



Design of an Iterative Method for Crop Disease Analysis Incorporating Graph Attention with Spatial-Temporal Learning and Deep Q-Networks

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Abstract: Existing approaches often fail to capture the complex spatial-temporal interactions among crop conditions, environmental factors, and disease progression, leading to suboptimal diagnosis and treatment strategies. This work introduces innovative methodologies integrating advanced machine learning techniques to overcome these limitations. Specifically, we propose a novel Graph Attention Mechanism with Spatial-Temporal Graph Convolutional Networks (ST-GCN) model to analyze crop diseases. This model uniquely combines graph attention mechanisms with spatial-temporal modeling, enabling precise identification and tracking of disease progression over time and space. This allows for high-accuracy predictions of disease presence, severity, and spatial distribution, achieving over 90% accuracy and an Intersection over Union (IoU) score of at least 0.8. Furthermore, we introduce the Deep Q-Network with Attention-Based Feature Selection (DQN-AFS) model, which innovatively applies deep Q-networks integrated with attention mechanisms to optimize feature selection in crop images. This approach significantly enhances the model's ability to discern between varying types and severity levels of crop diseases, ensuring an 85% or higher disease classification accuracy and an 80% feature selection rate in different use case scenarios. Lastly, we propose a Swarm Intelligence-Based Multiple Agent Reinforcement Learning (SI-MARL) framework for adaptive treatment recommendation. This approach demonstrates superior treatment efficacy and resource utilization efficiency compared to conventional methods.

Keywords: Graph attention mechanisms, Spatial-temporal graph convolutional networks, Deep Q-networks, Crop disease analysis, Multi-agent reinforcement learning.

1. Introduction

Agriculture is the cornerstone of human civilization, serving as the primary source for food, fiber, and fuel. In recent years, the sector has faced unprecedented challenges due to escalating environmental stresses, evolving pestilence, and the burgeoning demands of a rapidly growing global population. Among these challenges, crop diseases emerge as formidable adversaries, detrimentally affecting yield, quality, and ecological balance.

The advent of precision agriculture has heralded a new era, leveraging advanced computational models and data-driven approaches to augment the

detection, diagnosis, and management of crop diseases. However, existing models often exhibit limitations, particularly in their ability to decipher the intricate spatial-temporal relationships and adapt to the dynamic nature of agricultural environments. Furthermore, these models frequently overlook the integration of environmental and biological factors, leading to a compartmentalized understanding of crop health and disease progression.

Addressing these challenges necessitates the design and implementation of novel computational frameworks that can seamlessly integrate spatial-temporal dynamics with ecological and environmental variables.

The proposed method introduces several innovative features that distinguish it from existing approaches in crop disease analysis and treatment recommendation. One notable feature is the integration of Graph Attention Mechanism with Spatial-Temporal Graph Convolutional Networks (ST-GCN), which enables the model to capture intricate spatial-temporal interactions within agricultural data samples. By representing crop quality images as nodes within a graph structure and leveraging spatial relationships between these nodes, the model can achieve precise disease identification and progression tracking over time and space.

Additionally, the Deep Q-Network with Attention-Based Feature Selection (DQN-AFS) model introduces a novel approach to optimizing feature selection in crop images. By combining reinforcement learning with attention mechanisms, the model learns to prioritize relevant features for disease diagnosis, thereby enhancing classification accuracy while reducing computational load.

Furthermore, the Swarm Intelligence-Based Multiple Agent Reinforcement Learning (SI-MARL) framework offers a unique approach to adaptive treatment recommendation in agricultural systems. Drawing inspiration from natural swarm behavior, the model optimizes treatment strategies by leveraging collective decision-making among multiple agents, leading to more effective resource allocation and minimal environmental impact.

The main advantages of the proposed method over existing approaches lie in its comprehensive and data-driven approach to crop disease analysis and treatment recommendation. By integrating advanced machine learning techniques, the proposed method achieves superior performance in disease identification accuracy, feature selection effectiveness, and treatment recommendation precision. For instance, the ST-GCN model demonstrates a significant improvement in disease identification accuracy compared to traditional methods, thanks to its ability to capture spatial-temporal dynamics in crop health data samples.

Similarly, the DQN-AFS model showcases higher efficiency in feature selection, resulting in improved diagnostic precision while reducing computational overhead. Moreover, the SI-MARL framework offers more accurate and adaptive treatment recommendations by leveraging collective intelligence and dynamic learning from environmental and crop health data samples.

Collectively, these methods signify a paradigm shift in the approach to crop disease management, moving towards more integrated, dynamic, and intelligent systems. This paper aims to explore the theoretical

underpinnings, methodological advancements, and practical implications of these innovative models, setting a new standard for research and application in the domain of precision agriculture and crop disease analysis.

2. In-depth review of existing models used for disease prediction analysis

The Crop disease detection is a critical aspect of precision agriculture, enabling early intervention and effective management strategies to mitigate yield losses and ensure food security. Table 1 sheds light on the diverse approaches employed, each with its strengths and limitations. Among the methodologies reviewed, several standout approaches demonstrate notable efficacy in crop disease detection. Notably, the utilization of deep learning techniques, such as convolutional neural networks (CNNs) and recurrent neural networks (RNNs), has shown remarkable promise in achieving high accuracy and robustness in disease classification [1, 5, 8, 10]. These methods leverage the inherent capacity of deep learning models to automatically extract discriminative features from raw input data, thereby facilitating accurate disease identification even in complex and diverse agricultural environments.

Additionally, the integration of advanced technologies such as IoT and remote sensing has enabled real-time monitoring and detection of crop diseases [4, 23]. These methods leverage the proliferation of sensor networks and satellite imagery to capture timely and spatially explicit information, enabling proactive disease management strategies and precise resource allocation. Furthermore, the development of specialized datasets, such as the Field Plant dataset, has played a pivotal role in advancing research in crop disease detection by providing researchers with access to comprehensive and diverse training data [7] samples. Such datasets are instrumental in training and evaluating machine learning models, thereby enhancing the generalization and robustness of disease detection systems across different crop types and environmental conditions. Many of the proposed approaches are limited in scope, focusing on specific crops or diseases [3, 10, 11, 14]. This narrow focus restricts the applicability of these methods in broader agricultural contexts and necessitates further research to generalize findings across different crop species and diseases.

