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Bio-Inspired Optimization of Convolutional Neural Networks for Enhanced Maize Disease Detection in Precision Agriculture

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ABSTRACT

Objective: This study develops an automated, image-based system for early detection of four key maize diseases: *Puccinia sorghi*, *Cochliobolus carbonum*, *Bipolaris maydis*, and *Exserohilum turcicum* using Convolutional Neural Network (CNN) optimized through bio-inspired algorithms.

Design/methodology/approach: A dataset of 17,280 high-resolution images across six disease stages was preprocessed and used to train CNNs. Two metaheuristic algorithms, Spider Monkey Optimization (SMO) and Squirrel Search Algorithm (SSA), were applied to optimize weights and hyperparameters. An 80/20 training-validation split was used, and performance was assessed with standard classification metrics.

Results: The SMO-optimized CNN outperformed SSA, achieving 95.14% accuracy versus 89.74%. SMO also yielded better precision, recall, and F1-scores, showing strong performance even in distinguishing visually similar symptoms.

Study Limitations/Implications: SMO's computational demands may limit its usability in low-resource settings. Some classification confusion persisted, highlighting the need for improved feature extraction and broader datasets for increased generalization.

Findings/conclusions: CNNs optimized with SMO provide a robust tool for maize disease diagnosis, reducing analysis time and enabling more precise crop management. Future work will explore hybrid optimization methods to enhance scalability and real-time application in precision agriculture.

Keywords: Convolutional Neural Networks, Maize Disease Detection, Intelligent Precision Agriculture.

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INTRODUCTION

Maize (*Zea mays* L.) is a staple crop with significant global economic and nutritional relevance, particularly in regions where it underpins food security. Despite its importance, maize production is increasingly undermined by plant diseases, notably Common Rust (*Puccinia sorghi*), Gray Leaf Spot (*Cochliobolus carbonum*), Asphalt Spot (*Bipolaris maydis*), and Northern Corn Leaf Blight (*Exserohilum turcicum*). These pathogens disrupt photosynthetic processes and compromise overall plant health, often leading to considerable yield reductions (Pereira *et al.*, 2019; Sharma *et al.*, 2017).

Conventional approaches to disease diagnosis in the field, such as visual scouting by experts, are laborious, time-intensive, and subject to subjective error. Their effectiveness is further constrained in large-scale or resource-limited agricultural systems (Haug *et al.*, 2020). In recent years, advances in artificial intelligence (AI) and computer vision have paved the way for automated, image-based plant disease diagnostics. Among these, Convolutional Neural Networks (CNNs) have emerged as a particularly effective framework for high-accuracy classification tasks in agriculture (LeCun *et al.*, 2015; Goodfellow *et al.*, 2016).

CNNs can extract layered visual features directly from raw images, eliminating the need for manual feature engineering. Their capacity to capture subtle disease symptoms in complex agricultural scenes makes them well-suited for crop diagnostics (Krizhevsky *et al.*, 2012). However, CNN performance is highly sensitive to hyperparameter tuning and weight optimization, processes that are computationally demanding and prone to local minima.

To enhance training efficacy, bio-inspired optimization algorithms —such as Spider Monkey Optimization (SMO) and Squirrel Search Algorithm (SSA)— have been integrated into CNN frameworks. These algorithms replicate animal foraging behavior to more effectively navigate high-dimensional solution spaces, thereby improving convergence and predictive accuracy (Ali *et al.*, 2019; Mirjalili *et al.*, 2014).

This study presents a CNN architecture optimized with SMO and SSA to detect four major maize diseases. A dataset of 17,280 annotated images spanning multiple disease stages was employed. The central aim is to evaluate the efficacy of these optimization methods in enhancing CNN-based diagnostics and supporting the broader goals of precision agriculture.

MATERIALES Y METHODS

The method section of this study is based on Computer Vision, a field of AI that enables machines to interpret and understand visual data, similar to human vision. This technology automates tasks like image classification and object detection. In agriculture, it helps detect and classify crop diseases. This study uses a Computer Vision System to analyze maize leaf images and identify diseases. The system involves several steps: image acquisition with high-resolution cameras, preprocessing for noise reduction, feature extraction using CNNs, and classification to detect diseases. Post-processing refines the results, providing actionable recommendations, such as applying fungicides to prevent disease spread (Haug *et al.*, 2020).

