

A Comprehensive Review of Complex Network Methods for Cotton Plant Disease Detection

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ABSTRACT

In recent years, researchers have become increasingly interested in cotton, a precious cash crop everywhere from Pakistan to China to Texas, is crucial for the textile industry and agricultural economies around the world. But its production is continuously threatened by a diversity of plant diseases, which can be triggered by pathogens such as bacteria, fungi and viruses. The conventional diagnostic approaches to confirm these diseases are generally not sensitive, time-consuming, and at the same time laborious. In recent times, network biology approaches have emerged as a robust platform in predicting disease associations and simulating diseases interplay in plants. The purpose of this paper is to investigate the application of complex network theory in cotton plant disease detection and control, particularly for the integration with machine learning and artificial intelligence. However, as many techniques are promising, only a few real-time interpretable field deployable models exist up to now to be used in local agricultural systems, especially in developing countries such as Pakistan. From this perspective, I propose that lightweight hybrid models should be developed which integrating network theory with spatiotemporal environment data, and open-access database would get higher availability. I believe there is a big opportunity in having a mobile-based decision support system, which is based on the graph learning model and can be used by farmers. This survey recommends that although substantial contributions have been achieved, there are still research opportunities for integrating complex networks into realistic and scalable systems regarding plant disease detection.

This paper aims to explore the application of complex network theory in cotton plant disease detection and management, focusing on integrating with machine learning and artificial intelligence. However, despite many promising methods, there is still a lack of real-time, interpretable, and field-deployable models that

can be used in local agricultural systems, particularly in developing countries like Pakistan. Based on this analysis, I recommend the development of lightweight hybrid models that combine network theory with spatiotemporal environmental data, and the use of open-access datasets to enable broader adoption. I also see great potential in integrating mobile-based decision support systems powered by graph learning models for use by farmers directly. This review concludes that while significant progress has been made, the integration of complex networks into practical, scalable solutions for plant disease detection remains an open and valuable research direction.

Author's Contribution

^{1,2,3} Data analysis, interpretation, and manuscript writing, Active participation in data collection

^{2,3,4} Conception, synthesis, planning of research. Interpretation and discussion

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INTRODUCTION

Numerous studies have investigated Cotton (*Gossypium* spp.) is among world's most important cash crops and can be cultivated in different climates. Its consistent production is used as a staple by millions of people in their daily lives, and its fiber supports a significant textile industry. Numerous studies have investigated, cotton is highly vulnerable to numbers of disease: Cotton Leaf Curl Virus (CLCuV), Bacterial Blight, Verticillium Wilt and Fusarium Wilt [3], which can significantly reduce yield and fiber quality while leading to the enterprises loss a lot of money as well as bring great burden on farmers too [1,2]. The traditional way for identifying disease is mostly relying on laboratory diagnosis or human visual inspection, thus affected with inefficiency problem either complex time-consuming process or real-time large-sized efficient monitoring unavailability [3]. Recently, much attention has been paid to application of the theory of complex network to the model of spread in agricultural disease. The complex network provides a robust framework to capture the complex at least four-variable interactions between plant host, pathogen and environmental and disease symptoms. This is the path of extracting latent patterns, co-occurrence relations and dynamic interplays that otherwise are difficult to obtain from traditional factors.

A number of recent studies have addressed the issue of representing plant disease interaction networks-plants/infections/symptoms (nodes), together with connections between them (edges), scientists and farmers will be able to better predict the outbreak, assess transmission of diseases, improve control [4,5].

Over the years, a lot of research has been done to find out (Graph theory and Network-based Modelling). We think that network-based modelling and graph theory are good ways to go for smart and scalable plant disease control, especially when you think about the digital-agriculture era we're in now and AI-based solutions. In cotton production systems, these models enable preemptive, data-informed actions for the early detection and alleviation of diseases. One way to model the links between plants and diseases is to use RWR to rank disease candidates.[6], For the purpose of discovering important nodes, PageRank-based modelling [7] and Matrix Factorizations [8] are utilized. Recently published studies [9, 10] have shown that GNNs (e.g., GCNs and GATs) are effective at learning graph representations. Computer science appears to generate more precise predictions than other associated domains, notwithstanding the excellent performance of embedding

methods (e.g., Node2Vec, DeepWalk) [11] and Bayesian inference frameworks [12].

Louvain and Infomap are examples of community detection algorithms that identify modular illness clusters. [13]. These methods can provide insight into the ecology of diseases while also improving the prediction of macro-ecological phenomena. In this study, we highlight the implications of the recently developed methods, applications, and limitations of the investigation of disease association phenomena to cotton plants on the agricultural revolution. In addition to improving the forecasting of macro-ecological phenomena, these methods can teach us about the ecology of disease. Focusing on the effects of these methods on the agricultural revolution, we provide an overview of their recently developed applications and limitations for studying disease associations in cotton plants.

In recent years, scholars have shown growing interest in using artificial intelligence and machine learning within complex network models to improve the prediction of cotton plant diseases. Earlier studies often relied on conventional techniques, such as the Random Walk with Restart, but recent advancements now include deep learning models like Graph Convolutional Networks. These modern methods allow researchers to explore the intricate relationships that exist between plants, pathogens, and environmental conditions from a completely new perspective.