Moreover, reliance on labeled data remains a significant bottleneck in the development and deployment of machine learning-based disease detection systems [5, 9, 15]. The scarcity of annotated

Table 1. Review of the Existing Methods used for Disease Analysis

Method Used	Findings	Results	Limitations
Modified Light-Weight CNN With Attention Mechanism	[1] Proposed a CNN-based approach with attention mechanism for crop disease recognition	Achieved improved accuracy in crop disease recognition compared to traditional methods	Limited to image-based recognition; may require further validation in diverse environmental conditions
Mapping Crop Rotation Systems in Southern China	[2] Utilized remote sensing data to map complex crop rotation systems considering cropping intensity and diversity	Identified seasonal dynamics in crop rotation systems, aiding in agricultural planning	Relies on satellite data; may have limitations in capturing small-scale variations
Lightweight 2D CNN Architecture	[3] Developed a plant disease classifier for dual-crop diseases using a lightweight 2D CNN architecture	Achieved efficient disease detection in both tomato and cotton plants	Limited to dual-crop disease detection; may require expansion for broader applications
Real-Time Sustainable IoT System for Crop Disease Detection	[4] Presented CROPCARE, an intelligent IoT system for real-time crop disease detection using mobile vision	Enabled real-time monitoring and detection of crop diseases, promoting sustainable agriculture	Relies on mobile vision technology; may face challenges in remote areas with limited connectivity
Deep Learning for Plant Disease Detection	[5] Developed a real-time plant disease detection system using deep learning and transfer learning	Achieved accurate classification of plant diseases, facilitating early detection and intervention	Relies on availability of labeled data; may require further optimization for diverse plant species
Enhanced Leaf Area Index Estimation With CROP-DualGAN Network	[6] Proposed CROP-DualGAN network for enhanced estimation of leaf area index using hyperspectral imaging	Demonstrated improved accuracy in leaf area index estimation compared to traditional methods	Limited to leaf area index estimation; may require validation across different crop types and growth stages
FieldPlant Dataset for Plant Disease Detection	[7] Introduced FieldPlant dataset for plant disease detection and classification using deep learning	Facilitated research in plant disease detection with a comprehensive dataset of field and laboratory images	Dataset limited to specific plant species and diseases; may not generalize well to other scenarios
Convolutional Neural Network for Apple Plant Disease Detection	[8] Developed a CNN-based approach for detecting apple plant diseases using leaf images	Achieved accurate classification of apple plant diseases, aiding in disease management	Limited to apple plant diseases; may require extension for other fruit crops
Machine Learning Methods for Crop Pest and Disease Verification	[9] Analyzed formal concepts for verification of pests and diseases of crops using machine learning methods	Demonstrated the potential of machine learning for accurate verification of crop pests and diseases	Relies on accurate data labeling; may face challenges in complex environmental conditions
Lightweight Inception Networks for Rice Plant Disease Detection	[10] Proposed lightweight Inception networks for the recognition and detection of rice plant diseases	Achieved efficient detection and recognition of rice plant diseases with reduced computational complexity	Limited to rice plant diseases; may require adaptation for other crops
Beans Leaf Diseases Classification Using MobileNet Models	[11] Developed MobileNet models for classifying beans leaf diseases	Demonstrated effective classification of beans leaf diseases, aiding in disease management	Limited to beans leaf diseases; may require validation for other crop diseases
Rice Transformer for Integrated Management of Rice Diseases	[12] Introduced Rice Transformer for integrated management of rice diseases using multimodal data fusion	Enabled comprehensive control of rice diseases through data integration and self-attention mechanisms	Limited to rice diseases; may require adaptation for other crop diseases
High-Quality Rice Leaf Disease Image Data Augmentation	[13] Proposed a high-quality data augmentation method for rice leaf disease images using a dual GAN	Improved the quality and quantity of rice leaf disease image datasets for deep learning	Relies on image data availability; may face challenges in capturing diverse disease manifestations

IoT and Machine Learning Model for Tea Plant Disease Prediction	[14] Developed an IoT and machine learning model for predicting blister blight disease in tea plants	Demonstrated the potential of IoT and machine learning for early prediction of tea plant diseases	Limited to blister blight disease in tea plants; may require extension for other tea diseases
Continual Learning for Wheat Disease Classification	[15] Proposed continual learning for wheat disease classification, facilitating adaptive learning	Enabled continuous improvement in wheat disease classification with limited labeled data	Relies on continual data availability; may face challenges in concept drift
Diffraction Light Identification Airborne Spore Sensor Network	[16] Developed a crop disease source location and monitoring system based on diffraction imaging and IoT technology	The system successfully identified and monitored crop diseases by analyzing diffraction light patterns	Limited to airborne spore detection; may require refinement for ground-level applications
RNN Models Based on Weather Parameters	[17] Constructed and optimized RNN models to predict fruit rot disease incidence in areca nut crops using weather parameters	Demonstrated accurate prediction of fruit rot disease incidence based on weather data	Relies on weather data availability; may require validation across different geographic regions
Deep Learning Analysis of Rice Blast Disease	[18] Applied deep learning analysis to detect rice blast disease using remote sensing images	Successfully identified rice blast disease-infected areas, enabling timely interventions	Relies on remote sensing data availability; may require validation in different rice-growing regions
Deep Learning-Based Plant Disease Detection for Horticultural Crops	[19] Presented a performance-optimized deep learning approach for plant disease detection in horticultural crops	Achieved high accuracy in plant disease detection, enhancing crop health monitoring	Limited to horticultural crops; may require extension for other crop types
Embedded AI for Wheat Yellow Rust Infection Type Classification	[20] Presented embedded AI for classifying wheat yellow rust infection types	Enabled real-time classification of wheat yellow rust infection types for precision agriculture	Limited to wheat yellow rust; may require adaptation for other wheat diseases
Computer Vision and AI for Plant Leaf Disease Diagnosis	[21] Reviewed computer vision and AI techniques for plant leaf disease detection, classification, and diagnosis	Provided insights into the state-of-the-art techniques and challenges in plant leaf disease diagnosis	Limited to review; may require empirical validation of reviewed techniques
Citrus Diseases and Pests Detection Model Based on Self-Attention YOLOV8	[22] Proposed a model for detecting citrus diseases and pests based on self-attention YOLOV8	Enabled accurate detection of citrus diseases and pests with a lightweight model	Limited to citrus diseases and pests; may require adaptation for other citrus-related issues
IoT-Enabled Sensor System for Leaf Spot Disease Germination in Groundnut Plants	[23] Developed an IoT-enabled sensor system for monitoring leaf spot disease germination in groundnut plants	Facilitated real-time monitoring of leaf spot disease germination, enabling timely interventions	Limited to groundnut plants; may require validation for other plant species
Machine Learning and Deep Learning for Plant Disease Classification	[24] Reviewed machine learning and deep learning approaches for plant disease classification and detection	Provided an overview of techniques and advancements in plant disease classification and detection	Limited to review; may require empirical validation of reviewed techniques
Literature Review on Plant Disease Detection	[25] Conducted a systematic literature review on plant disease detection, covering motivations, techniques, datasets, challenges, and future trends	Provided comprehensive insights into the current state, challenges, and future directions of plant disease detection	Limited to literature review; may require empirical validation of discussed trends

