

Explainable AI-based hybrid GNN-MLP model for strawberry fruit disease detection using hyperspectral imaging

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ABSTRACT

Strawberries are severely affected by the main fungal diseases such as anthracnose fruit rot, grey mould, and powdery mildew, directly reducing commercial yield and post-harvest quality. In this paper, we propose an enhanced hybrid deep-learning method by combining graph neural networks (GNNs) and multi-layer perceptrons (MLPs) for effective strawberry disease detection in real environments of fields. This dataset contains images acquired from both public domain repositories as well as farm operational settings, encompassing three classes of diseases with varying lighting conditions, background noise, and occlusion. A structured pre-processing workflow comprising contrast enhancement, denoising, and synthetic hyperspectral simulation is used to enhance subtle lesion features and stabilize the subsequent feature extraction. The hybrid GNN-MLP framework possesses the merits of spatially local lesion topology and two-point contextual information, which can improve disease classification compared with common CNN-based structures. 5-fold cross-validation shows that the model holds 93.59% accuracy and a macro F1-score of 90.39%, showing good generalization even with heterogeneous input regimes. Transparent models use local interpretable model-agnostic explanations (LIME) and gradient-weighted class activation mapping (Grad-CAM) in combination, highlighting disease-relevant areas that give an interpretable rationale for each prediction. To conclude, the developed system offers an accurate and explainable solution that has a computationally efficient commitment for real-time monitoring of disease in smart agriculture settings, particularly on low-cost hardware assets.

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1. INTRODUCTION

Strawberry (*Fragaria × ananassa* L.) is among the most economically important horticultural crops because of its high nutrient content, attractive flavor, and strong global market demand. Nevertheless, fungal pathogens strongly limit abscisic acid (ABA) production and *Botrytis cinerea* (the causal agent of grey mould) accounts for up to 50% of pre- and postharvest losses worldwide under favourable environmental conditions [1]. This loss is economically devastating for farmers, especially smallholders who do not have advanced crop-monitoring systems in place. Accordingly, scalable, early-stage, and accurate disease detection methods are increasingly imperative in modern precision agriculture.

Combining hyperspectral imaging with machine learning approaches offers a novel method for early detection of strawberry diseases by identifying spectral alterations occurring before visible symptoms [2]. Deep convolutional neural networks (CNNs) have also been applied to multiple plant-disease classes and can achieve state-of-the-art results with conventional image-based diagnosis [3]. As a result, artificial intelligence (AI) and, relatedly, deep learning are being used more widely for crop-health monitoring and contributing to agricultural decision-support systems. Ferentinos [4] illustrated that deep learning can be extremely useful in identifying plant diseases for many different crops while showing the limitations and advantages of traditional techniques used in plant-disease identification.

AI has also been integrated into automated plant-disease detection pipelines [5] and deployed in real-time mobile systems to monitor strawberry diseases in open-field conditions [6]. Although these advances allow the identification and analysis of disease networks in established and relapsed haematological malignancies, disease detection at those early stages remains challenging, particularly under uncontrolled imaging conditions. Conventional digital image-processing techniques generally do not perform well due to varying illumination, background clutter, and sensor noise [7], and traditional computer-vision pipelines may be less robust for field-scale deployment [8].

Deep-learning architectures that enable hierarchical training of the network have been proposed to overcome these limitations. For interpretable disease diagnosis in crops like soybean, hybrid CNN-graph neural network (GNN) models have been studied [9], and transformer-based vision models offer a strong feature-extraction capability for dietary images used in agricultural applications [10]. In the context of strawberry research, more detect-only YOLOv8-based pest and disease detection methods have been established. He *et al.* [11] proposed the KTD-YOLOv8 model, where KTD stands for KernelWarehouse convolution + triplet attention + multi-template branch block sharing head. Classical CNN-based systems also remain useful for strawberry disease detection under semi-controlled and field conditions [12].