Computer vision is a field within computer science and artificial intelligence that enables machines to interpret and analyze visual data, similar to how humans use their eyes and brain. Through specialized algorithms and models, computers can extract meaningful information from images and videos. This technology is widely applied in industries such as robotics, healthcare, and automotive systems, supporting tasks like image classification, object detection, and facial recognition (Szeliski, 2010).

Computer Vision System

A Computer Vision System (also referred to as an Artificial Vision System) is designed to replicate the human ability to perceive, interpret, and analyze visual data from the world, enabling machines to make decisions based on visual input. These systems are increasingly used for a wide range of tasks, from image classification to object detection and facial recognition (Szeliski, 2010). The components of a computer vision system typically include the following stages:

Image Acquisition

The first step in a computer vision system is the acquisition of visual data, typically through cameras or other imaging devices. The quality and type of devices used depend on the specific application. These devices can range from high-resolution digital cameras and infrared cameras to specialized sensors. The images captured in this stage serve as the raw data for subsequent processing and analysis (Gonzalez & Woods, 2008).

Preprocessing

Preprocessing prepares images for analysis by enhancing quality and consistency. It includes:

- Noise Reduction: Filters like Gaussian blur remove visual artifacts that may obscure key features (Jain, 1989).
- Normalization: Adjusts brightness and contrast to standardize images under varying lighting conditions.
- Resizing and Cropping: Focuses on the region of interest (ROI) and reduces computational cost.
- Data Augmentation: Expands the dataset using rotations, flips, scaling, and color adjustments to improve model robustness (Perez & Wang, 2017).

Building Model

Feature Extraction

Once the image is preprocessed, the next step is featuring extraction. In traditional computer vision, the system identifies relevant visual patterns. While traditional methods relied on manual selection of features (edges, textures, shapes), deep learning —particularly Convolutional Neural Networks (CNNs)— now automates this process. CNNs detect simple elements in early layers and learn more complex, disease-specific patterns in deeper layers (LeCun *et al.*, 2015).

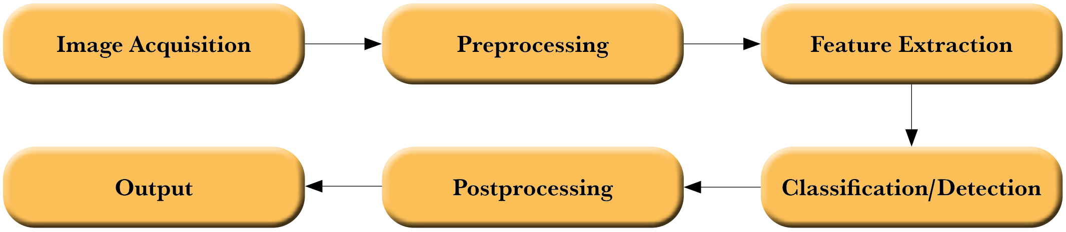

Figure 1. Diagram of Computer Vision System.

Optimization

Classification

After feature extraction, the system moves to the classification or detection phase, where the primary goal is to assign a label to the image or identify specific objects within it. Therefore, the system categorizes the image or identifies specific objects within it:

- Image Classification assigns a disease label to an image (*e.g.*, Common Rust or Gray Leaf Spot).
- Object Detection identifies and localizes diseased areas using bounding boxes.

Advanced systems apply semantic or instance segmentation, which classify pixels individually for more detailed analysis (He *et al.*, 2016; Long *et al.*, 2015).

Post-Processing

Post-processing refines model outputs by:

- Eliminating irrelevant or false detections.
- Smoothing segmentation boundaries to improve visual clarity and result accuracy (Ronneberger *et al.*, 2015).

These steps ensure the outputs are both precise and interpretable.

Output

The final stage generates actionable insights. In agriculture, this might include detecting Northern Corn Leaf Blight and recommending a fungicide. These outputs support real-time decision-making, helping farmers respond promptly and effectively to disease outbreaks (Haug *et al.*, 2020).

