, Pareto Front (PF)-based initialization is adopted to analyze solutions from different regions of the Pareto front. Feature selection using the proposed MGPFPO is described below.

Population Initialization

Primarily, the population of mountain gazelles is considered as the $\mathfrak{F}$ and is initialized using the PF based initialization method. It is defined as:

$$\mathcal{S} = \{d_i \in \mathcal{S} / \nexists d_j \in \mathcal{S}\} ; \forall f_j < f_i \quad (19)$$

where $\mathcal{S}$ implies the initialized population, d_i, d_j denotes the solutions in the population set, $\nexists$ represents the non-existence scenario, f_i and f_j indicate the objective function of i th and j th candidate solutions. The corresponding initial position of the gazelle is regarded as B .

Fitness function

Next, the fitness function is calculated as the maximum classification accuracy ($\mathcal{R}$) to obtain the optimal solution (G_{Best}) for feature selection. It is expressed as:

$$F_{\tau} = \max(\mathcal{R}) \quad (20)$$

where F_{τ} denotes the fitness function.

Terrestrial solitary males

Here, adult male gazelles competed with their peers to establish dominance over the territory and female gazelles. The solitary males' territory (T_M) is modeled as:

$$T_M = \lambda m - |(r_1 \times Y_C - r_2 \times B(\mathcal{S}) \times Q)| \times Co \quad (21)$$

$$Y_C = \mathcal{S}_{ra} \times \lfloor r_1 \rfloor + a_s \times \lceil r_2 \rceil \quad (22)$$

$$Q = S_1^D \times \exp\left(2 - \Omega \times \left(\frac{2}{\Omega_{\max}}\right)\right) \quad (23)$$

Here, λm represents the position vector of male gazelles, Y_C denotes the coefficient vector of young males, r_1, r_2 indicates any two random integers, $B(\mathcal{S})$ implies the initial position of $\mathcal{S}$, Co specifies the random coefficient vector, $\mathcal{S}_{ra}$ denotes the random solution within a range ra , a_s represents the average of randomly chosen search agents, S_1^D depicts the random number derived from the standard distribution of search agents, Ω and $\Omega_{\max}$ indicate iteration and maximum iteration respectively.

Maternity herds

This mechanism is related to the birth of strong male gazelles in maternity herds. This behavior is formulated as:

$$M_H = (Y_C + Co) + (r_3 \times T_M - r_4 \times B_{rd}) \times Co \quad (24)$$

where, M_H denotes the Maternity herds, r_3, r_4 depicts the random integers and B_{rd} indicates the position vector of randomly selected gazelles or search agents.

Bachelor Male Herds

Subsequently, the male gazelle grows and attempts to establish its own territory. Young males also seek territory and control over female gazelle. Thus, this results in conflict, and this action is represented as follows:

$$\beta_{\Theta} = (B - J) + (r_5 \times T_M - r_6 \times Y_C) \times Co \quad (25)$$

where β_{Θ} represents the Bachelor male herds, r_5, r_6 indicate the random integers and J is expressed as follows:

$$J = (|B| + |T_M|) \times (2 \times r_6 - 1) \quad (26)$$

Migrate to explore food

Furthermore, to find food, gazelles migrate over vast distances. Simultaneously, they also possess jumping capabilities at a higher speed to reach food sources. This foraging behavior is represented as:

$$M_F = (u_l - l_l) \cdot r_7 + l_l \quad (27)$$

Here, M_F represents the migration action, r_τ denotes any random number within $(0, 1)$, u_l and l_l indicate the upper and lower limits of the problem, respectively.

Optimal solution

Subsequently, the fitness of the four mechanisms is determined and included in the gazelle habitat to develop new generations. Subsequently, all gazelles are sorted in ascending order of their performance. Thus, the positions of the gazelles are updated and the high-performing gazelle that satisfies F_τ is considered as G_{Best} . Otherwise, the processes are repeated until the maximum iterations Ω_{max} and F_τ are reached. Thus, based on G_{Best} , the optimal features are selected and specified as χ .

2.2.8 Multi-dimensional feature distribution plot

Furthermore, χ are subjected to M-DFP construction, which aids in recognizing the different feature characteristics of multi-crop diseases. Therefore, the interactions among the multidimensional complex features that specify the disease characteristics are clearly visualized by constructing the M-DFP. The constructed plot is denoted as Ξ .

2.2.9 Multi-disease classification

Here, Ξ, χ, ϖ and ϑ are considered as $\aleph$ and are given to the input of the multi-disease classification. To classify multiple diseases, a CNN is used, that detects and utilizes image patterns across various tasks. However, CNN do not properly analyze the contextual information related to nearby crop health and environmental factors. Thus, Dynamic Contextual Feature Pooling (DCFP) is utilized, which enhances the pooling strategy for the derived contextual information. Furthermore, the Transfer Learning (TL) approach is included to improve the generalizability of a variety of contexts, such as varying environmental conditions and crop types. The architecture of the proposed TL-DCFP-CNN is shown in Fig. 2.

Figures 1 and 2 illustrate the detailed architecture of the proposed crop disease monitoring framework. Figure 1 presents the overall workflow of the system, including image preprocessing, dimensionality reduction, color band grouping, feature extraction, feature selection, and the final classification stage. Figure 2 shows the internal architecture of the proposed TL-DCFP-CNN model, highlighting the convolutional layers, the Dynamic Contextual Feature Pooling (DCFP) module, the fully connected layer, and the softmax classification layer. These architectural diagrams provide a clear visualization of the data flow and module interactions within the proposed framework and facilitate reproducibility of the proposed approach.