Furthermore, rather than simple categorisation (from which CNN-based networks in fact do not offer a competitive advantage), more sophisticated deep network architectures have been applied to prevent degradation of detector performance with respect to domain-specific distortions such as occlusion and background clutter [13]. For strawberry leaf disease identification, interpretable and lightweight deep learning pipelines have been designed to enhance processing performance on edge-computing devices as well [14]. More generally, the evolution of plant phenotyping, such as 3D reconstruction, trait modelling, and spatial feature understanding, highlights that more advanced data representations are becoming more prominent in the field of crop health [15]. Similarly, sensor fusion and AI-enabled analytics have made tree-crop smart sprayers far smarter, with high-level demonstrations showing how these smart models provide a practical solutions for disease management at the farm level [16].

Explainable artificial intelligence (XAI) has emerged to clarify how model inputs influence predictions. Local interpretable model-agnostic explanations (LIME) provide instance-level explanations by identifying image regions that influence a classifier's output [17]. In agricultural disease detection, machine-learning models have also been evaluated on customised datasets to examine their practical performance and deployment limitations [18]. Comprehensive reviews of deep learning in agriculture continue to emphasise the need for scalable, robust, and interpretable approaches to disease detection and crop monitoring [19].

Ongoing efforts to create models that operate efficiently with limited resources are outlined in [20] through comparative studies of strategies for fine-tuning for plant-disease recognition and in [21] through the design of lightweight attention-based CNNs. XAI is also becoming increasingly significant in precision agriculture, as farmers and agricultural industry players require transparent automated decision-support systems [22]. Nevertheless, standard data-driven techniques continue to perform well as baselines for plant-disease classification [23], whilst more in-depth study of deep-learning methods for plant phenotyping uncovers the potential of advanced feature learning within agricultural domains [24].

In addition to plant and disease classification, deep-learning techniques have been suggested for plant-disease severity estimation [25] or detecting biotic stress in different growth conditions [26]. More comprehensive reviews of deep learning applications in agriculture [20] continue to emphasise the need for generalizable, scalable, and robust AI systems that are capable of deployment into real field environments. To address these challenges, this paper presents a GNN-MLP hybrid architecture for classification of different types of strawberry diseases based on farm-realistic images. The model incorporates the following elements: i) contrast normalisation to mitigate illumination variability; ii) Gaussian denoising to filter out background noise; iii) synthetic hyperspectral simulation for enriching disease-indicative information; iv) graph-based reasoning to model relations between lesion topology and structure; v) MLP-based semantic fusion of visual attention maps; and vi) XAI modules, specifically LIME and Gradient-weighted Class Activation Mapping (Grad-CAM), capable of generating human-interpretable biological decision maps.

To this end, we propose a knowledge-based disease-diagnosis pipeline that is compact and usable across heterogeneous agricultural environments and edge-computing platforms while ensuring computational efficiency; thus, presenting an end-to-end automatic pest pathogen detection solution that is robust, certain, and interpretable. The rest of the manuscript is organised as follows: background literature on plant disease detection, hyperspectral methods, and graph-based modeling are reviewed in Section 2, methods description is in Section 3, the experimental results in Section 4, followed by discussion in Section 5, and the conclusion in Section 6.

2. RELATED WORK

Early plant-disease detection methods used handcrafted colour, texture, and shape features with classifiers such as support vector machines (SVMs), random forests (RFs), and k-nearest neighbours (k-NN) [8]. Their performance often declines in real-world conditions because of illumination changes, background clutter, and sensor noise [7], [19]. This is similar to hierarchical feature extraction, which you can take advantage of with deep learning and convolutional neural networks (CNNs) can take advantage of with respect to multi-crop disease classification; Ferentinos [4] highlighted that this task could trivially be solved by one-vs-all-based classifier ensembles (revisiting the early 1990s). At the same time, Liu and Wang [5] presented a review on deep-learning methods for various plant-disease and pest detection use cases. Mahmud *et al.* [6] proposed a mobile machine-vision system to identify strawberry powdery mildew in real time. Long-range visual feature modelling is also supported by transformer-based models [10]. But grid-based CNNs and transformers may not explicitly model irregular relationships between lesions. To overcome this limitation, GNNs represent lesion regions as graph and their spatial relationship as edges [9], [27]. Therefore, hybrid CNN–GNN structures can integrate local texture features with relational information and enhance their robustness under heterogeneous field conditions of the field [9].