Metrics

Evaluating the performance of the computer vision system is critical to ensuring its accuracy in detecting and classifying maize diseases. To achieve this, several key evaluation metrics were employed, including accuracy, precision, recall, F1-score, and a confusion matrix. These metrics provide a comprehensive understanding of the model's classification performance.

Precision

The proportion of true positive predictions among all predicted positives, measuring the model's ability to avoid false positives.

$$Precision = \frac{True\ Positives}{True\ Positives + False\ Positives} \tag{1}$$

Recall

The proportion of true positive predictions among all actual positives, assessing the model's ability to detect all instances of a specific disease.

$$Precision = \frac{True\ Positives}{True\ Positives + False\ Negatives} \tag{2}$$

F1-Score

The harmonic mean of precision and recall, providing a balanced measure of the model's performance.

$$F1 - Score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \tag{3}$$

Proposal Method

Convolutional Neuronal Networks

Convolutional Neural Networks (CNNs) are a specialized class of deep learning models designed to process structured grid data, such as images. Widely used in visual recognition tasks, CNNs excel in image classification, object detection, and semantic segmentation due to their ability to automatically learn hierarchical features from image data (LeCun, Bengio, & Hinton, 2015). In agriculture, CNNs are particularly effective for automating disease identification in crops like maize. By analyzing high-resolution images of leaves, these models can detect and classify plant diseases with high accuracy. Unlike traditional methods that require manual feature engineering, CNNs learn directly from raw pixel data through multiple layers that extract and refine visual patterns (Goodfellow *et al.*, 2016).

CNNs consist of several key layers that perform specific functions:

Step 1. Convolutional Layer

The convolutional layer is the core component of a CNN. It applies filters (also called kernels) that slide across the image to detect local features like edges, textures, and shapes. Early layers capture basic visual elements, while deeper layers learn more complex patterns, including object parts and disease-specific markers.

Step 2. Activation Function

After each convolution operation, an activation function like ReLU (Rectified Linear Unit) introduces non-linearity, enabling the network to model complex patterns. ReLU is commonly used because it accelerates training and helps prevent the vanishing gradient problem (Nair & Hinton, 2010).

Step 3. Pooling Layer

Pooling layers follow convolutional layers and reduce the image's spatial dimensions, lowering computational cost and minimizing overfitting. The most common method, max pooling, selects the highest value in each region, preserving key information from the feature map.

Step 4. Fully Connected Layer

After several convolutional and pooling layers, the network typically flattens the feature maps into a one-dimensional vector. This vector is passed through one or more fully connected layers, where each neuron is connected to all the neurons in the previous layer. The fully connected layer allows the model to make the final classification based on the extracted features.

Step 5. Softmax Activation

The CNN's output layer commonly uses a softmax activation function for multi-class classification. It assigns probabilities to each class —such as Common Rust or Gray Leaf Spot— allowing the model to determine the most likely maize disease (Krizhevsky *et al.*, 2012).

Spider Monkey Optimization

Spider Monkey Optimization is a bio-inspired algorithm that simulates the cooperative foraging behavior of spider monkeys. As part of the swarm intelligence family, SMO effectively balances exploration (searching new areas) and exploitation (refining promising solutions), making it well-suited for solving complex optimization problems. In SMO, each monkey represents a potential solution, and the group collectively moves toward better options based on shared knowledge and individual experience. The algorithm follows main phases:

- Initialization: A population of spider monkeys is randomly generated.
- Fitness Evaluation: Each solution is assessed using an objective function.
- Position Update: Individuals adjust their positions relative to the leader.
- Leader-Follower Mechanism: Monkeys are guided by the best performer while maintaining exploratory behavior.
- Termination Condition: The process stops when a set number of iterations or a satisfactory solution is reached.

In Spider Monkey Optimization, each monkey's position $X_i = \left(x_{i1}, x_{i2}, \ldots, x_{in}\right)$ represents a potential solution within the search space, where n is the number of decision variables. The fitness function evaluates how well a given position solves the problem.