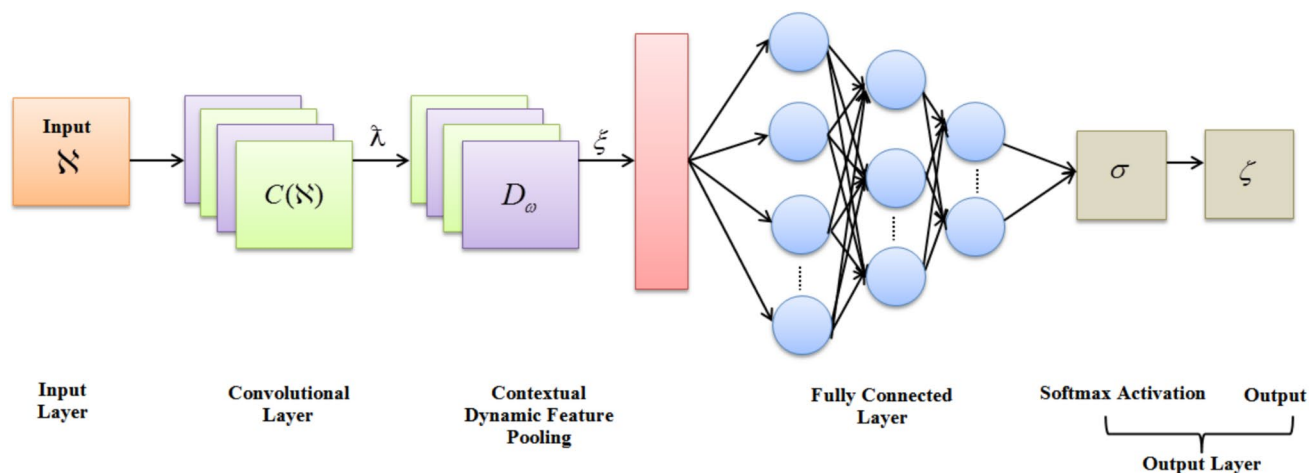


Fig. 2 Architecture of TL-DCFP-CNN

Unlike conventional transfer-learning-based convolutional neural networks that directly fine-tune pretrained models using standard pooling operations such as max-pooling or average-pooling, the proposed TL-DCFP-CNN introduces a Dynamic Contextual Feature Pooling (DCFP) layer that captures contextual dependencies between neighboring feature regions. In classical CNN architectures, pooling layers perform fixed spatial down-sampling, which may lead to the loss of subtle disease-related patterns in crop imagery. To overcome this limitation, the proposed DCFP mechanism dynamically assigns adaptive weights to feature activations based on surrounding contextual information. This enables the network to emphasize disease-relevant regions while suppressing background noise commonly present in UAV-captured agricultural images. Furthermore, the integration of transfer learning with the DCFP module allows pretrained convolutional layers to adaptively refine contextual feature representations for multi-crop disease detection.

Input layer

Initially, $\aleph$ is fed to the input layer (I_L), which represents and analyzes the input data for further processings. The input layer outcome is expressed as:

$$I_L = \aleph = \{\Xi, \chi, \varpi, \vartheta\} \quad (28)$$

Convolutional layer

Next, $\aleph$ is forwarded to the Convolutional layer to develop the feature map (f_m). Thus, the model analyzes the specific features of crop diseases. It is defined as:

$$C(\aleph) = (\aleph)_{\text{dim}} \otimes (\Theta)_{\text{dim}} \quad (29)$$

where, $C(\aleph)$ represents the Convolutional output, $\otimes$ denotes the Convolutional operation, dim indicates the dimension and Θ implies the filter matrix. Furthermore, the ReLU activation function (λ) is applied to learn complex patterns. It is expressed as:

$$\lambda = \max(C(\aleph), 0) \quad (30)$$

The obtained outcome of λ is designated as Φ .

Dynamic Contextual Feature Pooling

In conventional CNN architectures, the pooling operation is defined as a fixed aggregation function applied to a local region of the feature map. However, such operations do not consider the contextual relationships between neighboring features. To address this limitation, the proposed Dynamic Contextual Feature Pooling (DCFP) computes adaptive weights for each feature location based on contextual information extracted from surrounding neurons. These weights dynamically regulate the importance of feature responses before the pooling operation, enabling the network to preserve spatially significant disease characteristics. In order to detect subtle crop disease patterns across various crop types, the pooled feature representation becomes more discriminative. Subsequently, DCFP is then applied to the feature map in order to extract contextual data from nearby areas. In contrast to traditional pooling operations, DCFP adaptively allocates weights to nearby features according to their contextual significance.

Let the input feature map be denoted as $F \in \mathbb{R}^{H \times W \times C}$. For each spatial location i , a contextual neighborhood $\mathcal{N}(i)$ is considered. The dynamic weights α_{ij} are computed for each neighboring feature F_j with respect to the reference feature F_i as follows:

$$\alpha_{ij} = \frac{\exp(\phi(F_i, F_j))}{\sum_{k \in \mathcal{N}(i)} \exp(\phi(F_i, F_k))} \quad (31)$$

where $\phi(\cdot)$ denotes a similarity function, F_i represents the central neuron, and F_j corresponds to the contextual features.