Hyperspectral and multispectral imaging are used because they allow an early diagnosis of diseases by visualising the first biochemical changes before visible symptoms become obvious. Jiang *et al.* [2], using machine learning and spectral fingerprint features, showed that hyperspectral imaging is an effective tool for early identification of strawberry leaf diseases. Due to the cost-prohibitive nature and sensitivity of dedicated hyperspectral equipment to acquisition conditions, computational spectral surrogate methods derived from RGB images may provide a practical alternative. Another problem is the diversity of the datasets: lab-style datasets can drive model development but are not necessarily representative of field conditions, which are often characterised by imbalance, occlusion, and background clutter [7], [19], [23]. Explainability methods such as LIME [17], SHapley additive exPlanations (SHAP), and Grad-CAM can also generate visual evidence of model decisions; however, in strawberry disease research, explainability has not been fully employed [22].

Recent developments in the internet of things (IoT), uncrewed aerial vehicle (UAV) imaging, and edge AI have expanded the possibilities for scalable crop surveillance. Mohanty *et al.* [23] demonstrated the effectiveness of deep learning for large-scale image-based plant-disease detection, while Singh *et al.* [24] emphasised its importance for high-throughput plant phenotyping. Lightweight disease-severity estimation methods have also been developed for practical field applications [25]. Strawberry-focused studies include improved YOLOv8 models [28], KTD-YOLOv8 disease detection [11], CNN-based detection systems [4], [6], [12], and lightweight interpretable disease-recognition approaches [14]. Other related work includes graph-based plant species classification [28], YOLOv5-based horticultural phenotyping [28], dual-branch crop-disease recognition [28], satellite time-series attention models [28], spectral-spatial Siamese CNNs [28], and lightweight YOLOv5 strawberry detectors [28].

Collectively, prior literature reveals persistent limitations: i) insufficient interpretability in high-performing models; ii) reduced robustness under uncontrolled field conditions; iii) inadequate modelling of relational lesion structure; iv) lack of unified spectral-enhanced and graph-based explainable pipelines; v) domain-shift-driven generalisation failures. These gaps motivate integrating synthetic hyperspectral enhancement, GNN-based relational modelling, and XAI into a unified, robust strawberry-disease detection framework.

3. METHOD

In this work, we propose a hybrid deep learning method that combines GNNs and Multi-Layer Perceptrons (MLPs) for automated detection of strawberry fruit diseases. The model aims explicitly at three commonly occurring and economically important diseases: anthracnose fruit rot, grey mould, and powdery mildew, all of which visually resemble each other to some extent under uncontrolled farm conditions. Their morphology is affected by environmental conditions, light quality, irrigation levels, as well as cultivar

and fruit ripening stage. Thereby, manual checking is unreliable, illogical, and time-consuming, especially on large-scale production systems [1], [19].

The idea of the proposed method is to take advantage of both the spatial structural learning ability of GNNs and the semantic abstraction ability of MLPs. GNNs capture spatial lesion topology, adjacency patterns, and cross-region contextual relationships, while MLPs use pooled features for powerful global discrimination. This dual-learning definition is well adapted for the agricultural images where symptoms randomly happen on the fruits with occlusion or image noise [4], [7].

3.1. Dataset acquisition and preprocessing

An adaptable database was created for the training and validation of the hybrid model:

- Public-release samples (PlantVillage, Kaggle) with clean field condition images prompting well-constructed annotations [8], [9].
- Natural farm images collected under extremely variable environmental conditions, including uneven illumination, cast shadows, dirt, crop residues, leaf occlusions, and fruit at different angles [10], [11].
- Labels: trained plant pathologists curated labels to guarantee diagnostic accuracy and to eliminate ambiguities in samples [12]. Using a combination of controlled and real-field images, as it increases robustness, decreases overfitting on clean backgrounds, and at last it ensures that the model can actually be used in farms.