Monkeys adjust their positions based on the best-known solution X_{best}, using the update formula:

$$X_i^{new} = X_i + r \cdot \left(X_{best} - X_i\right) + \varepsilon \tag{4}$$

where: X_i is the current position of the i-th spider monkey. X_{best} is the position of the best solution found so far (the leader). r is a random factor between 0 and 1 that controls the extent to which the monkey moves towards the leader and explores new regions.

This leader-follower dynamic guides the population toward optimal regions while allowing for exploration. Followers move toward the leader but retain randomness in their search, helping the algorithm avoid local minima and discover better solutions over time (Ali *et al.*, 2019).

Optimization of CNN Parameters

In Convolutional Neural Networks, Spider Monkey Optimization is used to fine-tune both weights and hyperparameters. Each monkey's position represents a candidate parameter set, and its performance is evaluated through a loss function $L(W)$, typically categorical cross-entropy:

$$L(W)=\sum_{i=1}^{N} y_i \log\left(p_i\right) \tag{5}$$

where: N is the number of samples in the dataset. y_i is the true label of the i-th sample. p_i is the predicted probability for class y_i from the CNN output.

The fitness function $f(x)=L(W)$ determines how well each parameter set performs. SMO minimizes this loss by exploring the solution space, balancing exploration and exploitation to improve classification accuracy. Despite its computational demands, SMO is highly effective for optimizing CNNs in complex tasks like maize disease detection, making it a valuable tool for precision agriculture and other applied AI fields.

Squirrel Search Algorithm

The Squirrel Search Algorithm is a bio-inspired optimization technique based on the foraging behavior of squirrels. It has proven effective in solving complex problems in fields such as machine learning and artificial intelligence (Mirjalili *et al.*, 2014). In this study, SSA is applied to optimize the parameters of a Convolutional Neural Network for accurate classification of maize diseases, including common rust, gray leaf spot, asphalt spot, and leaf blight. SSA operates in two key phases: exploration, where squirrels search broadly for food (solutions), and exploitation, where they focus on the most promising regions. Each squirrel's position $X_i=\left(x_{i1},x_{i2},\ldots,x_{in}\right)$ represents a candidate solution in a $d-dimensional$ space. The position is updated:

$$x_i(t+1)=x_i(t)+\beta\left(X_{best}(t)-x_i(t)\right)+\alpha\cdot r(t) \tag{6}$$

where: $x_i(t)$ is the position of the squirrel at time t. $X_{best}(t)$ is the best position found by the squirrels up to time t. β is the step size toward the best solution. $\alpha\cdot r(t)$ is a random vector drawn from a uniform distribution between $[-1,1]$, which introduces stochasticity in the search process (Mirjalili *et al.*, 2014).

Integration of SSA with Convolutional Neural Networks

Integrating the Squirrel Search Algorithm with Convolutional Neural Networks aims to optimize both weights and hyperparameters to improve classification performance in maize disease detection.

In this approach, each squirrel's position represents a unique set of CNN hyperparameters —such as learning rate, number of layers, filter size, and batch size. SSA explores the search space to identify combinations that minimize classification error or maximize accuracy on a validation dataset.

By applying SSA, the CNN achieves improved accuracy in identifying diseases like common rust, gray leaf spot, asphalt spot, and leaf blight. This nature-inspired strategy enhances the CNN's ability to generalize and adapt, offering a valuable method for optimizing deep learning models in agricultural applications.

Maize

Maize (*Zea mays*) is one of the world's most important staple crops, providing essential nutrients and energy. However, its productivity is frequently threatened by foliar diseases such as Common Rust, Gray Leaf Spot, Asphalt Spot, and Northern Corn Leaf Blight, which reduce photosynthetic efficiency and crop yield if not managed promptly.

RESULTS AND DISCUSSION

The integration of computer vision systems in agriculture marks a crucial advancement in crop health monitoring. As global food demand grows and plant diseases become more prevalent, there is an urgent need for accurate, efficient, and scalable diagnostic tools. Traditional methods —based on manual inspection and expert judgment— are often slow, error-prone, and impractical for large-scale farming.