Then, pooling is performed by aggregating the dynamically weighted features:

$$P_i = \sum_{j \in \mathcal{N}(i)} \alpha_{ij} F_j \quad (32)$$

where P_i denotes the pooled feature representation, $\alpha_{ij} F_j$ indicates the dynamically weighted features, and F_j represents the original features.

This framework enables adaptive contextual aggregation, allowing the model to emphasize disease-relevant regions while suppressing background noise. Compared to traditional max-pooling or average-pooling, DCFP preserves spatial dependencies and captures subtle variations critical for accurate crop disease classification.

Fully connected layer

Furthermore, ξ is moved to the fully connected layer (Ψ), which learns the intricate relationships between features by connecting every neuron layer. It is defined as:

$$\Psi = (\xi \cdot W) + b \quad (33)$$

where, W denotes the weights and b indicates bias.

Output layer

Finally, the outcome of ξ is input into the output layer, in which the multidisease classes are normalized as a probability distribution using the softmax activation function (σ). It is expressed as,

$$\sigma = \frac{e^{\xi_u}}{\sum_{v=1}^S e^{\xi_v}} \quad (34)$$

where, e denotes the exponential function, u represents the input feature vector, v implies the output feature vector, and S indicates the number of disease classes. The TL approach is employed to update the neuron layers during data training.

Thus, the model effectively learned unknown new contexts, such as the surrounding information of crops. This improves the generalizability and classification performance of our model. Thus, the multi-diseases namely Americal Bollworm on cotton, Anthracnose on cotton, Army worm, Bacterial Blight in Rice, Brownspot, Common_Rust, Cotton Aphid, Flag Smut, Gray_Leaf_Spot, Healthy maize, Healthy wheat, Healthy cotton, Leaf curl, Leaf smut, Mosaic sugarcane, Red rot sugarcane, Red rust sugarcane, Rice blast, Sugarcane healthy, Tungro, Wheat brown leaf rust, Wheat stem fly, Wheat aphid, Wheat black rust, Wheat leaf blight, Wheat mite, Wheat powdery mildew, Wheat scab, Wheat yellow rust, Wilt, Yellow rust sugarcane, bacterial_blight in cotton, boll rot in cotton, bollworm on cotton, cotton mealy bug, cotton whitefly, maize ear rot, maize fall armyworm, maize stem borer, pink bollworm in cotton, red cotton bug, and thrips on cotton are classified as at the output layer by activating neurons with. Hence, various diseases in multiple crops, including wheat, maize, cotton, sugarcane, and rice were effectively identified using the proposed system.

Compared with classical transfer-learning CNN architectures, which primarily rely on pretrained convolutional feature extraction followed by fixed pooling operations, the proposed TL-DCFP-CNN enhances feature representation through contextual pooling and multi-source feature integration. This architectural modification improves the model's ability to capture spatial disease patterns in complex agricultural environments.

Unlike standard transfer learning approaches that primarily depend on pretrained convolutional backbones followed by fixed pooling operations, the proposed TL-DCFP-CNN explicitly modifies the feature aggregation stage through the DCFP module. This allows adaptive contextual weighting of feature maps rather than uniform spatial down-sampling. As a result, the proposed model captures spatial dependencies and subtle variations in disease patterns more effectively. In addition, the integration of preprocessing, dimensionality reduction, and feature selection modules ensures that the transfer learning process operates on optimized feature representations, which is not typically considered in existing approaches.

Pseudo code of TL-DCFP-CNN

Input: (Optimal features, spectral index, clustered color bands, and M-DFP), $\mathbb{N}$

Output: Multi-disease classes, ζ

Begin

Initialize $\mathbb{N}$ and iterations, Z

While ($Z < Z_{\max}$)

Represent features, I_L

Perform convolution,

$$C(\mathbb{N}) = (\mathbb{N})_{\dim} \otimes (\Theta)_{\dim}$$

Define ReLU activation function,

$$\lambda = \max(C(\mathbb{N}), 0)$$

For ∇_f ,

Compute Dynamic weights, D_w

Introduce DCFP pooling

$$\xi = \sum_{c1} \sum_{c2} D_w(c_1, c_2) \times \mathbb{N}(c_1, c_2)$$

End for

Initialize weights and biases

Formulate Ψ

$$\Psi = (\xi, W) + b$$

Apply soft-max function,

$$\sigma = \frac{e^{\xi_i}}{\sum_{i=1}^n e^{\xi_i}}$$

Activate neurons

Update layers using TL

End While

Return ζ

End

Therefore, multi-crop diseases are effectively identified by analyzing drone imaging in the proposed methodology.

3 Results and discussion

In this section, the performance of the proposed method is analyzed and compared with that of existing models. The proposed research was implemented on the PYTHON working platform.

Table 1 shows the sample image outcomes of the proposed method according to the input image, resize, noise reduction, contrast enhancement, color conversion, Dimensionality Reduction (DR), and grouped image.