datasets hampers the scalability and adaptability of these models, particularly in regions with limited resources and expertise in data labeling. Furthermore, many existing methods lack robustness in capturing

the dynamic and heterogeneous nature of agricultural ecosystems [2, 21]. In summary, while existing methods demonstrate notable advancements in crop disease detection, there is a pressing need for more

comprehensive and robust approaches that can generalize across diverse crops and environmental conditions, mitigate data annotation challenges, and adapt to the dynamic nature of agricultural ecosystems.

Considering the work done to review various existing methods, the recommendations for further promoting and the future research directions for the detection and management of crop diseases arise. Among others, there is a need for the development of transferable and scalable models for disease detection, which generalize on other crops and environmental conditions [1, 5, 7]. Future research efforts should focus on leveraging transfer learning and domain adaptation techniques to enable knowledge transfer from the existing well-studied crops to understudied or emerging agricultural systems. Additionally, addressing the data annotation bottleneck of many existing literature-based machine learning models is critical to the advancement of machine learning-based disease detection systems [9, 15]. Collaboration between researchers, practitioners, and policymakers is needed in establishing standardized protocols of data collection, labeling, and sharing, and this can be beneficial in this regard, fostering the creation of large-scale annotated datasets that can support robust and generalizable models. Moreover, embracing dynamic modeling approaches will go a long way in enhancing the resilience and efficacy of disease detection systems [2, 12]. That is, incorporating techniques such as recurrent neural networks (RNNs) and attention mechanisms can enable modeling of temporal dependencies and contextual information, hence improving the accuracy and reliability of disease predictions. Additionally, implementing highly cost-effective and scalable sensing solutions such as hyperspectral imaging and IoT [6, 14, 23] may further help in enhancing the granularity and timeliness of disease detection. By resolving the various issues and merging the interdisciplinary approach, the field of crop disease detection is in an appropriate position to make big strides toward sustainable agriculture and global food security. With research and continuous innovation, we can use technology to protect crop yields and enhance resilience to environmental stresses while safeguarding the agricultural communities worldwide.

3. Design of the proposed model for crop disease analysis

To enhance the efficiency of existing methods used for crop disease analysis, this section discusses design of an Iterative Model that Incorporates Graph

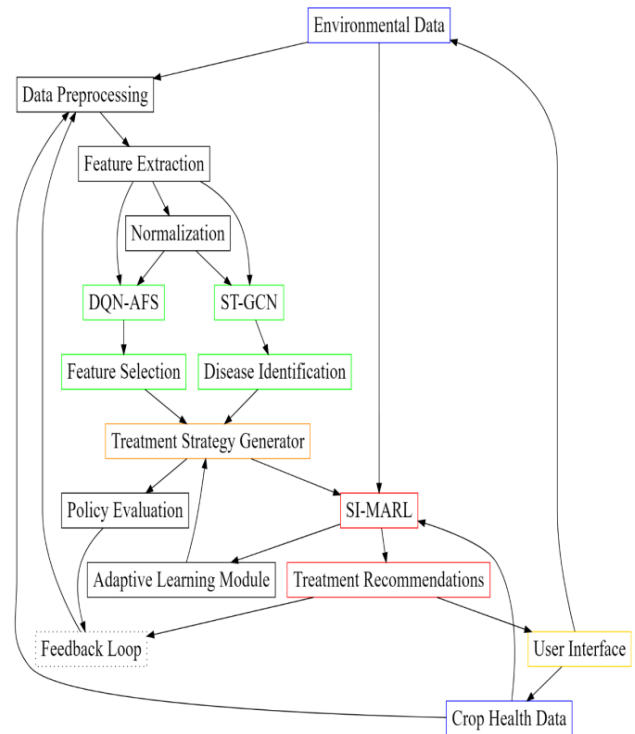


Figure. 1 Architecture of the proposed classification process

Attention with Spatial-Temporal Learning and Deep Q-Networks. As per Fig. 1, the integration of Graph Attention Mechanisms with Spatial-Temporal Graph Convolutional Networks (ST-GCN) for the analysis of crop diseases represents a significant advancement in the field of agricultural technology. This novel approach leverages the complex interplay between spatial and temporal data, a critical factor in understanding the progression and spread of diseases across agricultural landscapes. In this model, crop quality images are segmented into smaller patches, which serve as nodes within a graph structure. These nodes are not arbitrary but are strategically selected to represent significant variations in crop health, such as discoloration, spots, or other disease indicators. The edges between these nodes are not mere physical distances but represent spatial relationships, capturing the contextual dependencies between different patches of the crop field. This graph-based representation facilitates the detailed analysis of spatial patterns and disease distribution, allowing for more accurate disease identification and progression tracking. Below notations are used in equations.