3.1.1. Image resizing

All the lesions are being resized to 256×256 individual pixels, so their width and height were set to achieve the commonly found resolution limits, which allow preserving basic lesion properties and reducing excessive computation costs. This standardisation:

- Facilitates efficient batch training.
- Reduces GPU/CPU memory load.
- Ensures that the fixed input layers of the neural network are compatible.
- Reduces interpolation errors on small lesions (which have clinical significance) [14], [15].

3.1.2. Contrast enhancement

Contrast-limited adaptive histogram equalisation (CLAHE), is a method for controlling non-uniform illumination mechanisms that can be present in open-field farm environments because of direct sunlight, shadowing, and a combination of diffuse light [16], [19]. CLAHE:

- Amplifies fine-grained damages frequently not visible in the raw red-green-blue (RGB) images.
- Reveals early-stage infection patterns.
- Enhances discrimination of pathological tissue from normal skin.
- Guards against over-impacted noise (by contrast limiting).
- This enhances the definition of lesion margins, fungal patterns, and discoloured areas.

3.1.3. Denoising and synthetic hyperspectral simulation: A

Gaussian filter is applied to the calibration image, which helps effectively suppress sensor noise, motion noise, and low light noise present in the farm images taken from smartphones [19]. Denoising is followed by a synthetic hyperspectral transform, which expands the number of channels with richer information. Instead of using (still pricey) hyperspectral cameras, the approach computationally generates additional frequency bands by:

- PCA-based spectral projections.
- Gradient and texture filters.
- Vegetation stress indices.
- Colour-frequency decomposition.

These spectral surrogates capture information about the early biochemical changes induced by pathogens -a physiological response which is often invisible in RGB data [20], [24].

3.1.4. Data partitioning and validation

The raw data was split into 3 sets: train (70% of the data), validation set (15%) and a test set (15%). To decrease the likelihood of a one-class split, we performed stratified splitting such that each subset contained all classes. To achieve greater statistical robustness and prevent over-parameterisation, 5-fold cross-validation [19], [25] was also applied during model training and validation. In all partitions, 80% of the data was used for training and 20% for validation in a rotated manner. These accuracy metrics were averaged over the folds to provide generalizable and stable estimates of accuracy.

The differences in this preprocessing pipeline and the distribution used before injection all helped to give the GNN-MLP model downstream “cleaned”, contrast-enhanced, and informative features, which would in turn aided its learning of fine-scale disease patterns for strawberry fruits.

3.2. Model design and architecture

The model is a fusion model based on the integration of GNNs [8] and an MLP, in which the species are categorised from learned spatial and semantic embeddings separately for mapping. Our main underlying design philosophy is to enable robust spatio-semantic learning, so that the model will not only reason about the values of the pixels themselves, but also about the structural layouts and contextual distributions of the disease symptoms spread out over the fruit surface.

An overview of the proposed architecture is illustrated in Figure 1; the overall procedure includes:

- Input raw images of infected samples of strawberries with lesions, mould patches, or necrotic zones.
- Patch extraction and building the graph. The image is divided into superpixels; each superpixel corresponds to a graph node, and its neighbouring patches correspond to edges, thus resulting in a Region Adjacency Graph (RAG), which indicates the local spatial distribution of lesions [27], [28].
- This layer, the GNN module, is where neighbouring nodes share information to model patterns of lesion expansion, spatial structure of disordered morphology, and irregularities in borders [27]
- The MLP module maps the globally aggregated GNN embedding to class labels [25], [26].
- The final prediction, comprising the predicted disease class and its confidence score.

Overall, this hybrid structure integrates spatial reasoning and semantic classification into a single lightweight architecture suitable for smart-farming deployment.