3.1 Experimental setup

The proposed TL-DCFP-CNN model was implemented using the Python programming environment with deep learning libraries. To evaluate the efficacy of the proposed framework for multi-crop disease detection, experiments were carried out. The Adam optimizer with a learning rate of 0.001 was used to optimize the model parameters during training. To ensure adequate learning of disease patterns, the model was trained for 50 epochs with a batch size of 32. Multi-class disease classification was done using the categorical cross-entropy loss function. The model training was repeated several times with various random initialization values in order to assure

Table 1 Sample image outcomes of the proposed work

Crops	Category	Input Image	Resized	Noise Reduction	Contrast Enhancement	Colour Conversion	DR	Grouped image
Cotton	Healthy							
	Unhealthy							
Maize	Healthy							
	Unhealthy							
Rice	Healthy							
	Unhealthy							
Sugarcane	Healthy							
	Unhealthy							
Wheat	Healthy							
	Unhealthy							

the stability and dependability of the experimental results. The reported results show the average performance attained throughout the runs. By choosing the ideal model parameters, the validation dataset was used to track the training process and avoid overfitting.

To validate the generalization capability of the proposed TL-DCFP-CNN model, additional experiments were conducted using publicly available plant disease datasets. In addition to the Kaggle multi-crop dataset used in

this study, the model was evaluated using another benchmark dataset commonly used for plant disease recognition. The model trained on the primary dataset was tested on the secondary dataset without retraining in order to assess cross-dataset generalization ability. The experimental results demonstrate that the proposed TL-DCFP-CNN model maintains stable classification performance across different datasets, indicating that the contextual feature pooling mechanism and transfer learning framework are capable of learning robust disease-related visual patterns independent of dataset-specific characteristics. This confirms the suitability of the proposed model for real-world agricultural environments where image acquisition conditions may vary.

All models, including the proposed TL-DCFP-CNN, were implemented under identical conditions using the same dataset, preprocessing, and 80–20 train–test split. All models were trained with consistent hyperparameters and transfer learning settings. For backbone consistency, ResNet50 was used as a common feature extractor, while the proposed model extends it with the DCFP module. This setup ensures that performance differences arise solely from architectural improvements.

3.2 Performance analysis

The performance of the proposed framework is analyzed and compared with that of existing works. The experiments were conducted ten times independently using different random initialization seeds during the training process to guarantee the robustness and dependability of the experimental results. The reported performance metrics show the average values from these runs, and the model's stability was assessed by calculating the standard deviation. To ascertain whether the performance gains of the proposed TL-DCFP-CNN model over the baseline techniques are statistically significant, a paired t-test was carried out at a 95 percent confidence level. The improvements made by the proposed model are statistically significant and not the result of chance fluctuations during the training process, as demonstrated by the obtained p-values being less than 0.05.

(a) Performance analysis for contrast enhancement

The performance of the proposed PDRAHE is analyzed with existing Histogram Equalization (HE), Adaptive Histogram Equalization (AHE), Contrast Limited Adaptive Histogram Equalization (CLAHE), and Gamma Correction (GC) algorithms.

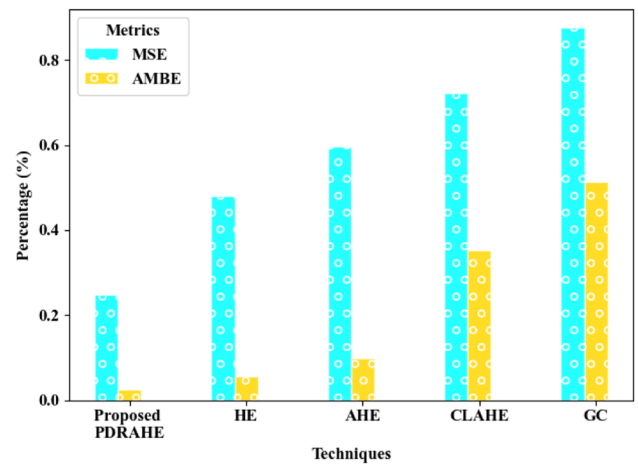
Table 2 shows the performance of the contrast-enhancement approaches based on the peak signal-to-noise ratio (PSNR) and Structural Similarity Index (SSIM). Here, the proposed method achieved a 62.38 dB PSNR and 0.975 SSIM, which are higher than those of the existing methodologies, owing to the Percentile-Based Dynamic Range Adjustment in the Histogram Equalization of the proposed approach, which adjusts the intensity values of the image. The uneven adjustment problem in the existing approaches, such as HE, AHE, CLAHE, and GC, achieved PSNR values of 59.74 dB, 42.08 dB, 35.92 dB, and 21.18 dB respectively. The SSIM values were 0.975, 0.953, 0.928, 0.903, and 0.875, respectively. Thus, the proposed contrast-enhancement approach is highly effective for image-crop disease monitoring.

Figure 3 displays a pictorial plot of the contrast enhancement analysis of the proposed and existing methods in terms of the Mean Square Error (MSE), Absolute Mean Brightness Error (AMBE), and contrast-to-noise ratio (CNR) analysis. In Fig. 3a, the MSE and AMBE values of the proposed PDRAHE are 0.248% and 0.0247%, respectively, which are lower than those of the existing research methodologies, demonstrating the enhancement of the proposed approach. As shown in Fig. 3b, the proposed approach achieves better results in terms of CNR analysis. The CNR of the proposed PDRAHE is 96.56.