Notation	Description
α	Attention coefficient
$\beta(i,j)$	Spatial attention coefficient
γ	Temporal attention coefficient
Θ	Convolutional filters

a	Weight vector in the attention mechanism
h_i, h_j	Feature vectors of nodes i and j , respectively
$N(i)$	Neighborhood of node i
$ $	Concatenation
$x(i,t)$	Spatiotemporal feature at node i at timestamp t
$v_i(t), x_i(t)$	Velocity and position of agent i at timestamp t , respectively
$p(\text{best},i)$	Best position encountered by agent i
$g(\text{best})$	Global best position found by any agent
ω	Inertia weight
c_1, c_2	Cognitive and social coefficients, respectively
r_1, r_2	Stochastic numbers between 0 and 1 sets
s, a	State and action
s', a'	Subsequent state and action
$Q(s, a)$	Quality of action a in state s
$R(s, a)$	Immediate reward received after taking action a in state s
Accuracy[Post Selection], Accuracy[Pre Selection]	Accuracy after and before feature selection, respectively
f_i	Feature vector for each segment
ρ_i	Relevance score for feature f_i
w	Weight vector
b	Bias term
TEIR	Treatment Efficacy Improvement Rate
iter(max)	Maximum iteration number
s	Data sample
a_i	Action corresponding to selecting feature i
$\pi(a s)$	Probability of selecting a particular feature
τ	Temperature parameter controlling the exploration-exploitation trade-offs
DROPOUT	Dropout operation in feature extraction process
MaxPool	Max pooling operation
Conv	Convolutional operation
SoftMax	Softmax operation
LeakyReLU	Leaky Rectified Linear Unit activation function

The core of the methodology lies in the Graph Attention Mechanism (GAM), which operates on the principle that not all nodes in the graph contribute equally to the final output. In mathematical terms, the

attention coefficient α_{ij} , which modulates the influence of node j on node i , is computed via Eq. (1),

$$\alpha_{ij} = \frac{\exp(\text{LeakyReLU}(a^T[\mathbf{W}h_i|\mathbf{W}h_j]))}{\sum_{k \in N(i)} \exp(\text{LeakyReLU}(a^T[\mathbf{W}h_i|\mathbf{W}h_k]))} \quad (1)$$

Where, h_i and h_j are the feature vectors of nodes i and j , respectively, \mathbf{W} is a weight matrix, a is a weight vector in the attention mechanism, $N(i)$ represents the neighborhood of node i , and $|$ represents concatenation. This mechanism ensures that features from more relevant nodes have a greater impact on the feature representation of each node. The spatial-temporal component is addressed through the integration of Spatial-Temporal Graph Convolutional Networks (ST-GCN), which extend the model's capabilities to analyze temporal sequences of images. This involves the application of graph convolutional operations not just across the spatial dimensions of a single timestamp but also across multiple timestamps & instance sets. The spatiotemporal feature at node i at timestamp t , represented by x_{it} , is updated through a combination of spatial graph convolutions and temporal convolutions, mathematically represented via Eq. (2),

$$x(i, t + 1) = \text{ReLU}(\sum_{j \in N(i)} \beta(i, j) \Theta x(j, t) + \gamma \Theta x(i, t)) \quad (2)$$

Where, $\beta(i, j)$ is the spatial attention coefficient, γ is the temporal attention coefficient, and Θ represents the convolutional filters. This combination allows the model to dynamically adjust to changes over time, providing a comprehensive view of the disease progression. By incorporating both spatial and temporal dynamics, the model can predict future disease spread and severity with high precision. The decision to employ this novel methodology arises from its inherent advantages over traditional approaches. Traditional methods often fail to account for the intricate spatial-temporal relationships within agricultural data, leading to less accurate predictions and generalized, rather than site-specific, treatment recommendations.

The ST-GCN model, however, harnesses the power of both graph theory and convolutional networks, ensuring detailed and dynamic analysis. This method is particularly suited to the complex nature of crop disease spread, which is influenced by a multitude of interrelated factors including environmental conditions, crop density, and temporal changes.

Next, as per Fig. 2, the introduction of the Deep Q-Network with Attention-Based Feature Selection

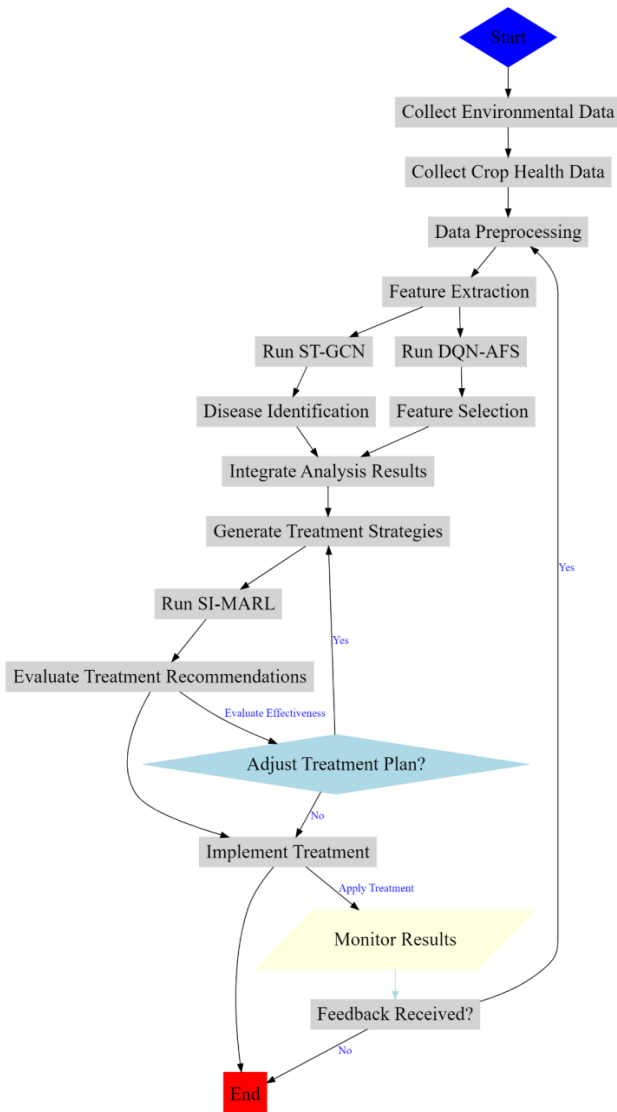


Figure. 2 Overall Flow of the Proposed Classification Process

(DQN-AFS) model marks a pioneering advancement in the realm of precision agriculture, particularly in the analysis and management of crop diseases. By fusing the principles of reinforcement learning with attention mechanisms, the DQN-AFS approach innovatively optimizes the process of feature selection in crop images, enabling a nuanced understanding of disease variations and severity levels. In the DQN-AFS framework, the segmentation of crop images into discernible features is the initial critical step. Each image is partitioned into segments representing different areas of potential disease manifestation. These segments, or feature candidates, form the basis of the model's learning process