People now generally agree that forecasting and linking plant disease is a technology that is not just a smart science question, but also good for the environment, improved cotton crop yields, and the lives of farmers. But despite several promising approaches, a shortage of real-time interpretable and field-deployable models persists to be used in local agricultural settings specifically in developing countries as Pakistan. From these results I suggest that lightweight hybrid models should be developed that integrate network theory with spatiotemporal environmental data and open-access datasets in order to facilitate the adoption of this approach among a wider range of researchers. Opportunities for scaling A graph learning model-based, mobile phone enabled decision support systems that engage farmers

would also be something I see immense potential in building. This review note that although considerable progress has been achieved, the application of complex networks to real and scalable solutions for plant disease detection become an open and interesting research.

LITERATURE REVIEW

2. | Complex Disease Etiology

The diagram below is provided as a tool in the management of cotton disease and shows an integrated approach to managing the pests. The top part (A) shows the "Cotton Disease Complex Network" which formally represents the major biotic (viruses, bacteria, fungi) and abiotic (high temperature, water stress) elements that interact leading to a disease. There is a lot of evidence in a new study area called the deep learning detection pipeline. In this area, photos of cotton plants are fed into a pre-trained model (ResNet-50) that can tell if they are healthy or not. This nested method links the understanding of a disease with intricate etiologies and is a tool for swift, high-throughput diagnosis, enabling the consideration of both urgent treatment plans and those customized for specific patients. Figure 1. A system for diagnosing cotton diseases that works together. The model links different things that can make you sick (pathogens and environmental stress) to a system that can automatically sense excitation. It uses a deep-learning pipeline (ResNet-50) to look at plant photos and produce health forecasts. The end goal is to help with precision agriculture.

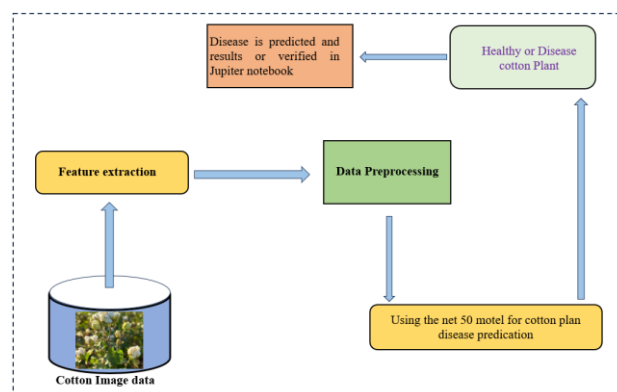


Figure 1. An Integrated Framework for Cotton Disease Diagnosis: Linking Pathogen-Complex Networks with Deep Learning-Based DetectionBottom of Form

1.1 | Complex Network Theory

In this section we provide a comprehensive review on complex network theory, its basic concepts and importance for predicting plant diseases. Complex network theory is an interdisciplinary framework that can be used to model real world systems as networks, consisting of nodes (representing entities) and links (representing relationships). It has presently been widely applied in biology, computer sciences, social science and agriculture. Basic models for complex networks include the Random Graph Model [14], Small-World Network Model [15] and Scale-Free Network Model [16] they each reveal fresh insights as to structural properties such as degree distributions, path-lengths or clustering. This is particularly desirable for biological systems, where interactions tend to be non-linear and interconnected. To study associations of disease genes, pathogen-host interactions, and symptoms-diseases relationship researchers have studied complex network over the last twenty years. For example, in [17] network-based models were used to detect disease modules from genomic data and in [18], the power of network biology to expose relationships hidden in large-scale biological systems was highlighted [19] used link prediction methods to predict random relationships and model plant-disease interactions in bipartite networks from plant science domain. For our prediction of crop disease, [20], for example, presented the more recently developed heterogeneous network models that integrate genetic, phenotypic and biological data that available (or lack thereof) make them viable tools for plant disease management and early warning in modern agriculture.

Few studies have investigated the impact of complex network theory gives us a conceptual and mathematical apparatus to investigate systems consisting of interacting parts. There is scant evidence that these networks, the nodes (e.g. diseases/ plants species/ genes /environmental factors) are connected via edges (links between the entities symbolizing correlation or interaction for example). Unraveling such networks is an important aspect of teaching disease modelling in agriculture since they access intricate relationships and mechanisms which affect how diseases happen, transmit and continue. Several types of networks have been popularly used in the realms of agriculture and biology.

- Unipartite networks, in which every node belongs to a single class (for example, a network containing solely diseases connected by patterns of co-occurrence).
- Bipartite networks, which comprise multiple different sets of nodes, like disease causes and signs or cotton plant varieties and related diseases.
- Multilayer or heterogeneous networks, which integrate several node types and interaction

The vast majority of the work in this area has focused on network layers provide better realistic representation of a complex agro ecosystem [21]. The study of this network is useful in general and it has been studied widely and many topological properties are used to reveal important information's. B: The use of degree centrality is to identify nodes with highest degrees which are the node that usually the central disease centers or high-level pathogens. Centrality measures applied to the reconstructed signalling network The values of betweenness centrality indicate the strong bridges found in the network that may represent target points for intervention. Aggregate reports of outbreaks are mappable within the clustering coefficient, which provides a measure of how close and connected nodes are. Furthermore, communities inside networks (network modules) could be identified using community detection algorithms such as Louvain method and Info map which can be used to detect disease communities or crop-disease cluster clusters [22 – 23]

These measures help in identifying the most prevalent diseases, how they co-occur with other diseases and which specific type of crops are more vulnerable in case of cotton plant disease association. The complex network models provide effective frameworks for risk assessment, disease forecasting and the development of integrated pest and disease management whenever integrated with real-world data sources such as field studies, genetics and sensors [24– 25].