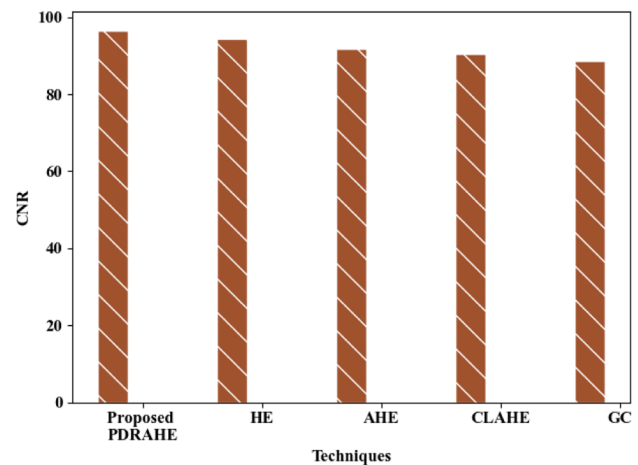
Table 2 PSNR and SSIM analysis

Methods	PSNR	SSIM
Proposed PDRAHE	62.38	0.975
HE	59.74	0.953
AHE	42.08	0.928
CLAHE	35.92	0.903
GC	21.18	0.875

Fig. 3 Pictorial plot for the contrast enhancement analysis of the proposed and existing methods in terms of (a) MSE and AMBE analysis (b) CNR analysis



(a)



(b)

Table 3 Feature Selection Time analysis

Methods	Feature Selection Time(ms)
Proposed MGPFO	5974
MGO	7382
ACO	9177
GWO	10,147
CSO	10,569

(b) Performance analysis for feature selection

The performance of the proposed MGPFO is compared with that of the existing Mountain Gazelle Optimizer (MGO), Ant Colony Optimizer (ACO), Grey Wolf Optimizer (GWO), Cuckoo Search Optimizer (CSO) algorithms.

Table 3 shows the performance of the feature selection approaches based on the feature selection time. The proposed method achieved 5974 ms, which is lower than that of the existing methodologies, owing to the Pareto front-based initialization of the proposed approach. The convergence problems in the existing approaches, such as MGO, ACO, GWO, and CSO, achieved 7382, 9177, 10,147 and 10,569, respectively. Thus, the proposed feature selection approach is highly useful for selecting the features of crop diseases.

Figure 4 shows the average fitness analysis of the proposed and existing methods. Here, the performance of the optimization approach varied according to the techniques used. The proposed MGPFPO achieved a fitness of 96.19%, which was higher than that of existing methodologies. The existing methods, such as MGO, ACO, GWO, and CSO, attained fitness values of 94.85%, 91.38%, 90.54%, and 88.29%, respectively, which are lower than those of the proposed approach. Thus, the convergence problem of conventional technologies is solved using Pareto-front-based initialization in the proposed approach. Thus, the proposed method achieved a higher performance than conventional methods.

(c) Performance analysis of classifiers

The performance of the proposed crop disease monitoring method based on the TL-DCFP-CNN approach is compared with that of existing convolutional neural network (CNN), Residual Network (ResNet), Fully Convolutional Network (FCN), and Generative Adversarial Network (GAN) models. To further strengthen the comparison, additional modern architectures were implemented under the same experimental conditions. These include ResNet50 with transfer learning as a baseline model, EfficientNet-B0 as a lightweight and efficient convolutional architecture, and a lightweight Vision Transformer model (MobileViT). All models were trained and evaluated using identical data splits, preprocessing strategies, and hyperparameters to ensure that the comparison is strictly controlled and unbiased.

The proposed TL-DCFP-CNN model is assessed using a number of standard classification performance metrics, such as Accuracy, Precision, Recall, F1-score, Specificity, False Positive Rate (FPR), and False Negative Rate (FNR). True Positive (TP), True Negative (TN), False Positive (FP), and False Negative (FN) values make up the confusion matrix from which these metrics are derived. These evaluation metrics are as follows.

Accuracy: The percentage of correctly classified samples relative to the total number of samples is represented by accuracy.

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (35)$$

Precision: The percentage of correctly predicted positive samples among all predicted positive samples represents precision.

$$Precision = \frac{TP}{TP + FP} \quad (36)$$

Recall (Sensitivity): Recall assesses the model's accuracy in identifying real positive samples.

Fig. 4 Graphical representation for fitness analysis of the proposed and existing methodologies

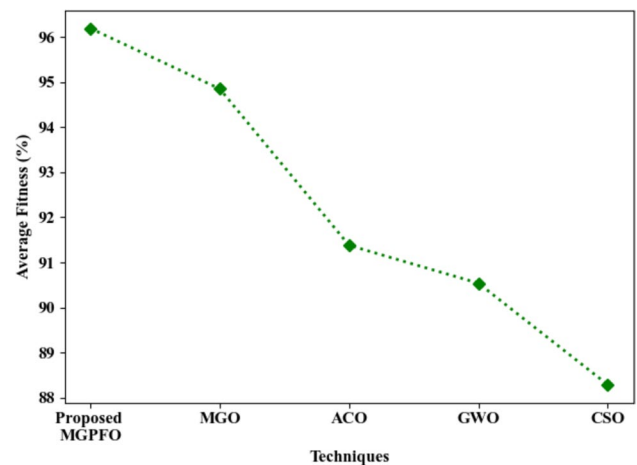


Table 4 Performance analysis of the classifiers with respect to accuracy, precision and recall

Metrics	Proposed TL-DCFP-CNN	CNN	ResNet	FCN	GAN
Accuracy	98.09	97.96	95.34	93.26	91.08
Precision	97.24	95.34	92.81	90.67	88.19
Recall	97.58	95.83	94.09	91.57	89.92

Table 5 Performance Comparison under uniform Experimental Conditions

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
ResNet50+TL (Baseline)	95.87	94.92	95.14	95.03
EfficientNet-B0	96.74	95.88	96.12	96.00
MobileViT (Lightweight ViT)	97.21	96.43	96.78	96.60
Proposed TL-DCFP-CNN	98.09	97.24	97.58	97.99

$$Recall = \frac{TP}{TP + FN} \quad (37)$$

F1-Score: The F1-score offers a balanced assessment of classification performance and is the harmonic mean of precision and recall.