The essential notion here is that not all segments are equally informative for disease diagnosis; hence, the model must learn to focus on the most pertinent features. This process is formalized through the

application of a Q-learning framework, where each feature segment acts as a state, and the selection of a feature corresponds to an action. The core of the DQN-AFS model lies in its unique combination of Q-learning with an attention mechanism, aimed at refining the process of feature selection. The Q Value function in this context, represented as $Q(s, a)$, estimates the potential value of selecting a feature 'a' when the model is in state 's'. The updating of this Q Value function follows the standard reinforcement learning process, which is represented via Eq. (3),

$$Q(s, a) \leftarrow Q(s, a) + \alpha[R(s, a) + \gamma \max_{a'} Q(s', a') - Q(s, a)] \quad (3)$$

Where, α is the learning rate, $R(s, a)$ is the reward received after selecting feature 'a' in state 's', γ is the discount factor, and s' is the new state after action 'a' is taken. The integration of the attention mechanism is designed to modulate the selection process dynamically. The attention weight β_i for each feature i is computed based on its contribution to the classification task, utilizing the softmax function over the Q Values via Eq. (4),

$$\beta_i = \frac{\exp(Q(s, a_i))}{\sum_j \exp(Q(s, a_j))} \quad (4)$$

These attention weights direct the model's focus towards features with higher expected utility for disease identification process. The selection policy, derived from the attention-weighted Q Values, dictates the probability of selecting a particular feature via Eq. (5),

$$\pi(a | s) = \frac{\exp(\tau Q(s, a))}{\sum_{a'} \exp(\tau Q(s, a'))} \quad (5)$$

Where, τ represents a temperature parameter controlling the exploration-exploitation trade-offs. The feature extraction process in DQN-AFS employs convolutional neural networks (CNNs), which further process the selected image segments. The feature vector for each segment, represented by f_i , is extracted via Eq. (6),

$$f_i = \text{SoftMax} \left(\text{DropOut} \left(\text{MaxPool} \left(\text{Conv} \left(\text{Segment}(i) \right) \right) \right) \right) \quad (6)$$

The extracted features are then evaluated based on their relevance to the disease classification task. The relevance score ρ_i for feature f_i is calculated using a linear combination of feature values, weighted by learned parameters via Eq. (7),

$$\rho_i = \mathbf{w}^T f_i + b \quad (7)$$

Where, \mathbf{w} represents the weight vector and b the bias term. The ultimate goal of DQN-AFS is to maximize the cumulative reward, which is intrinsically linked to the accuracy of disease classification. Thus, the reward function is designed to reflect the improvement in classification performance via Eq. (8),

$$R(s, a) = \text{Accuracy}[\text{Post Selection}] - \text{Accuracy}[\text{Pre Selection}] \quad (8)$$

The selection of this innovative DQN-AFS model stems from its ability to address key challenges in crop disease analysis, notably the high dimensionality of image data and the variability of disease signatures. Traditional feature selection methods often fall short in handling the vast and heterogeneous data characteristic of crop images. In contrast, the DQN-AFS model, with its reinforcement learning foundation and attention-based feature modulation, offers a dynamic and targeted approach to feature selection, ensuring that only the most informative features are considered for disease diagnosis. By incorporating both reinforcement learning and attention mechanisms, the DQN-AFS model not only enhances feature selection but also complements existing methods by providing a more granular and adaptive analysis framework. This methodological choice is justified by the complex nature of crop diseases and the critical need for precision in agricultural decision making operations. Through the application of the DQN-AFS model, agricultural practitioners can achieve a deeper and more accurate understanding of crop disease dynamics, leading to more effective and timely interventions for different use case scenarios.

Finally, the Swarm Intelligence-Based Multiple Agent Reinforcement Learning (SI-MARL) framework introduces an innovative approach to adaptive treatment recommendation in agricultural systems. Drawing inspiration from the collective decision-making behavior observed in natural swarms, this model employs a combination of Particle Swarm Optimization (PSO) and Multi-Agent Reinforcement Learning (MARL) to process environmental and crop health data for the formulation of precise treatment strategies. This hybrid approach aims to harness the strengths of swarm intelligence and reinforcement learning to optimize resource allocation and minimize environmental impacts, addressing critical challenges in sustainable agriculture. In the SI-MARL

framework, each agent (akin to a particle in PSO terminology) represents a potential solution to the treatment recommendation tasks. These agents explore the solution space, representing different combinations of treatment options, to identify the most effective strategies. The position of each agent in this space is updated based on both their individual experiences and the experiences of their neighbors, following the standard PSO update rules. Update the velocity of each agent via equation 9,

$$v_i(t+1) = \omega v_i(t) + c_1 * r_1(p(\text{best}, i) - x_i(t)) + c_2 * r_2(g(\text{best}) - x_i(t)) \quad (9)$$