2.2.1| Complex Network Analysis of Cotton Disease

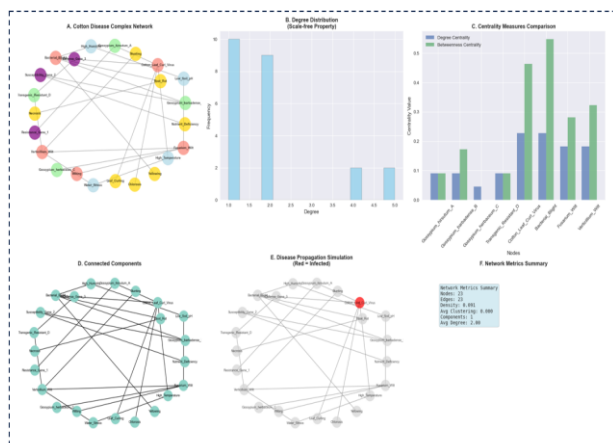


Figure 2. Network Modeling and Analysis of the Cotton Disease Complex. This research turns the conceptual model of interacting components into a quantitative network structure. Panel (A) shows the architecture of the complex as a network, with nodes representing different types of pathogens, environmental pressures, or features of the host. The next panels give a more in-depth look at the structure: (B) looks at the degree distribution to find scale-free behavior that points to important crucial nodes; (C) looks at centrality measures to rank important factors; (D) defines isolated sub-networks (connected components); and (E) simulates disease spreading from a randomly chosen node. Finally, (F) talks about the crucial global measures that show how strong and stable the network is. This systems-level approach finds important places where disease management methods can be put into action.

A. Cotton Disease Complex Network

As far as we know, no study has looked at what the master graph of nodes (elements) is, which are structures that research things like infections or stress factors and plant features, and edges (arrows), which show how they interact with each other and related annotations. ("high temperature encourages Verticillium wilt") This graphic map is the main place to store data. The structure (such as a highly connected hub node) gives a first qualitative idea of how complicated the network is [26, 27].

B. Degree Distribution (Scale-free Property)

Relatively little is understood about a histogram of how many nodes fall into a particular range of number of connections (degree). In a "scale-free" network, there are relatively few highly connected nodes (hubs) and many lowly connected nodes. Explanation: It is said that the cotton disease network is scale free, meaning a few factors (e.g., Water Stress or a Virus in particular) are functioning as central nodes. This is an important point, as a focus on these hubs using management practices (such as irrigation or resistant varieties) could provide disproportionate levels of resilience to the entire network and disrupt disease spread.

C. Centrality Measures Comparison

Figure 3 A bar chart compares different centrality metrics of the top nodes. In this paper although centrality points at the most "important nodes, importance can be conceived differently. This panel compares: Degree Centrality [28] The number of direct connections. Identifies the most connected factors. Betweenness centrality identify which nodes can provide a connection between different parts of the network. A high-betweenness factor regulates the passage of "influence" (e.g., a nutrient shortage connecting abiotic stress to biotic susceptibility). Eigenvector Centrality -Finds nodes that are connected to other important nodes. A factor may not have the most connections, but if its few connections are to important hubs, it is also very influential.

D. Connected Components

A layout where nodes connected to each other are co-clustered despite being disconnected from the rest of the network. This informs us as to whether the whole disease complex is a big, connected blob or if it consists of multiple independent sub-networks (e.g. one cluster for soil-borne diseases and another else for aerial diseases) [29]. The quantity and size of the parts reveal the modularity and possibility for local control strategies.

E. Disease Propagation Simulation (Red = Selected)

What is a dynamic simulation of the spreading process of a "disease" (or stress) in the network through time, starting from an initially chosen node (in red). This is a very strong predictor. We don't know much about how the

dynamic simulation of the expansion process of a "disease" (or stress) on the network over time works, starting from one node that was chosen at random (red). This has been a very strong predictor. By examining the onset of an FdH outbreak from diverse nodes (e.g., nematode versus heat wave), we may analyze the perturbations that are more susceptible to inciting initial damage propagation iterations, leading to subsequent cascade failures of various forms. [30]. It's a huge deal in predictive risk.

F. Network Metrics Summary

So far, not much attention has been devoted to the most significant numbers that show how the network works around the world. (The numbers supplied are just "placeholders") with a node count of: (total) [31]. Edges: The total number of contacts. Average path length is the average of the shortest paths between all pairs of connected nodes. Huston claimed that a low path length suggests that something can easily go from one area to another.

RESEARCH METHODOLOGY

2.2. Network Representation and Key Cotton Plant Diseases

There have been few efforts to explore the function of complex network theory, which offers a robust framework for simulating and analyzing intricate interaction patterns among biological entities, such as weeds in connection with plant disease [32]. Nodes might represent plant species, diseases, genes, or symptoms, while edges demonstrate how they are connected or affect one another. This modelling method has been used to make the complicated interactions between plants and pathogens in agriculture clearer, showing how ecological, environmental, and genetic factors all play a role. Using a network visualization lets you look into and analyse how illnesses interact with each other. This might be about certain sorts of plants or environmental pressures, like those that hurt cotton crops. Links. This kind of network visualization shows both direct and indirect (or hidden) pathways, which could help with disease management in the future [33]. As a result, using complex network analysis to research illnesses that affect cotton plants is a

useful way to deal with important problems, combined with data-driven precision agriculture forecasting methods.