This study aimed to develop an AI-based system using Convolutional Neural Networks to automatically classify four major maize diseases: *Puccinia sorghi* (Common Rust), *Cochliobolus carbonum* (Gray Leaf Spot), *Bipolaris maydis* (Asphalt Spot), and *Exserohilum turcicum* (Northern Corn Leaf Blight). The following section details the development process of the computer vision model designed for disease detection.

Image acquisition (Data Collection)

The initial step in developing a computer vision system for maize disease detection involves assembling a comprehensive and diverse dataset of high-resolution maize leaf images. In this study, a total of 17,280 images were collected, with 4,320 images representing each of the four target diseases: *Puccinia sorghi* (Common Rust), *Cochliobolus carbonum* (Gray Leaf Spot), *Bipolaris maydis* (Asphalt Spot), and *Exserohilum turcicum* (Northern Corn Leaf Blight). Each disease was documented across six distinct stages of progression, ranging from early infection to advanced symptoms, enabling the model to learn variations in visual patterns over time.

Images were captured using a 12-megapixel wide-angle camera (f/1.6 aperture) equipped with optical image stabilization, ensuring sharp, high-fidelity captures under diverse field conditions. Photographs were taken under controlled lighting and from multiple leaf orientations to enhance the model's robustness and generalization capability. To ensure broad visual coverage, images were acquired from six different regions of the plant, capturing varied textures, angles, and symptom presentations. Additionally, the dataset was balanced to include both healthy and infected leaves, providing a solid foundation for training a Convolutional Neural Network (CNN) capable of accurate and scalable disease classification in maize.

Preprocessing

Following image collection, preprocessing is a critical step to prepare data for analysis by CNN. The objective is to standardize the data set, reduce noise, and introduce variability to enhance model robustness. In this study, a structured preprocessing pipeline was implemented, incorporating normalization, resizing, and data augmentation to ensure consistency and improve learning performance.

Normalization

To standardize the pixel intensity values, all images were normalized by scaling the values from their original range of 0-255 to a range of 0-1. The normalization was performed using the following formula:

$$Normalized = \frac{Pixel\,Value}{255} \tag{7}$$

Resizing

For consistency and compatibility with the CNN input requirements, All images were resized to 480×480 pixels to standardize dimensions and meet CNN input requirements while preserving visual detail.

Rotations

Images were rotated by 0°, 30°, 60°, 90°, 120°, 150°, 180°, 210°, 240°, 270°, 300° and 330°. This step increases the robustness of the model in recognizing disease patterns from different angles.

Zoom

Images were zoomed in (120%) and out (80%) to simulate distance variability between the camera and the leaf.

Random Cropping

Random subregions were extracted to vary disease positioning, improving model generalization.

Brightness and Contrast Adjustments

Brightness was scaled by 1.2 and 0.8 to reflect different lighting scenarios in the field.

Perspective Transformations

Slight corner distortions simulated camera angle changes, helping the model adapt to different viewpoints.

Flipping

Horizontal and vertical flips added variation in leaf orientation.

Noise Addition

Gaussian noise was introduced to mimic real-world imperfections, enhancing the model's resilience to noisy data.

Feature Extraction Using CNN (Building Model)

The core of the maize disease detection system is a Convolutional Neural Network (CNN), which automatically extracts hierarchical features from raw images. Unlike traditional models requiring manual feature engineering, CNNs learn complex spatial patterns critical for accurate classification.

The architecture consists of multiple layers, each contributing to the feature extraction process. Table 1 summarizes the structure of the network.

To ensure optimal accuracy and efficiency, several hyperparameters were fine-tuned during model development. These include filter size, which determines how much spatial information is captured, and stride, which controls how the kernel moves across the image. Kernel dimensions define the receptive field of each convolutional layer.

By carefully adjusting these hyperparameters based on validation performance, the CNN achieves a balance between classification accuracy and computational cost. This enables practical deployment of the model in real-world maize disease monitoring applications.

Model Training

Once the CNN architecture is established, the next step is training the model on the labeled dataset. The CNN is trained using supervised learning, where the model is provided

Table 1. CNN Architecture Layer by Layer Summary.