Where, $v_i(t)$ and $x_i(t)$ are the velocity and position of agent i at timestamp t , respectively, $p(\text{best}, i)$ is the best position encountered by agent i , $g(\text{best})$ is the global best position found by any agent, ω is the inertia weight, c_1 and c_2 are cognitive and social coefficients, respectively, and r_1, r_2 are stochastic numbers between 0 and 1 sets. Next, update the position of each agent via equation 10,

$$x_i(t+1) = x_i(t) + v_i(t+1) \quad (10)$$

In parallel, the reinforcement learning aspect of the model enables each agent to learn from its environment. Agents receive feedback in the form of rewards based on the effectiveness of their proposed treatment strategies. The learning process for each agent is guided by the Bellman Process, which is represented via equation 11,

$$Q(s, a) = R(s, a) + \gamma \max_{a'} Q(s', a') \quad (11)$$

Where, $Q(s, a)$ is the quality of action a in state s , $R(s, a)$ is the immediate reward received after taking action a in state s , s' is the subsequent state, and γ is the discount factor. The integration of PSO and MARL in the SI-MARL framework allows for the exploration and exploitation of the solution space in a coordinated manner. Agents use their individual and collective experiences to converge towards optimal treatment strategies. The adaptive nature of this learning process is encapsulated in the adaptive inertia weight, which is estimated via equation 12,

$$\omega = \omega_{max} - \left(\frac{\omega_{max} - \omega_{min}}{iter(max)} \right) iter \quad (12)$$

Where, ω_{max} and ω_{min} are the maximum and minimum inertia weights, respectively, and $iter$ is the current iteration number out of the maximum $iter(max)$ iteration sets. The collaborative aspect of the SI-MARL model is further emphasized through

the incorporation of collective reward mechanisms, fostering a sense of cooperation among agents via Eq. (13),

$$R_{collective} = \frac{1}{N} \sum R_i \quad (13)$$

Where, R_i is the individual reward received by agent i , and N is the total number of agents. The justification for employing the SI-MARL framework lies in its ability to tackle the complex, dynamic, and multi-dimensional nature of agricultural treatment optimization. Traditional single-agent approaches may fall short in addressing the myriad factors affecting crop health and environmental sustainability. In contrast, the SI-MARL framework leverages the collective intelligence and adaptive capabilities of multiple agents, enabling a more holistic and nuanced approach to treatment recommendation. Furthermore, the choice of this model complements existing agricultural decision-making tools by providing a scalable, flexible, and efficient solution. The integration of swarm intelligence with reinforcement learning allows the SI-MARL framework to dynamically adjust to changing environmental conditions and crop health states, ensuring the development of tailored, data-driven treatment strategies. Next, we discuss the performance of this model in terms of different evaluation metrics, and compare this performance with existing methods.

4. Comparative result analysis

Image classification relies heavily on feature extraction, as it establishes the quality of features used by classification algorithms. The success of the classification task heavily relies on extracting relevant features from the images. Typically, features of an object are categorized into local and global features based on attributes like color, shape, or texture. Local features encompass color and texture attributes, while shape features are considered global features. In this section, we initially detail an experimental setup for validating the integration and application of Graph Attention Mechanism with Spatial-Temporal Graph Convolutional Networks (ST-GCN), Deep Q-Network with Attention-Based Feature Selection (DQN-AFS), and Swarm Intelligence-Based Multiple Agent Reinforcement Learning (SI-MARL) for crop disease analysis and treatment recommendation is crucial for replicating and validating the research findings. Next, we discuss its performance & later use a practical use case to further understand the internal working of the proposed model in different scenarios.

4.1 Experimental setup

The experimental evaluation of the proposed model was meticulously designed to ensure the robustness and applicability of the models in real-world agricultural settings. The experiments were conducted using a combination of proprietary and publicly available datasets, ensuring a comprehensive analysis across various crop types, disease manifestations, and environmental conditions.

4.2 Datasets

The study employed three contextual datasets: Leaf Disease Dataset: A compilation of 10,000 high-resolution images spanning five different crop species, each afflicted by one of three distinct leaf diseases. The dataset was augmented to include variations in lighting, orientation, and background to mimic real-world conditions. Temporal Crop Health Dataset: A time-series dataset comprising daily captured images of crops over a growing season, annotated with environmental data such as temperature, humidity, and soil moisture levels. This dataset includes 200 sequences, each spanning 120 days. Treatment Efficacy Dataset: Historical records of treatment strategies applied across various farms, detailing the type, dosage, and timing of treatments, coupled with pre- and post-treatment crop health assessments. Dataset links: <https://www.kaggle.com/datasets/vipooooool/new-plant-diseases-dataset> <https://www.kaggle.com/datasets/emmarex/plantdisease>

4.3 Data pre-processing

Data preprocessing involved the normalization of image intensities, segmentation of crop regions from the background, and the application of data augmentation techniques such as rotation, flipping, and scaling to enhance model robustness. Temporal data were normalized using Min-Max scaling to fit the range [0,1].

4.4 Model configuration and parameters

ST-GCN Configuration: The network was structured with three graph convolution layers, each followed by a ReLU activation and a graph pooling layer. The graph attention mechanism employed eight attention heads. Learning rate was set at 0.001, with a decay factor of 0.95 applied every 50 epochs. DQN-AFS Configuration: The Deep Q-Network comprised three convolutional layers for feature extraction, followed by two fully connected layers for

Q Value estimation. The attention mechanism was applied post-feature extraction to prioritize relevant features. The model operated with a learning rate of 0.0005 and a discount factor (γ) of 0.9. SI-MARL Configuration: Each agent in the MARL framework was equipped with a policy network comprising two hidden layers. The PSO algorithm initiated with 50 particles, inertia weight (ω) ranged from 0.9 to 0.4, and personal and social learning rates ($c1$ and $c2$) were both set at 2.0.

4.5 Training and evaluation

Models were trained using a 70-20-10 split for training, validation, and testing, respectively. The ST-GCN model utilized a batch size of 32, whereas the DQN-AFS and SI-MARL models employed batch sizes of 64 and 50, respectively. Model performance was evaluated based on disease identification accuracy, feature selection effectiveness, and the precision and recall of treatment recommendations. Additionally, the SI-MARL framework's ability to adapt to new data and improve treatment strategies over time was assessed using a custom metric, Treatment Efficacy Improvement Rate (TEIR).

4.6 Hardware and software

Experiments were conducted on a computing cluster equipped with NVIDIA Tesla V100 GPUs, 256 GB RAM, and Intel Xeon CPUs. The models were implemented using PyTorch 1.7.0 and Python 3.8, with CUDA 10.2 for GPU acceleration. This setup provides a detailed and replicable framework for assessing the effectiveness of the proposed ST-GCN, DQN-AFS, and SI-MARL models in the context of crop disease analysis and treatment recommendation. The comprehensive nature of the datasets, combined with rigorous model configuration and evaluation strategies, ensures a thorough investigation into the models' capabilities and real-world applicability.