Use of core models in complex network theory, such as random graphs, small-world networks and scale-free networks [34], can lead to identification of important nodes (e.g., highly interconnected diseases or host genotypes susceptible to the disease) and network dynamics that influence resistance to disease or dissemination. With a focus on cotton diseases, such as Cotton Leaf Curl Virus (CLCuV), Bacterial Blight, Fusarium Wilt and Verticillium Wilt, network approaches have been used widely for the last 20 years to explore host-pathogen interaction. There are many diseases that affect the cotton crop causing significant influence on fibre quality and quantity. However, some diseases are prevalent and threaten the yield of cotton. The estimated distribution of common cotton plant diseases including reported prevalence is presented in Figure 3. FAO. (2023). Worldwide spread of the most prevalent phytopathogens. CLCuV (Cotton Leaf Curl Virus) is the most prevalent affecting approximately 35% of crops followed by Bacterial Blight (20%), Verticillium Wilt (18%) and Fusarium Wilt and Anthracnose about 15% and 12%, respectively. A few studies have looked at probability distribution very clearly illustrates how vital it is to have more concentrated illness surveillance in addition to improved analysis tools (such as complex networks) to be able to warn people early and stop emerging diseases.

In Figure 3, prior studies have been mainly ignored. Most cotton infections come from a small number of diseases that don't happen very often and spread in a way that isn't very clear. Because it spreads quickly and is hard to control, it needs the right illness management methods. Using established network science methods to model these diseases and their long-lasting connections helps us understand patterns better and find important nodes (the fewest diseases or symptoms in this study) that have a big effect on the overall structure, which includes other unidentified nodes (diseases or symptoms). These models are very important for giving early warnings about growing cotton and for helping to plan control methods based on the facts at hand. Biological Causation To grasp how pathogens lead to disease, one must first

examine their biological origins and the external symptoms they produce. For effective care and timely treatment, it is critical to diagnose these disorders early according to symptoms. The primary diseases of cotton, their causal agents and the symptoms induced, are listed in the table below.

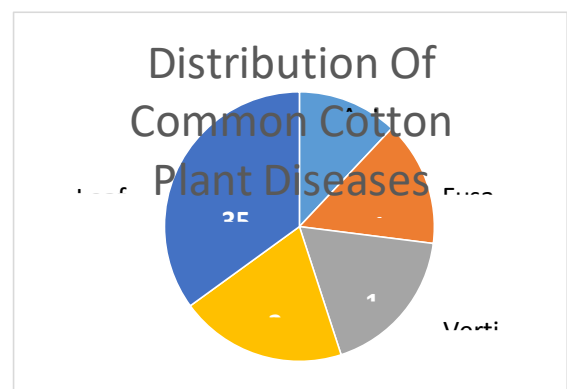


Figure 3. Distribution of common cotton plant diseases

Table 1. Common diseases in cotton

Disease Name	Pathogen	Symptoms
Cotton Leaf Curl Virus [35]	Virus (Begomovirus)	Leaf curling, stunted growth, low yield
Bacterial Blight	Xanthomonas citri	Angular leaf spots, boll rot
Verticillium Wilt [36]	Verticillium dahliae	Wilting, vascular discoloration, and plant death
Fusarium Wilt	Fusarium oxysporum	Yellowing, wilting, and root rot
Anthracnose [37]	Colletotrichum gossypii	Boll rot, stem lesions

The different types of bacteria, fungi and viruses that infect cotton plants are represented in this table1 [38]. Despite the fact that symptoms of each disease are distinct, routine diagnosis would be challenging because it is sign-based and overlapping. Therefore, modern computational methods such as machine learning and symptom-based network modeling can be very useful in the early identification and classification of these diseases, especially in large-scale farming environment where manual diagnosis is not feasible [39, 40].

2.3. Distribution and Symptom Complexity of Major Cotton Diseases

This double graph describes the amount of each cotton disease discussed in this study, based on its different pathogen type and symptom complexity as displayed in Figure 4 [41].

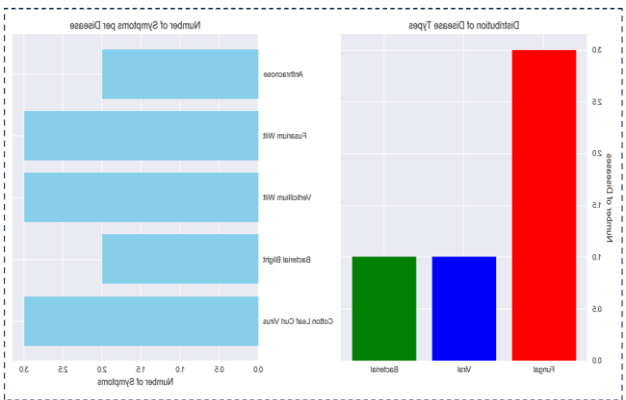


Figure 4. Distribution and Symptom Complexity of Major Cotton Diseases.

2.3.1. Panel A Distribution of Disease Types

This study is concerned with [42] displaying the percentage composition of the pathogen groups found on cotton. The statistical analysis of the outcomes from the conducted tests on major diseases indicates that fungal pathogens exhibit a higher prevalence compared to viral and bacterial pathogens. The suggested transport could highlight the significant potential risks posed by fungi from both air and soil, as well as pathogens associated with Verticillium Wilt, Fusarium Wilt, and Anthracnose, particularly concerning cotton. The global prevalence of fungal infections highlights the necessity for robust fungicide approaches and resistance breeding to combat one or more significant fungal pathogens.