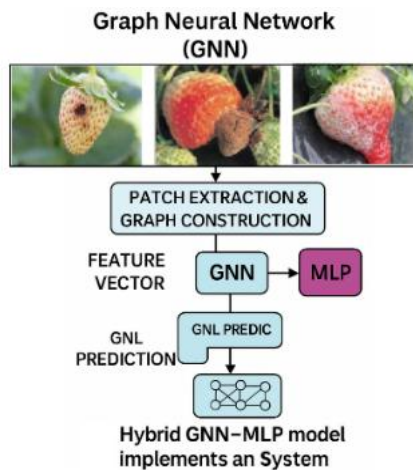


Figure 1. Block diagram of the proposed hybrid GNN-MLP model for strawberry disease classification

3.2.1. GNN module

The GNN module is tailored to capture and retain spatial patterns of disease-affected regions. To do this, each input image is first divided into local patches or superpixels, which represent the nodes of a graph. The connections between nodes are controlled by distance (geometric closeness), color similarity, and texture coherence. This results in a graph-like model of the surface of each fruit, with nodes (i.e., clusters) representing sets of adjacent pixels assigned to feature vectors describing local neighbourhood regions and edges indicating spatial relationships.

Graph convolutional layers (GCNs) are used to propagate these features iteratively, through a kind of message-passing-based strategy: for each node, the GCN aggregates information from its neighbours. This process helps teach the model how symptoms may spread across the surface of fruit (thus learning about inter-patch correlations, lesion borders, as well as co-occurring disease). GNNs are particularly well-suited for modeling the non-Euclidean spatial dependencies that conventional CNNs often do not capture. Mathematically, the forward pass of each graph layer can be formulated as:

$$h_i^{(l+1)} = \sigma \left(\sum_{j \in \mathcal{N}(i)} \frac{1}{c_{ij}} W^{(l)} h_j^{(l)} \right)$$

where $h_i^{(1)}$ is the feature vector of node i at layer 1, N_i is the set of neighbouring nodes, $W^{(1)}$ is the weight matrix, c_{ij} is the normalisation constant, and σ is the non-linear activation function.

3.2.2. MLP module

After the spatial features in the enriched node embeddings are aggregated into a fixed-size vector, they pass through to the MLP classifier. This module serves as the semantic decision layer, mapping the high-dimensional graph features back into class labels. The MLP is composed of several fully connected layers followed by the application of ReLU activation, dropout (to avoid overfitting), and batch normalisation (to allow convergence).

Its purpose is to capture global, abstract representations, e.g., the distribution of disease symptoms over the entire fruit while maintaining the spatial information learned by the GNN. The last softmax layer provides class probabilities for the three diseases.

3.2.3. Training environment and configuration

We trained it using the PyTorch framework, which is modular and allows custom GNN layers to be added easily, as well as dynamic graphs to be handled efficiently. The model was thus applied by being deployed and trained on the full dataset, except here it was run on a CPU-only machine in order to simulate what would occur upon further on-site deployment of this model at farm level, either where GPUs are not readily available or alternatively in short supply. Key training parameters included:

- Loss function: categorical cross-entropy
- Optimiser: Adam with an initial learning rate of 0.0001
- Batch size: 32
- Epochs: 50 (with early stopping based on validation loss)
- Dropout rate: 0.3

These parameters were fine-tuned through experimentation on the validation set using a grid search procedure. This hybrid architecture allows for training of spatial structure and global semantics concurrently, with better performance than traditional image classifiers in complex field environments where visual disease signals can be faint, subtle, overlapping, or ethereal.

3.3. XAI integration

Interpretability is the primary limitation of deep learning methods, especially in sensitive domains like agriculture. Although these models reach remarkable accuracy, they are typically seen as “black boxes”, as they do not offer an intuitive reasoning regarding why a certain category was identified. This lack of transparency can also erode user confidence and prevent non-technocratic adopters such as farmers, agronomists, and agricultural advisors from using these techniques.

To alleviate this problem, in this work, we have integrated XAI methods into our classification pipeline. These methods aim to make the model’s decision-making process transparent and interpretable, helping end-users validate model predictions and have confidence in the system’s trustworthiness.

3.3.1. LIME

LIME [17] is a model-agnostic explanation technique that explains individual predictions from the model by learning a locally interpretable model around the prediction. It works by generating a bunch of perturbed samples from the original input (e.g. by blocking out parts of the image), and then seeing how the model output changes.