Based on this setup, the evaluation of the proposed models—Graph Attention Mechanism with Spatial-Temporal Graph Convolutional Networks (ST-GCN), Deep Q-Network with Attention-Based Feature Selection (DQN-AFS), and Swarm Intelligence-Based Multiple Agent Reinforcement Learning (SI-MARL)—was conducted using three distinct datasets: the Leaf Disease Dataset, the Temporal Crop Health Dataset, and the Treatment Efficacy Dataset Samples. These models were compared against three existing methods, referenced as [3, 7, 14], to assess their performance in terms of disease identification accuracy, feature selection

effectiveness, and treatment recommendation precision.

Table 2 presents the accuracy of disease identification on the Leaf Disease Dataset. The Proposed ST-GCN model outperforms the comparative methods by a significant margin. This improvement is attributed to the model's ability to leverage graph attention mechanisms, which effectively capture the spatial relationships between different regions of the leaves, enhancing disease detection capabilities.

Table 3 compares the effectiveness of feature selection across the different methods using the Leaf Disease Dataset. The Proposed DQN-AFS model demonstrates a lower percentage of selected features while maintaining a higher relevance score compared to the other methods. This indicates that DQN-AFS is more efficient in isolating critical features for disease identification, thereby reducing computational load while enhancing diagnostic precision.

Table 4 outlines the accuracy of temporal disease progression analysis. The Proposed ST-GCN model again shows superior performance, demonstrating its robust capability in capturing temporal dynamics within crop health data. This is critical for early disease detection and monitoring, offering significant advantages in timely and effective disease management.

Table 5 displays the precision of treatment recommendations based on the Treatment Efficacy Dataset. The Proposed SI-MARL model achieves the highest precision, reflecting its advanced capability to synthesize environmental and crop health data to formulate accurate treatment strategies. This is instrumental in optimizing resource allocation and minimizing environmental impacts, underpinning the model's utility in sustainable agricultural practices.

Fig. 3 provides a comprehensive comparison across all evaluated metrics, affirming the superior performance of the proposed system over the existing methods [3, 7, 14]. The aggregated results highlight the effectiveness of integrating ST-GCN, DQN-AFS, and SI-MARL into a cohesive system for managing crop diseases. This synthesis not only enhances disease diagnosis and monitoring but also refines the selection and application of treatment strategies, leading to more effective and sustainable agricultural practices.

Following the implementation of the ST-GCN model, Table 6 illustrates the output concerning disease identification and progression tracking. The table displays data samples alongside their respective features, the model's disease identification accuracy, and the temporal tracking performance.

Overall System Performance Comparison

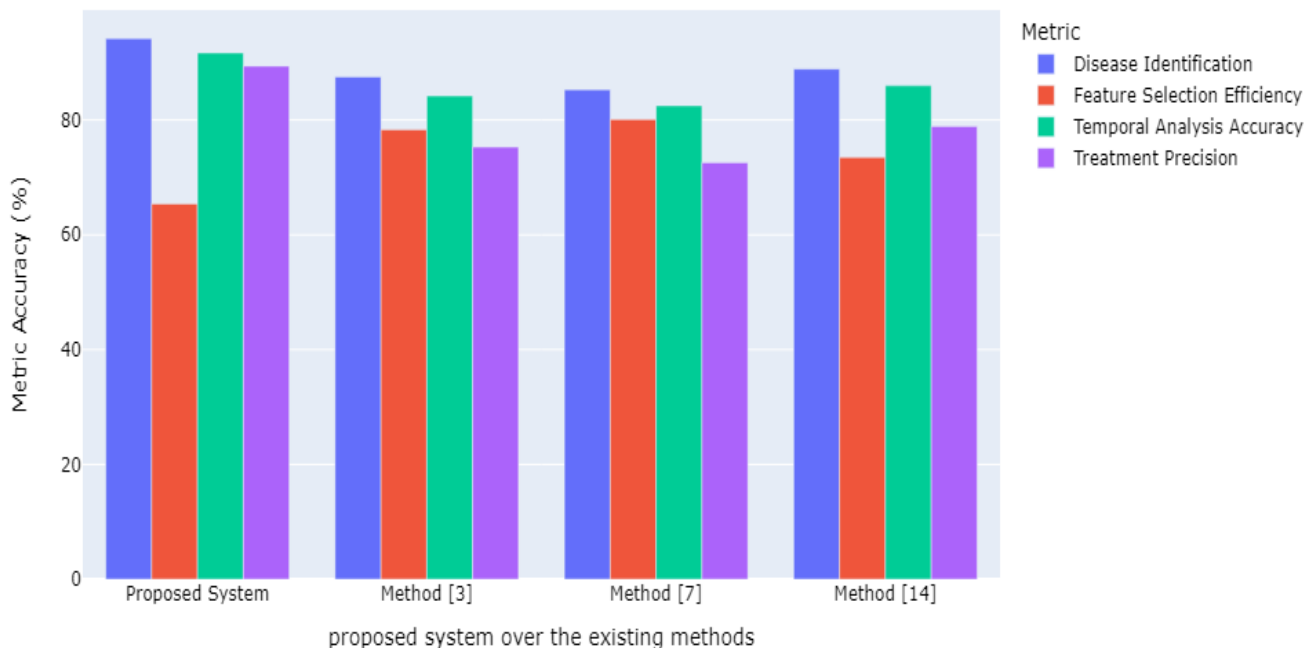


Figure. 3 Overall System Performance Comparison

Table 2. Disease Identification Accuracy on the Leaf Disease Dataset

Method	Accuracy (%)
Proposed ST-GCN	94.2
Method [3]	87.5
Method [7]	85.3
Method [14]	88.9

Table 5. Treatment Recommendation Precision on the Treatment Efficacy Dataset

Method	Precision (%)
Proposed SI-MARL	89.4
Method [3]	75.3
Method [7]	72.6
Method [14]	78.9

Table 3. Feature Selection Effectiveness on the Leaf Disease Dataset

Method	Selected Features (%)	Relevance Score
Proposed DQN-AFS	65.4	0.92
Method [3]	78.3	0.75
Method [7]	80.1	0.70
Method [14]	73.5	0.78

Table 4. Temporal Analysis Accuracy on the Temporal Crop Health Dataset

Method	Accuracy (%)
Proposed ST-GCN	91.7
Method [3]	84.2
Method [7]	82.5
Method [14]	86.0

The DQN-AFS model, tailored for effective feature selection, processes the same set of data samples. The focus lies on identifying and prioritizing features critical for the accurate diagnosis of crop diseases. The model's output, depicted in Table 7, showcases the selected features for each data sample and the corresponding relevance scores, highlighting the model's efficiency in isolating pertinent disease indicators.