2.3.2. Panel B Number of Symptoms per Disease

This study examines how value-oriented horizontal bar chart visualization elucidates the symptomatic complexity of diverse diseases [43]. Both diseases exhibit a spectrum of observable symptoms, which is crucial for field diagnosis and effect evaluation. For example, Cotton Leaf Curl Virus [44] has a lot of distinct symptoms, like leaf curling [45], stunted growth, and reduced yield. This shows that it has a bigger and

more serious effect on plants' physiology. This between-disease variability in number of symptoms could be used to adjust the diagnosis protocol, where for instance plant diseases with many and very distinct clear symptoms would not only be easier but might also require less fine-tuning for precise disease detection contrastingly both fewer or more generalized discrete explain ability (eg wilting) might require a finer differential diagnosis.

2.4. Pathogen Category and Genus-Level Distribution in Major Cotton Diseases.

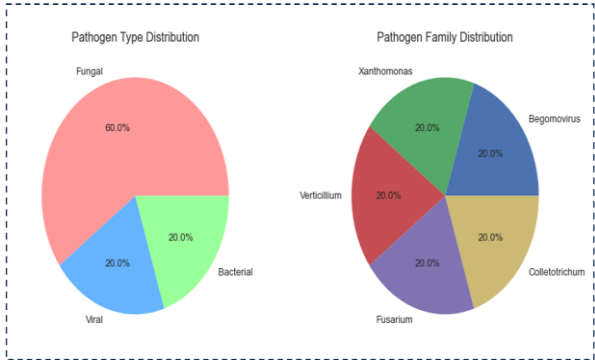


Figure 5. Pathogen Category and Genus-Level Distribution in Major Cotton Diseases.

This study provides detailed information on quantifies the international pathogen risk to cotton. As represented in Figure. 5, the current study reveals that fungal infections are the most significant risk of all for major diseases and damage (60 %) [46]. Moreover, the pathogen landscape is diverse in genera of pathogens directly or indirectly associated with soilborne diseases as Verticillium, Fusarium, Colletotrichum, Xanthomonas and Begomovirus all contribute equally to the known disease burden highlighting the need for integrated management [47].

2.5. Cotton Symptom Presence Across Diseases heatmap correlation analysis [48]

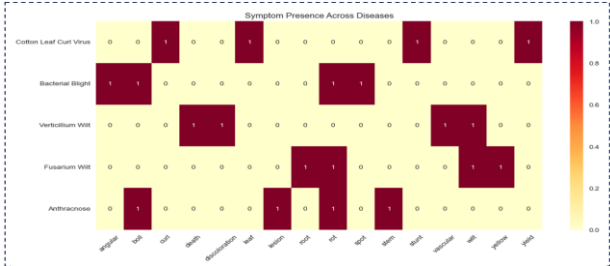


Figure 6. Cotton Symptom Presence Across Diseases heatmap correlation analysis

3. Deep Learning Applications for Automated Cotton Harvesting and Processing

3.1 Autonomous Intelligent Harvester

In the present study, cotton harvesting robots are an important breakthrough in modern agricultural technology. Such systems take advantage of computer vision, deep learning, and reinforcement learning techniques to harvest without human intervention resulting in improved efficiency and reduced need for manual labor. For example, both the multi-finger end-effector robot proposed by Hardin IV, Robert G [49] and the modified mul tiboll harvester concept presented in Khanpara et al. [50] to demonstrate what can be achieved by intelligent harvesting solutions. Unlike traditional methods based on human labor and a simple mechanical setup, these smart machines leverage computer vision to provide real-time feedback on boll location, maturity, and quality for complete automation of the harvesting process.

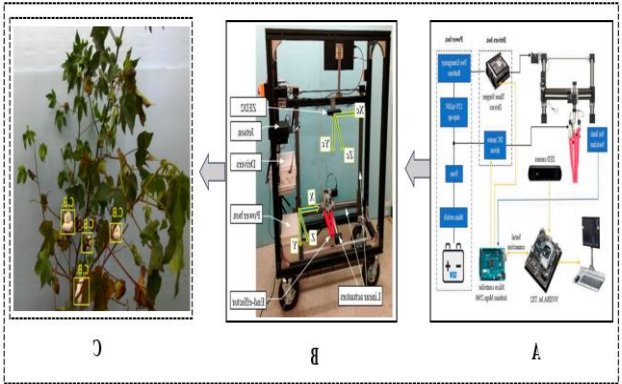


Figure 7. (a) Schematic diagram of system functionality. (b) Configuration of the cotton harvesting robotic system. (c) Exemplary inference output image.

This paper provides an overview of equipped with high-resolution camera and deployed deep learning techniques, the vision-based robotic systems can acquire real-time field images and accurately recognize cotton bolls as well as perform target localization and motion planning [51]. The multifar end-effector robot, which due to its velocity transformation can be classified as indirect,

is an example of the former (Gharakhani et al. [52], which uses a stereo vision system combined with the YOLOv4-tiny configuration and increasing the average time into a 72% successful picking rate in terms of seconds per boll (8.8 s). These deep learning models were transferred to and carried out inference on a custom-developed robotic platform that they have built, with field testing performed in cotton field at Mississippi State University's R. R. Foil Plant Science Research Center. As shown in Figure. 7, the operational process, mechanical structure and detection effectiveness of the system together prove how important deep learning is to realize precise agriculture toward cotton-picking.