Layer	Output Dimensions
Input Layer	480×480×3
Conv2D+ReLU	480×480×16
Max Pooling	240×240×16
Conv2D+ReLU	240×240×32
Max Pooling	120×120×32
Conv2D+ReLU	120×120×64
Max Pooling	160×60×64
Flattening	230,400
Fully Connected Layer	4

with images labeled with the corresponding disease type (or "healthy" for non-diseased leaves). The model learns to map input images to their correct labels by minimizing the loss function during training.

Data Split

The dataset included 17,280 images evenly distributed across four maize diseases: *Puccinia sorghi*, *Cochliobolus carbonum*, *Bipolaris maydis*, and *Exserohilum turcicum*. To ensure reliable model performance, the data was divided into 80% for training (13,824 images) and 20% for validation (3,456 images).

The training set was used to optimize the CNN's weights, while the validation set provided an unbiased measure of generalization. This strategy helps the model learn disease features effectively while minimizing the risk of overfitting to the training data.

Loss Function

Given the multi-class nature of this classification problem, categorical cross-entropy was selected as the loss function. This function quantifies the discrepancy between the predicted probability distribution and the true label distribution, ensuring the model effectively learns to differentiate between classes. The mathematical definition is provided in Equation 4.

Optimizer

To enhance the performance of the CNN from the outset, three key optimization strategies were employed: Squirrel Search Algorithm and Spider Monkey Optimization.

Weight Initialization

Squirrel Search Algorithm draws inspiration from squirrel foraging behavior to efficiently explore the solution space. It initializes candidate weights and hyperparameters, refining them iteratively based on the categorical cross-entropy loss from the validation set. Spider Monkey Optimization simulates social foraging to fine-tune hyperparameters and weight configurations. By enhancing both global and local search, SMO helps the model converge toward an optimal setup for maize disease classification.

Hyperparameter Tuning

In addition to optimizing the weights, the SSA and SMO played crucial roles in tuning key hyperparameters of the CNN. These algorithms explored various configurations of:

- Learning Rate: The Squirrel Search Algorithm and Spider Monkey Optimization were essential in fine-tuning the learning rate, dynamically exploring configurations to balance convergence speed and training stability. During the optimization phase, learning rates were adjusted to prevent divergence and promote efficient loss minimization.
- Dropout Rate: To reduce overfitting, SSA and SMO were used to optimize the dropout rate, determining the proportion of neurons deactivated during training.

By evaluating various configurations in the fully connected layers, these algorithms improved the model's generalization through stochastic regularization, balancing overfitting prevention with learning capacity.

- Number of Filters: The SSA and SMO were used to fine-tune the number of filters in each convolutional layer, balancing feature extraction and computational efficiency. By dynamically adjusting filter counts, the algorithms tailored model complexity to the dataset, enhancing representation while reducing unnecessary processing.

The SSA and SMO achieve this by simulating the behavior of animals foraging for resources, enabling both exploration of diverse hyperparameter configurations and exploitation of promising solutions.

The performance of the proposed computer vision system for maize disease classification was evaluated across different training epochs, comparing two configurations: CNN's+SMO (Spider Monkey Optimization) and CNN's+SSA (Spider Subspace Algorithm). The results, as shown in Table 2, include training and validation loss functions and accuracy metrics.

Table 2 indicates that the CNN combined with Spider Monkey Optimization (SMO) consistently outperformed the CNN with Squirrel Search Algorithm (SSA) across all epochs, achieving higher accuracy and lower loss during both the training and validation phases. These results suggest that SMO significantly enhances the training and optimization of the CNN, rendering it more effective for the task of maize disease classification.

The metrics were computed for each class to assess the model's capability to handle imbalanced datasets, where certain diseases are underrepresented. Table 3 provides a comparison of the classification performance of two bio-inspired optimization algorithms, Spider Monkey Optimization and Squirrel Search Algorithm, implemented in a Convolutional Neural Network for maize disease classification. The evaluation focuses on four key metrics: Precision, Recall, F1-Score, and Accuracy, measured across different training epochs (10, 20, 30, and 40).

Table 2. Summary Results.