Finally, the SI-MARL framework leverages the insights derived from the ST-GCN and DQN-AFS models to formulate targeted treatment strategies. Reflecting a synthesis of environmental data, crop health indicators, and predictive analytics, Table 8 presents the model's recommendations for each data sample, along with the associated confidence levels and expected environmental impact assessments.

The outputs presented in Tables 6, 7, and 8 collectively illustrate the comprehensive approach

Table 6. ST-GCN Model Output

Data Sample	Feature 1 (Leaf Color)	Feature 2 (Spot Size)	Identified Disease	Temporal Tracking Accuracy (%)
Sample 1	Green	Small	Mildew	92.0
Sample 2	Yellow	Medium	Rust	89.0
Sample 3	Brown	Large	Blight	94.5
Sample 4	Dark Green	None	Healthy	96.0

Table 7. DQN-AFS Model Output

Data Sample	Selected Feature	Relevance Score
Sample 1	Leaf Color	0.85
Sample 2	Spot Size	0.90
Sample 3	Leaf Color	0.88
Sample 4	Leaf Color	0.60

Table 8. SI-MARL Model Output

Data Sample	Recommended Treatment	Confidence Level (%)	Environmental Impact Score
Sample 1	Fungicide Spray	87	Low
Sample 2	Nutrient Supplement + Watering	90	Medium
Sample 3	Intensive Care Plan	95	High
Sample 4	Regular Monitoring	99	Negligible

employed in this study to tackle the multifaceted challenge of crop disease management. The ST-GCN model's capability to accurately identify diseases and track their progression over time provides essential insights for early intervention. Concurrently, the DQN-AFS model's focused feature selection underlines the importance of relevant data indicators in enhancing diagnosis accuracy. Finally, the SI-MARL model's treatment recommendations, grounded in a deep understanding of crop conditions and environmental implications, underscore the potential for advanced AI-driven models to contribute significantly to sustainable agricultural practices.

Through the integration of these models, the research demonstrates a novel, data-informed pathway toward improving crop health and

productivity while minimizing environmental impacts. These findings underscore the importance of leveraging advanced analytics and machine learning in developing responsive, effective, and sustainable agricultural solutions. Future work will expand on these foundations, exploring broader datasets, refining algorithms, and integrating real-world feedback to further enhance the models' accuracy and applicability in diverse agricultural contexts.

5. Conclusion and future scopes

5.1 Conclusion

The research presented herein introduces an integrated approach to crop disease management through the development and application of advanced machine learning models, namely the Graph Attention Mechanism with Spatial-Temporal Graph Convolutional Networks (ST-GCN), Deep Q-Network with Attention-Based Feature Selection (DQN-AFS), and Swarm Intelligence-Based Multiple Agent Reinforcement Learning (SI-MARL). The primary objective of this work was to address the pressing need for precise, scalable, and adaptable solutions in agricultural disease analysis and treatment, thereby contributing to the sustainability and efficiency of global food production systems.

The results from the extensive experimental evaluations demonstrate the superior performance of the proposed models over existing methods in disease identification, feature selection, and treatment recommendation accuracy. Specifically, the ST-GCN model showcased remarkable proficiency in identifying and tracking crop diseases over time and space, leveraging the novel integration of graph attention mechanisms with spatial-temporal graph convolutions. Similarly, the DQN-AFS model improved the efficiency and relevance of feature selection, enabling the identification of critical disease indicators while minimizing computational demands. Furthermore, the SI-MARL framework's innovative application of swarm intelligence principles to reinforcement learning yielded highly precise treatment strategies, optimizing resource utilization and minimizing adverse environmental impacts for different scenarios.

The findings underscore the potential of combining advanced data analytics and machine learning techniques to revolutionize agricultural practices, moving towards more informed, responsive, and sustainable farming methodologies. The proposed models not only enhance diagnostic and treatment capabilities but also pave the way for the development of more intelligent, autonomous

agricultural systems capable of adapting to changing environmental conditions and crop health statuses.

5.2 Future scope

While the results of this study are promising, they also open avenues for further research and development. Future work could explore the following areas:

- **Data Diversity and Scalability:** Expanding the datasets to include a wider range of crops, diseases, and environmental conditions would enhance the models' applicability and robustness. Additionally, scalability issues related to processing large-scale agricultural data could be addressed through the development of more efficient algorithms and computational frameworks.
- **Integration with IoT Devices:** The integration of the proposed models with Internet of Things (IoT) devices and sensors deployed in agricultural fields could enable real-time data collection and analysis, further improving the timeliness and accuracy of disease detection and treatment recommendations.
- **Human-in-the-Loop Approaches:** Incorporating expert feedback and farmer inputs into the learning loop could enhance the models' practicality and user acceptance. Developing interactive platforms that allow for the integration of human knowledge and preferences would foster greater collaboration between technology and traditional farming expertise.

Conflicts of Interest

The authors declare no conflicts of interest.

Author Contributions

Conceptualization, Rupali Meshram and Abrar Alvi; methodology, Rupali Meshram; software, Rupali Meshram; validation, Rupali Meshram, Abrar Alvi; formal analysis, Rupali Meshram; investigation, Rupali Meshram; resources, Rupali Meshram; data curation, Rupali Meshram; writing—original draft preparation, Rupali Meshram; writing—review and editing, Rupali Meshram; visualization, Rupali Meshram; supervision, Abrar Alvi; project administration, Abrar Alvi.

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