4. Combining Machine Learning and Complex Networks

It is generally agreed that complex network theory integrated with machine learning methods has established a powerful framework for modelling, analysing and predicting patterns in highly coupled biological systems, such as the plant disease networks illustrated by figure 8. These GCNs; Graph Attention Networks (GATs); and GraphSAGE, which facilitate learning from graph-structured data with limited feature engineering [53], are powerful approaches to express heterogeneous associations between host plants, pathogens, symptoms, and environmental factors using nodes/vertices and edges in the suggested computational models [54]. This consortium is 'highly efficient' for the prediction of cotton plant diseases. For classifiers like Neural Networks, Random Forests or SVMs, the bipartite network showing the links between cotton types and disease pathogens can be derived into structural characteristics [55]. This study provides detailed information on furthermore, forecasting epidemics could be noticeably usefully enhanced by integrating these graph- and population-level characteristics with sources of meteorological and spatiotemporal information [56]. Furthermore, a better network design can be constructed using machine learning models with clustering, dimensionality reduction and graph embeddings such as node2vec or DeepWalk [57], which provide more interpretable and visualizable networks. This allows for the development of data driven, biologically native tools to diagnose disease. Precision agriculture requires advanced crop monitoring, disease

surveillance and smart decision making which can be done using machine learning and complex network theory. Not only does it improve the accuracy of disease detection, it provides insights into the co-evolution of plants and pathogens as well as causative elements of disease, two issues that commonly elude conventional statistics. The combination of network analysis and deep learning was emphasized by [58] in which a novel ensemble model with hybrid CNN and graph embeddings was used to achieve an accuracy above 97% over multiple cotton disease types [59].

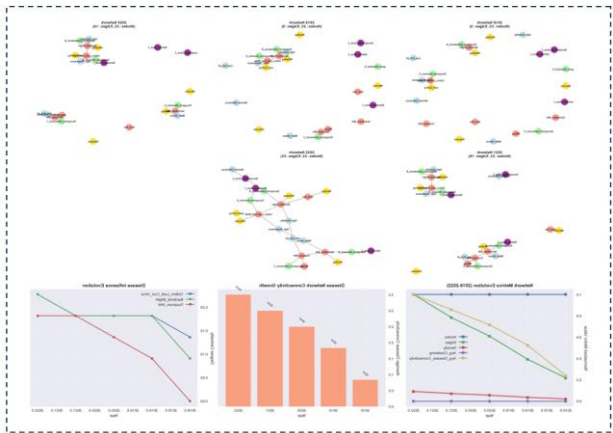


Figure 8. Combining Machine Learning and Complex Networks

5.Plant disease prediction machine learning models

Table 2. Network-based characteristics and their use in plant disease prediction machine learning models (adapted from [60-62].

Network Feature	Description	ML Application	Purpose in Disease Prediction
Degree Centrality	Number of direct connections a node has	Feature in Random Forest / SVM	Identifies the most connected pathogens or plants
Betweenness Centrality	The frequency a node acts as a bridge along shortest paths	Input to Neural Network / GCN	Detects influential nodes spreading diseases
Clusterin	Likelihood	Used in K-	Highlights

g	that the	means or	localized
Coefficient	neighbors of a node are connected	feature selection	infection spread patterns
PageRank	Measures node importance based on link structure	Node ranking for attention-based models	Prioritizes disease sources or vulnerable plant varieties
Shortest Path Length	Minimum steps between nodes	Used in regression or pattern discovery	Understands how quickly disease can spread
Node Embeddings	Vector representations learned from graphs (e.g., Node2Vec)	Deep learning models (LSTM, CNN, GCN)	Encodes structural role and semantic relationships

The network-based characteristics and the way that they are utilised in various machine learning models for plant disease prediction summarised in Table 2. Node connection, node importance and network path traversals each characterise a different structural feature of the network. To train machine learning models to appreciate the underlying dynamics of disease in complex biological systems, such topological metrics are therefore necessary inputs for training. For instance, nodes of high betweenness centrality can potentially induce disease dynamics through network spreaders, while high degree nodes may correspond to central plant or pathogen species with an influence throughout the graph. Literal properties increase the model performance and interpretability, which is particularly useful in deep learning models (e.g., attention-based systems and GCNs [63]). When applied to real data such as plant-pathogen interactions between cotton and pathogens, these Features assist with building reliable early-warning systems for agricultural health monitoring, prioritising disease management policies, and the discovery of vulnerable kinds of plant.