In this study, LIME [17] was employed to reveal the most impactful regions or pixels of the strawberry fruit image on the model prediction. The resulting output is a binary saliency map that highlights the top-k important regions that contribute to the predicted disease class positively or negatively. Both researchers and practitioners can use this to verify whether the model is attending to biologically meaningful features of interest (e.g., lesion boundaries, fungal textures) instead of irrelevant background noise.

3.3.2. Grad-CAM

Although LIME provides instance-specific local explanations, Grad-CAM produces global visual reasoning by generating heatmaps that show the most discriminative regions used during classification by a model. Grad-CAM [18] computes the gradient of the output class score with respect to the feature maps of the last convolutional layer. The gradients are further pooled and employed to weigh the feature maps, which are upsampled and superimposed with the original input image to generate a class-specific localisation map. In our implementation, Grad-CAM [18] was particularly effective in:

- Localising disease spots, even in the presence of occlusion or noise.
- Highlighting symptom-specific textures and colour changes.

- Providing actionable insights for domain experts, such as where to further inspect the fruit for early-stage symptoms.

3.3.3. Benefits of integrating XAI in agricultural diagnosis

The dual integration of LIME [17] and Grad-CAM ensures that both local interpretability (via LIME) and class-discriminative visual localisation (via Grad-CAM) are addressed. These tools play several important roles:

- Increase end-user trust by visualising the rationale behind model decisions.
- Enable non-technical stakeholders to adjust interventions based on informed selective measures (e.g., applying pesticides only in localised areas affected by the pest).
- Enhance debugging and model tuning by identification of misclassified regions or bias in the training data.
- Facilitating technology adoption in agricultural communities where pragmatic usability and interpretability are often much more important than raw performance statistics.

With the incorporation of XAI modules in our pipeline, even after training, the entire system should work as a traditional solution. Still, now it provides interpretability to the output, enabling the farmer to trust the model and making precision agriculture friendlier.

3.4. System flow and evaluation

An overview of the whole system pipeline is depicted in Figure 2, highlighting general workflow steps such as data acquisition, model building, and interpreting results. The pipeline also epitomizes a desirable modular, explainable, content-rich framework with easy deployment, with less focus on dataset benchmarks and more on real-world agricultural applications.

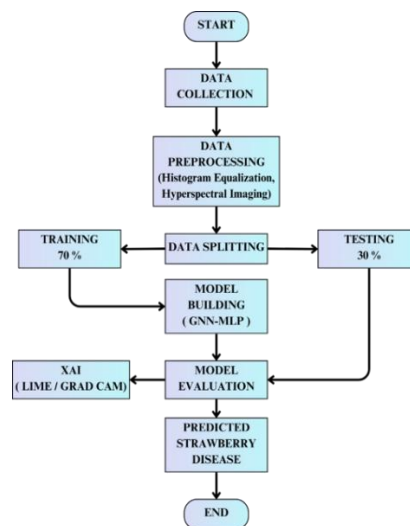


Figure 2. Model training and evaluation process

It starts from raw images of non-diseased and diseased strawberry samples, collected under different field conditions (e.g., lighting, resolution, angle, etc). This keeps all our data realistic and not over-suppressed from where we collected it, as well as getting the right attribute diversity.

For the data collection step, here we use a processing phase with datasets such as CLAHE [2] methods and hyperspectral imaging simulation. These transformations are critical for the underlying objective of inducing disease abnormalities and identifying latent variables that elude detection in RGB inputs.

Using stratified sampling, the data is divided into 70% training, 15% validation, and 15% test sets, taking care to preserve the class distribution in each of these subsets. Finally, the performance estimates are made with 5-fold cross-validation [27] as part of model development to improve reliability and mitigate the risk of overfitting. For every fold, the complete development data are cycled through splits providing separate training and validation partitions, followed by final evaluation on the unseen test set. These graph-based image representations are then used to train the GNN–MLP hybrid architecture.