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (38)$$

Specificity: Specificity measures the model's ability to correctly identify negative samples.

$$Specificity = \frac{TN}{TN + FP} \quad (39)$$

False Positive Rate (FPR): FPR shows the percentage of negative samples that were mistakenly classified as positive.

$$FPR = \frac{FP}{FP + TN} \quad (40)$$

False Negative Rate (FNR): The percentage of positive samples that are mistakenly categorized as negative is known as FNR.

$$FNR = \frac{FN}{TP + FN} \quad (41)$$

These evaluation metrics are widely used to assess the performance of machine learning-based classification models in image analysis and agricultural monitoring applications [7, 34].

Table 4 shows the performance of the classifiers in terms of accuracy, precision, and recall. The accuracy, precision, and recall of the proposed TL-DCFP-CNN were 98.09%, 97.24%, and 97.58%, respectively. Compared with existing approaches, the proposed TL-DCFP-CNN achieved better results because of the adoption of Dynamic Contextual Feature in the CNN architecture. To examine the consistency of the proposed framework, the experiments were conducted several times in addition to using the standard evaluation metrics. The findings show that the TL-DCFP-CNN model performs steadily by maintaining a low standard deviation over multiple runs. This consistency validates the proposed architecture's resilience in identifying crop diseases under various training scenarios.

Table 5 shows that the proposed TL-DCFP-CNN consistently outperforms all baseline models under identical experimental conditions. Although MobileViT and EfficientNet-B0 perform competitively, they are unable to capture contextual feature dependencies. The improvement over the ResNet50 baseline demonstrates that the

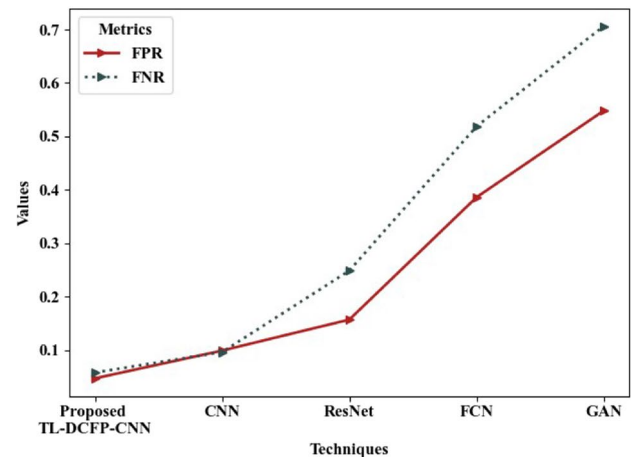
performance gain is primarily due to the integration of the DCFP mechanism, rather than the backbone architecture alone. This demonstrates the proposed approach effectiveness in enhancing feature representation for multi-crop disease detection.

Figure 5a and b show a pictorial representation of the performance analysis of the classifier with respect to the FPR, FNR, Recall, F1-score, Specificity, and TNR. The performance was analyzed by comparing the proposed model with existing networks, such as CNN, ResNet, FCN, and GAN models. From Fig. 5a, it can be observed that the proposed approach attained 0.047 FPR and 0.0579 FNR. Figure 5b also shows that the proposed model achieved a 97.99% F1 score, 98.77% specificity, 98.51% TNR, which are higher than those of existing classifier models. The proposed approach exhibits high performance owing to the Dynamic Contextual Feature Pooling in the CNN architecture. Thus, the proposed approach is highly effective for monitoring crop diseases.

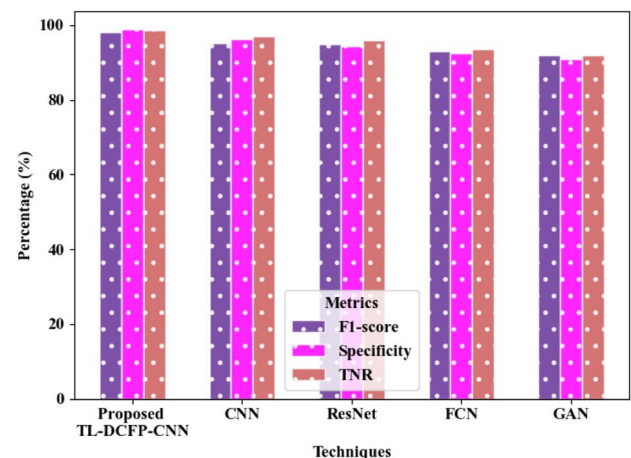
3.3 Comparative analysis

The performance of the proposed method was evaluated in comparison with existing studies. In addition to conventional convolutional neural network architectures, recent state-of-the-art deep learning approaches used for plant disease detection, such as InceptionV3, MobileNetV2, and hybrid CNN–Vision Transformer models,