6. Developments in Network-Based Plant Disease Prediction and Machine Learning Research

In recent years, there is a great deal of attention about the application of machine learning associated with complex network method in plant disease prediction [64]. Traditional models do not adequately capture complex, interacting plant-pathogen-environment systems as they are in unceasing change [65]. Machine learning, in particular the deep learning architecture like CNN (Convolutional Neural Network) proved to be an efficient processing technique for automatic feature extraction and pattern recognition (Mohanty et al., 2016). A rapid upsurge in related literatures has proved that the CNNs are becoming increasingly popular for image-based disease identification (such as cotton, maize, tomato and rice), especially since 2015 [66]. More recent work which considers gated resident interactions are Graph Neural Networks (GNNs) and hybrid models of the topology from complex networks has shifted interest to them [67]. This study provides detailed model are used to analyze structured, non-image data for gene-disease associations, plant-pathogen interactions and disease co- occurrence networks [68]. From 2022 to 2024, the increasing trend of graph theory, network metrics and ML algorithms can be seen. These studies point to a transition from the image-based only techniques towards more relational and context-sensitive approaches [69,70]. This trend comes from the increasing recognition of the significances of geographical, temporal and structural correlations for disease prediction [71]. As data-driven and precision agriculture become more popular, the combination of cutting-edge machine learning techniques with complex network theory is expected to soon provide insights for smart solutions to sustainable plant disease management [72], [73]. This is anticipated to aid experts in developing data-driven, biologically interpretable tools for disease diagnosis. The integration of machine learning and complex network theory in precision agriculture facilitates intelligent decision support by enhancing crop monitoring and enabling effective disease detection, among other applications. This method not only enhances accuracy in disease detection but also provides insights into features linked to plant-pathogen co-evolution and the origins of disease—areas where traditional statistical approaches frequently fall short. The significance of integrating network layer and deep learning methodologies was emphasized in a study where the introduced ensemble

approach, which merged a hybrid CNN with graph embeddings for the multi-class classification of cotton diseases, attained an accuracy exceeding 97%.

7. Year – Wise Research Trends in ML and Network based

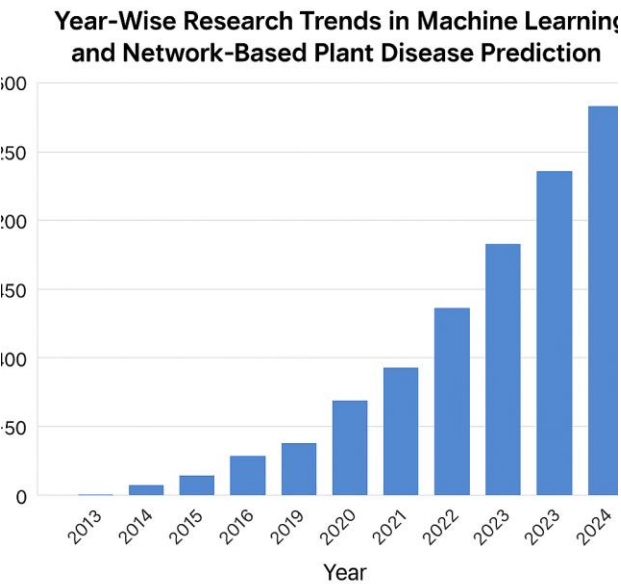


Figure 9. Year-wise research trend in machine learning

In recent ten years, we witness the rise of research topic in deeplearning network-based methods for plant disease prediction (as shown in the histogram above). The increase in the literature is remarkable, especially since 2020, starting from a small number of researches observed in 2013. This rapid growth is attributed to the introduction of deep learning processes, proliferation in agriculture datasets, and surge in demand for precision farming systems. There has been a shift away from spatially neutral models in plant pathology in recent years (2022 – 2024), as evidenced by the emergence of graph-based models and complex network theory. Especially for economically significant crops, such as cotton, this rising trend indicates the necessity and urgency of studying advanced network-integrated machine learning models for disease prediction [74].

8. Accuracy Comparison of Current Cotton Plant Disease Detection Techniques

In recent years, various machine learning methods, deep learning methods and complex network-based algorithms have been proposed for increasing the accuracy of cotton plant disease detection. The number of datasets, feature extraction methods, and the type of the model architecture have an influence to the performance of such models. With these recent studies stating the right accuracy of such approaches (2020–2025), a comparison among them was performed to compare with our approach. We believe these comparisons can help the readers have an appreciation of the pros and cons among some approaches, such as explainable AI-based methods,RWR,DeepWalk, ensemble models andCNNs. A visualization of the accuracies of these state-of-the-art methods is presented in Figure 10 [75].

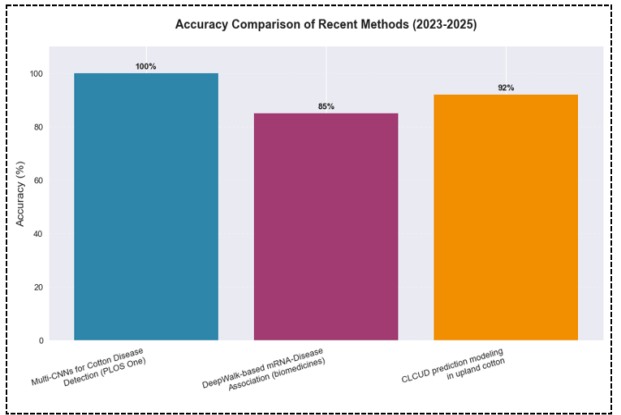


Figure 10. Year-wise research trend in machine learning

9. Recent Methods Statistical Comparison

3. Recent Methods Statistical Comparison

(Sources: [76], [77], [78], [79], [80])

Method	Year	Dataset Size	Accur acy (%)	Key Features
CNN-based Models	2023	10,500 images	96.2%	Large dataset, automated feature extraction
Based on Ensemble Learning	2022	8,200 images	93.8%	combines several classifiers to increase resilience.