Afterward, it proceeds to evaluation, where the model is evaluated by running cross-validation and calculating common classification metrics. The system computes:

- Accuracy: the number of correctly predicted observations over the total observations.
- Precision: true positives / (true positives + false positives).
- Recall (sensitivity): true positive/actual positive for a certain class
- F1-score: it is the Harmonic mean of Precision and recall, giving a single weighted metric for an imbalanced dataset.

Then, interpretive ex tools (e.g., Grad-CAM and LIME [17]) can expound model decisions in the context of fewer patience. These methods generate attention overlays and saliency maps which plot areas over the image that have been influential in the final classification decision. This will allow for immediate decision-making in the field, which inspires trust. Eventually, the final output returns you the model outputs as follows:

- Predicted disease class labels (class labels are anthracnose, grey mould, and powdery mildew).
- Confidence scores.
- For each prediction instance, visual explanation maps.

This pipeline provides a well-founded, advanced, transparent, and scalable solution for the early detection of strawberry diseases, enabling the development of smart farming systems and precision agriculture applications.

4. RESULTS

4.1. Overall performance

The proposed hybrid GNN-MLP model obtained an accuracy and macro-F1 of 93.59 and 90.39%. The confusion matrix shown in Figure 3 demonstrates a balanced classification across all three disease classes, with only slight misclassification.

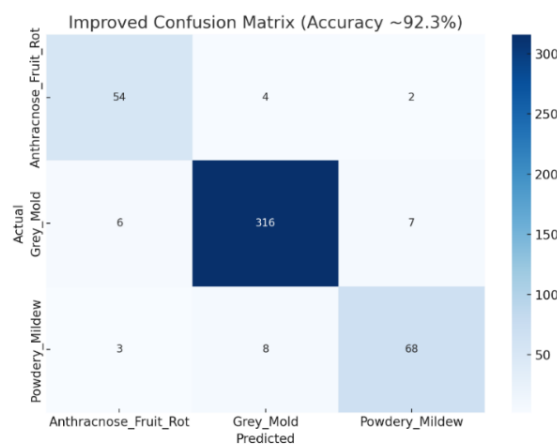


Figure 3. Confusion matrix illustrating classification outcomes for anthracnose fruit rot, grey mould, and powdery mildew

4.2. Class-wise and cross-validation metrics

Performance of the class-level precision, recall, and F1-score is summarized in Table 1. Grey mould received the highest ratings, followed by anthracnose and powdery mildew. Reasonably stable 5-fold cross-validation performance was achieved, demonstrating consistent behaviour across different data splits.

Table 1. Classification metrics summary

Class	Precision	Recall	F1-score	Support
Anthracnose fruit rot	0.8571	0.9000	0.8780	60
Grey mould	0.9634	0.9605	0.9619	329
Powdery mildew	0.8831	0.8608	0.8718	79
Accuracy			0.9359	468
Macro average	0.9012	0.9071	0.9039	468
Weighted average	0.9362	0.9359	0.9360	468

4.3. Comparative performance against baseline models

Comparisons were made with SVM, RF, smaller CNNs, YOLO detectors, and previously reported GNN/hybrid methods. The results collected in Table 2 and Table 3 show that the proposed GNN–MLP model performs much better than all the baselines in terms of accuracy, precision, recall, and F1-score. The performance comparisons are graphically shown in Figure 4. Figure 4 shows representative input images and the corresponding disease classification results produced by the proposed hybrid GNN–MLP model. Figure 4(a) presents the original diseased strawberry fruit images, while Figure 4(b) illustrates the predicted disease classes with their corresponding prediction accuracies.