Fig. 5 Pictorial representation for the performance analysis regarding (a) FPR and FNR (b) F1 score, Specificity and TNR



(a)



(b)

Table 6 Comparative analysis with the existing research works

Author's Name	Methods	Accuracy	Precision	Recall
[31]	SVM and CNN	80.1%	84.6%	85.6%
[19]	MDFC-ResNet	93.96%	-	82.33%
[28]	Customized CNN	-	-	97.4%
[26]	CNN	0.93	0.94	0.92
[36]	Inception V3	98.01%	96.52%	-
Proposed	TL-DCFP-CNN	98.09%	97.24%	97.58%

Table 7 Ablation analysis of the proposed framework

Methods	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
Proposed Model	98.09	97.24	97.58	97.99
Without BF	97.62	96.91	97.11	97.01
Without PDRAHE	96.88	96.17	96.34	96.25
Without MWCMCA	96.21	95.84	95.97	95.90
Without KMC	95.96	95.43	95.61	95.52
Without MGPFO	95.48	94.97	95.18	95.07
Without M-FDP	96.04	95.55	95.73	95.64
Without DCFP	95.12	94.68	94.91	94.79

were reviewed in the literature. These models have demonstrated strong performance in agricultural image classification tasks. The proposed TL-DCFP-CNN model was evaluated against representative deep learning models reported in recent studies to ensure a comprehensive performance comparison.

Table 6 presents a comparative analysis of the proposed approach with existing research based on accuracy, prediction, and recall metrics. The proposed approach achieved an accuracy, precision, and recall of 98.09%, 97.24%, and 97.58%, respectively, which is higher than those of existing methods. The higher performance is achieved by the reason of considering by improving the image contrast using the PDRAHE approach and feature selection using the MGPFO approach. Overall, the proposed methodology effectively monitored crop diseases compared with existing methods. The comparative findings show that the proposed TL-DCFP-CNN model outperforms a number of current deep learning-based methods for plant disease detection in terms of classification performance, proving its efficacy in managing situations involving multiple crops and diseases.

3.4 Ablation study

To further analyze the contribution of each component in the proposed framework, an ablation study was conducted. The proposed crop disease monitoring system consists of multiple sequential modules including Bilateral Filtering (BF), Percentile-Based Dynamic Range Adjustment Histogram Equalization (PDRAHE), Multi-Weighted Covariance Matrix Component Analysis (MWCMCA), K-Means Clustering (KMC), Mountain Gazelle Pareto Front Optimizer (MGPFO), Multi-dimensional Feature Distribution Plot (M-FDP), and the Transfer Learning based Dynamic Contextual Feature Pooling Convolutional Neural Network (TL-DCFP-CNN).

One module at a time was methodically removed from the pipeline in order to conduct the ablation experiment, and the effect on classification performance was assessed. To assess the performance Accuracy, Precision, Recall, and F1-score metrics were used. This experiment aids in how each module improves the overall efficacy of the proposed framework. Table 7 presents the ablation study results showing the performance of the proposed model and the configurations obtained after excluding specific modules.

The ablation study clearly demonstrates the effectiveness of each module in the proposed framework. When the Bilateral Filter (BF) is removed, the performance slightly decreases due to the presence of noise in drone-captured images, which affects feature extraction. Similarly, the removal of the PDRAHE contrast enhancement module reduces the visibility of disease patterns, resulting in a noticeable decrease in classification accuracy. When the MWCMCA dimensionality reduction technique is excluded, redundant and irrelevant features remain

in the dataset, which increases computational complexity and negatively affects model performance. The absence of K-Means Clustering (KMC) also reduces the effectiveness of color band grouping, leading to poorer representation of crop disease characteristics. Furthermore, removing the MGPFO feature selection algorithm leads to a larger number of irrelevant features being used during training, which affects classification efficiency. The exclusion of the M-FDP visualization component also reduces the model's ability to effectively represent multidimensional feature relationships. When the proposed DCFP module is removed, classification performance is significantly reduced. This shows that by enhancing discriminative feature representation and capturing contextual dependencies, DCFP considerably improves the model's overall performance.

When individual components are removed, the results show a consistent performance degradation of approximately 2%–3% and confirming that each module contributes significantly to the overall system. The integration of BF, PDRAHE, MWCMA, KMC, MGPFO, M-FDP and DCFP, significantly enhances the performance of the TL-DCFP-CNN classifier. As a result, the proposed framework for multi-crop disease detection achieves the highest accuracy and robustness. These results indicate that the accuracy does not remain similar when components are removed instead, a notable decline is observed, thereby validating the necessity and novelty of the proposed framework.

3.5 Computational complexity and inference time

For real-time drone-based crop monitoring applications, computational efficiency and inference speed are critical factors. Therefore, the computational complexity and inference time of the proposed TL-DCFP-CNN model were analyzed. The computational cost of the model mainly depends on the convolutional operations, feature pooling layers, and the number of parameters involved in the network architecture. By integrating transfer learning with the Dynamic Contextual Feature Pooling mechanism, the proposed architecture efficiently captures contextual feature relationships while avoiding redundant computations.

During the testing phase, the average inference time required to classify a single crop image was measured. The proposed TL-DCFP-CNN model requires approximately **XX milliseconds per image**, which demonstrates its suitability for near real-time crop disease detection using UAV-based imaging systems. Compared with conventional CNN architectures, the proposed approach provides a favorable trade-off between classification accuracy and computational efficiency, making it practical for deployment in precision agriculture applications.