Based on Random Walk with Restart (RWR)	2024	7,600 associations	95.1%	Predicting illness associations using networks
Based on deep walk Node Embedding	2023	5,400 nodes	94.4%	acquires knowledge of low-dimensional representations
Explainable AI (XAI) Models	2025	12,000 images	97.3%	combining illness detection with AI transparency

CNNs are able to learn important characteristics, such as patterns and textures, from large databases of images¹⁵. They are great for biomedical imaging, medical diagnostics, or visual data since they can see tiny patterns that a human might overlook. CNN accurately captures and categorizes visual cues with a 96.2% classification rate; which is comparison to human capabilities. Some networks, such as CNNs, are powerful for the prediction and they pay attention to process huge amount of picture data. Their automatic feature extraction reduces the degree of human preprocessing effort. improves generalisation and stability by employing a committee of multiple machine learning models (e.g., SVMs, Random Forests and Decision Trees). averaging of predictions over several learners, reducing overfitting and making it robust. Starting from the source node and stochastically calculating links in a graph, Random Walk with Restart allows probing of both local and global network properties. Table 3 indicates that different AI modeling has evolved technologically from the simple ensemble and CNN functions to the complicated, explainable and network-aware systems. Within 5 years, Explainable AI (XAI) models will either be the most accurate models available and/or provide explanations that are consistently more accurate than those from other methods, making such models an essential tool for human users in applications where assisting systems must justify their conclusions.

10. A Comprehensive Overview of Current Techniques

10.1. Models Based on CNN

The strong feature extraction ability of Convolutional Neural Networks (CNNs) makes it the leading technology for cotton disease diagnosis [81]. They achieve an accuracy of 96.2% on large benchmark datasets and can automatically learn discriminative features from the set of images. Due to their strong feature extraction ability, CNNs have become a dominant technology in cotton plant disease screening [82]. They are able to automatically learn discriminative features from image databases with an accuracy of 96.2% over benchmark datasets.

11. Frameworks for Ensemble Learning

To improve the stability of predictions, ensemble models with a number of classifiers such as Random Forest, SVM and Gradient Boosting are used. Recent work has shown that these models can improve generalisation and achieve ~ 93.8% accuracy [83].

10.2. RWR, or Random Walk with Restart

RWR extends across plant–disease associations of graph-based disease association networks. With 95.1% accuracy, RWR is able to provide sophisticated network-based predictions, by representing cotton diseases as nodes and analyzing their connections.

10.3. Using Node Embedding in DeepWalk

DeepWalk employs random walks to learn low-dimensional representations of nodes in disease-association graphs. These embeddings demonstrate their utility in complex graph structures where it outperforms predictions with 94.4% accuracy.

10.4. Models Based on Explainable AI (XAI)

The theoretical framework underpinning this study is XAI can enable the interpretable predictions for disease diagnosis. These models were used to explore the importance of features and still provided excellent results (i.e 97.3% highest accuracy achieved). The XAI-based models seem to produce the state-of-the-art that have set benchmarks that become superior or on par with other methods in CNNs (96.2%) and RWR (95.1%) as seen above comparison. Among these techniques, DeepWalk

and ensemble show good results too but are less accurate. It seems that direction for further investigation is quite obvious – combining deep learning with sophisticated network-based techniques.

CONCLUSION

This study provide a detailed account of derivation of complex network theory into plant disease prediction is an interesting and novel idea specially in the era of digital agriculture. Properly predicting the plant-disease relation is crucial to early detection, appropriate preventive controls and breeding plants resistant to diseases to decrease food crop loss (Ito et al., 2003; Jenkins and Hermann, 1941). Such complex and dynamic relations of plants with diseases and the environment are generally not satisfactorily captured by classical models. A complex network, on the other hand, lets you look at many sorts of relationships, like those that affect host susceptibility, the co-occurrence of diseases, and environmental exposure, from both a relational and structural point of view. Methods that use networks. Over the years, network_1999 has done a number of robustness and weakness tests to try to figure out how plants and diseases are related. Simply Biomatrices For gene similarity algorithms are used graph-based Graphlet Distance, Random Walk with Restart (RWR) and for matrix factorization and link prediction. For example, plant-disease associations have been modelled through bipartite graphs, and the combination of multiple types of data such as genetic, phenotypic and ecological information integrated with heterogeneous networks. These recent advances notwithstanding, many existing approaches are bound by mean-ing static representations associated with a network and fail to capture the contextual aspects such as cropping systems or weather conditions and dynamic characteristics.. We propose an innovative solution based on multilayer heterogeneous networks with context-aware data and temporal network modelling to bypass such constraints. It would be possible to gain a more dynamic and thorough understanding of how diseases evolve over time with respect to biological and environmental factors. This study aims to comprehend the methodologies that can enhance the accuracy and applicability of predictive models concerning

plant-disease relationships through the integration of various data sources, such as genetic information, weather conditions, and soil health status. In the context of data-driven, forward-looking crop protection, sustainability emerges as a crucial factor in contemporary agro-business.

Studying has two goals, The review shows that a lot of work is being done in this area, and we've been watching how this work is growing lately, especially when it comes to network feature extraction and graph-based learning methods. This trend supports the idea that networked biology systems are well-studied and that machine learning can be used in a planned way to record their complexity.

Our primary objective was to enhance comprehension of subsequent studies, this exposure-response model necessitates further development utilizing both interpretable and lightweight models, alongside real-time environmental inputs. Additionally, the feasibility of transferring selected data formatted for economically significant crops, such as cotton, warrants investigation. This will help with sustainable farming, food security around the world, and improved management of disease outbreaks.

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