Training Epochs	Proposed	Loss Function		Accuracy	
		Training	Validation	Training	Validation
10	CNN's+SMO	1.2541	1.8752	0.8904	0.8754
	CNN's+SSA	1.4587	1.7691	0.8879	0.8014
20	CNN's+SMO	0.7587	0.9872	0.9106	0.9047
	CNN's+SSA	0.9458	1.0567	0.9054	0.8381
30	CNN's+SMO	0.5891	0.7655	0.9358	0.9213
	CNN's+SSA	0.7841	0.9871	0.9245	0.8712
40	CNN's+SMO	0.3248	0.4218	0.9758	0.9514
	CNN's+SSA	0.6241	0.7861	0.9442	0.8974

Table 3. Classification Metrics for CNN with SMO and SSA Across Epochs.

Epochs	Proposed	Precision	Recall	F1-Score	Accuracy
10	CNN's+SMO	0.80	0.79	0.79	0.8754
	CNN's+SSA	0.77	0.74	0.75	0.8014
20	CNN's+SMO	0.84	0.82	0.83	0.9047
	CNN's+SSA	0.79	0.77	0.78	0.8381
30	CNN's+SMO	0.88	0.87	0.87	0.9213
	CNN's+SSA	0.83	0.8	0.81	0.8712
40	CNN's+SMO	0.92	0.91	0.91	0.9514
	CNN's+SSA	0.88	0.85	0.86	0.8974

The comparison of performance between SMO and SSA highlights SMO's superior optimization capabilities across all metrics and epochs. As training progresses, both methods exhibit improvements, suggesting that the model benefits from extended training.

Epoch-Wise Comparison

Epoch 10:

SMO achieved a Precision of 0.80, Recall of 0.79, F1-Score of 0.79, and an Accuracy of 87.54%, outperforming SSA, which recorded a Precision of 0.77, Recall of 0.74, F1-Score of 0.75, and Accuracy of 80.14%. At this early stage, SMO demonstrates a clear advantage, with a 7.4% higher accuracy, indicating faster convergence and better initial learning.

Epoch 40:

SMO reached its best performance with a Precision of 0.92, Recall of 0.91, F1-Score of 0.91, and an Accuracy of 95.14%. In contrast, SSA achieved 0.88, 0.85, 0.86, and 89.74%. SMO's 5.4% higher accuracy, combined with better balance across all metrics, underscores its overall superiority in optimizing the CNN for maize disease classification.

The spider monkey optimization consistently demonstrates superior performance, particularly during extended training periods, likely due to its enhanced global and local search capabilities. Although less effective than SMO, the squirrel search algorithm produces competitive results in the early stages of training, suggesting its viability as an alternative when computational resources or time are limited. Both optimization methods exhibit steady improvements with increasing epochs, highlighting the critical importance of adequate training duration in achieving high classification accuracy. By epoch 40, SMO achieves near-perfect accuracy 95.14%, underscoring its suitability for real-world applications requiring high reliability and precision. In contrast, SSA reaches a peak accuracy of 89.74%, indicating that further fine-tuning or additional training epochs could potentially reduce the performance gap. For high-stakes scenarios, such as precision agriculture, where accuracy and dependability are crucial, SMO emerges as the preferred optimization technique. Nonetheless, SSA remains a valuable option in situations where computational efficiency is prioritized over incremental improvements in accuracy.

The results presented in Table 3 confirm the superiority of SMO in optimizing Convolutional Neural Networks for maize disease classification, particularly in achieving higher precision, recall, and F1-scores across all epochs. While slightly less effective, SSA remains a viable alternative for scenarios where faster convergence and computational efficiency are critical. Its potential for further improvement underscores the importance of continued research in this area.

The confusion matrix provides a detailed analysis of the model's classification performance across four maize disease categories: Asphalt Spot, Gray Leaf Spot, Common Rust, and Leaf Blight. Each cell represents the number of instances for a given true class (rows) versus the predicted class (columns). The diagonal values, representing true positives, reveal the model's high accuracy, with 411 correctly classified instances for Asphalt Spot, 406 for Gray Leaf Spot, 431 for Common Rust, and 415 for Leaf Blight. These results underscore the model's strong performance and reliability in maize disease classification. This high level of accuracy was achieved using a Convolutional Neural Network optimized with SMO and trained over 40 epochs, showcasing its effectiveness as a robust tool for precision agriculture applications. The corresponding confusion matrix is shown in Figure 2 below.