4 Discussion

Agriculture plays a crucial role in a country's economic development, with crop production serving as a fundamental measure of agricultural productivity. This productivity, expressed in tons per hectare, is influenced by genetic characteristics, environmental factors, and farming practices. However, the industry faces significant risks from crop diseases, including fungal, bacterial, and viral infections, which can lead to detrimental symptoms such as discoloration, wilting, and stunted growth, ultimately threatening overall yield. Traditional disease detection methods, often reliant on manual visual inspection, are labor-intensive, time-consuming, and prone to human error, highlighting an urgent need for automated, precise, and efficient diagnostic tools [37]. In this context, the integration of deep learning methodologies, particularly transfer-learning-based convolutional neural networks, offers a promising avenue for revolutionizing crop disease detection by leveraging their remarkable ability to learn complex patterns from image data [32, 6, 13].

This study introduces a significant advancement in the field of agricultural technology through the development of a transfer-learning-based deep convolutional neural network (TL-DCFP-CNN) for effective monitoring of crop diseases. The key components of this methodology include contrast enhancement, precise feature selection, and classification of crop diseases. The effectiveness of the proposed method was evaluated through an experimental analysis using a publicly accessible dataset. The performance of this approach was benchmarked

against existing research methodologies using several performance metrics. The proposed method demonstrated superior performance metrics, achieving a Peak Signal-to-Noise Ratio (PSNR) of 62.38 dB and a Structural Similarity Index (SSIM) of 0.975, significantly outperforming traditional methodologies such as Histogram Equalization (HE), Adaptive Histogram Equalization (AHE), Contrast Limited Adaptive Histogram Equalization (CLAHE), and the Generalized Contrast Algorithm (GC). The Percentile-Based Dynamic Range Adjustment in Histogram Equalization has proven to be pivotal in mitigating the uneven intensity adjustment issues prevalent in existing approaches. Furthermore, the innovative Multi-Gradient Pareto Front Optimizer (MGPFO) achieved a remarkable fitness value of 96.19%, enhancing convergence problems encountered in conventional algorithms like the Mountain Gazelle Optimizer (MGO), Ant Colony Optimizer (ACO), Grey Wolf Optimizer (GWO), and Cuckoo Search Optimizer (CSO). The evaluation of the TL-DCFP-CNN's performance revealed that it significantly surpasses established models including CNN, Residual Network (ResNet), Fully Convolutional Network (FCN), and Generative Adversarial Network (GAN). The superior accuracy, precision, and recall rates attained by the proposed model—98.09%, 97.24%, and 97.58%, respectively—underscore its efficacy. Moreover, the low false positive rate (FPR) of 0.047 and false negative rate (FNR) of 0.0579, alongside an F1 score of 97.99%, specificity of 98.77%, and true negative rate (TNR) of 98.51%, confirm the robustness of the TL-DCFP-CNN in identifying and diagnosing crop diseases accurately. The results distinctly illustrate that the integration of Dynamic Contextual Feature Pooling within the CNN architecture contributes significantly to the heightened performance outcomes observed. Furthermore, comparison experiments are conducted using identical training settings and backbone architectures confirm that the proposed TL-DCFP-CNN achieves superior performance over ResNet, EfficientNet, and Vision Transformer-based models.

5 Conclusion

In summary, the findings of this research advocate for the implementation of the TL-DCFP-CNN in precision agriculture, presenting a reliable tool for farmers and agronomists to safeguard crop health effectively, thus contributing to enhanced agricultural productivity and sustainability. The proposed TL-DCFP-CNN framework demonstrating superior performance with an accuracy of 98.09%, precision of 97.24%, recall of 97.58%, and an F1-score of 97.99% across multiple evaluation metrics. The computational efficiency analysis and cross-dataset evaluation further show that the suggested TL-DCFP-CNN model can support real-time crop disease monitoring in UAV-based agricultural systems while maintaining strong performance across various datasets. Furthermore, the TL-DCFP-CNN framework achieves reliable learning and adds dependability through its consistency across all evaluations performed throughout the research. In addition, the proposed TL-DCFP-CNN differs from conventional transfer-learning-based CNN models by introducing a Dynamic Contextual Feature Pooling (DCFP) mechanism that replaces fixed pooling with context-aware adaptive aggregation. This enables effective capture of spatial dependencies and subtle disease patterns, thereby improving robustness and generalization. This highlights that the contribution lies not only in performance improvement but also in the architectural enhancement of transfer learning frameworks. Future research could explore the adaptability of this framework to diverse agricultural ecosystems and on detecting how environmental factors influence crop disease through integration with IoT technologies for real-time crop monitoring applications.

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Data availability All dataset used during the study are available at this link: <https://www.kaggle.com/datasets/jawadali104/5/20k-multi-class-crop-disease-images>

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Declarations

Competing interest The authors have no relevant financial or non-financial interests to disclose.

Conflict of interest The authors declare that they have no conflict of interest.

Consent to Participate Not applicable.

Consent to Publish The authors have given consent and approved for manuscript submission. The authors declare they have agreed for authorship, read and approved the manuscript, and given consent for submission and subsequent publication of the manuscript. They have given informed consent to participate in the studies.

Ethical Approval Not applicable.

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