The off-diagonal values in the confusion matrix represent misclassifications, providing further insight into the model's performance across the four maize disease categories. For Asphalt Spot, 19 instances were misclassified as Common Rust, and 2 as Leaf Blight. Gray Leaf Spot was misclassified as Asphalt Spot in 8 cases, and 9 instances were misclassified as both Common Rust and Leaf Blight. Common Rust had 1 instance misclassified as Asphalt Spot, while Leaf Blight was misclassified as Asphalt Spot and Gray Leaf Spot in 9 and 3 cases, respectively. The most significant misclassification

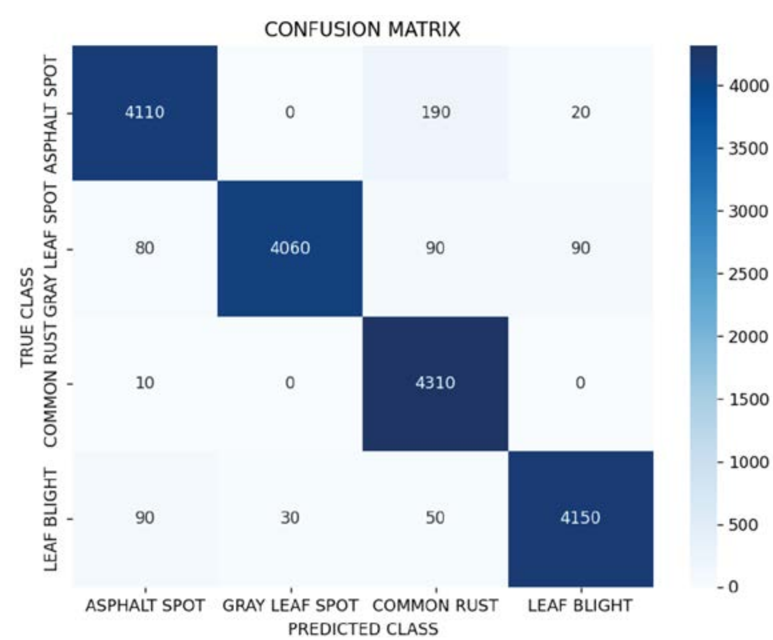

Figure 2. Confusion Matrix of CNN's+SMO for 40 Epochs.

occurred between Asphalt Spot and Common Rust (19 instances), suggesting potential feature overlap between these diseases. Despite these errors, the majority of predictions align with the diagonal, indicating high classification accuracy across all categories. Notably, symmetric misclassification was observed between Gray Leaf Spot and Leaf Blight (9 instances each), highlighting potential overlap in visual features such as texture or color. These findings, as illustrated in Figure 2, suggest areas for further improvement, such as refining feature extraction or incorporating additional data to better distinguish between similar disease patterns.

CONCLUSION

The implementation of convolutional neural networks for the automated identification of four major maize diseases —Common Rust, Gray Leaf Spot, Asphalt Spot, and Northern Corn Leaf Blight— demonstrated high classification accuracy and robustness. Using Spider Monkey Optimization to optimize the CNN, the model achieved a precision of 92%, a recall of 91%, and an F1-score of 91% after 40 training epochs, with an overall accuracy of 95.14%. These results highlight the advantages of integrating bio-inspired optimization algorithms with deep learning techniques, resulting in improved feature extraction and classification capabilities. The model's ability to minimize misclassifications, particularly between Asphalt Spot and Common Rust (19 cases), underscores its robustness in distinguishing visually similar categories. This optimized approach provides a well-supported and reliable framework for automating disease detection, enabling timely and accurate interventions in precision agriculture.

Furthermore, the study emphasizes the importance of balanced datasets and sufficient training epochs, which contributed to the model's solid performance and dependability. By automating the disease identification process, the proposed system can significantly reduce diagnostic time and enhance crop yield management, potentially saving farmers up to 30% in crop loss costs annually. Future research should focus on further refining the CNN architecture and exploring hybrid optimization techniques to address remaining misclassification challenges and improve the system's scalability for large-scale agricultural applications.

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