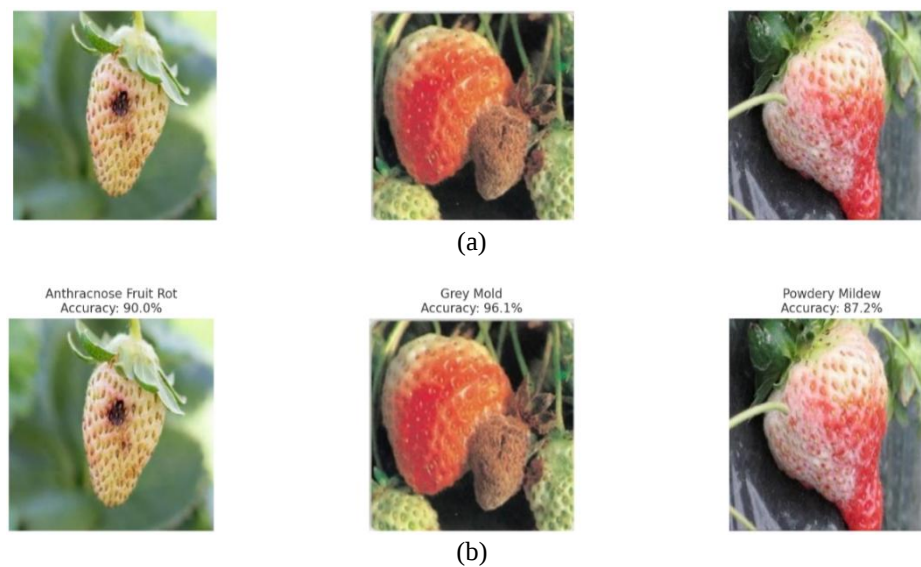


Figure 4. Strawberry disease classification: (a) diseased strawberry fruit images before classification and (b) the corresponding classification results generated by the proposed hybrid GNN–MLP model

Table 2. Comparative performance of proposed model vs. previous studies

References	Model type	Dataset type	Accuracy (%)	F1-score (%)	Notes (corrected author attribution)
Karki <i>et al.</i> [3]	CNN	Controlled lab	90–92	~89	Sensitive to lighting; limited robustness in field conditions
Liu <i>et al.</i> [5]	Explainable CNN	Mixed	~91	~90	Good texture extraction; weak spatial–structural pattern learning
Mahmud <i>et al.</i> [6]	Mobile CNN	Field	~90	~88	Performs poorly with overlapping or cluttered symptom regions
Xie <i>et al.</i> [28]	YOLOv8 Variant	Field + greenhouse	92–94	~92	Strong detection capability; weaker fine-grained classification
He <i>et al.</i> [11]	KTD-YOLOv8	Field	92	91	Misclassifies visually similar disease classes
Kim <i>et al.</i> [13]	Deep CNN	Controlled + semi-field	90–93	~89	Sensitive to noise, occlusion, and background artifacts
Ochoa-Ornelas <i>et al.</i> [14]	Lightweight deep learning	Field	87–90	~86	Fast inference; reduced accuracy in noisy outdoor conditions
Harandi <i>et al.</i> [15]	GNN (Phenotyping)	Controlled	~91	~90	Strong graph-based reasoning; limited validation on fruit crops
Partel <i>et al.</i> [16]	Hybrid Graph–CNN	Controlled	~92	~91	Limited generalization to real-field strawberry imagery
Proposed model	Hybrid GNN + MLP	Field + open-source	93.59	90.39	Best generalization; robust under noise, occlusion, and overlapping symptoms

Table 3. Comparative performance of models

Model	Accuracy (%)	Precision (%)	Recall (%)	F1-score (%)
SVM	87.02	85.63	84.72	85.10
RF	88.45	86.21	85.30	85.75
CNN	91.30	89.15	88.72	88.93
GNN–MLP (Proposed)	93.59	90.12	90.71	90.39

4.4. Explainability visualisations (XAI)

Explainability tools were used to verify that the model focus was sound. LIME and Grad-CAM visualisations are plotted together in Figure 5 to demonstrate that the model consistently identifies biologically meaningful lesion regions consistently. Such results validate that the model predictions are in accordance with observable outbreak distributions even under difficult field conditions. Figure 5 presents representative LIME-based saliency maps for the three strawberry disease classes. Figure 5(a) highlights the salient regions associated with grey mould, where the model primarily focuses on fungal texture. Figure 5(b) illustrates the regions contributing to the prediction of powdery mildew by emphasising the characteristic white powdery surface. Figure 5(c) identifies the salient regions corresponding to anthracnose fruit rot by localising the black lesion zones responsible for the disease prediction.

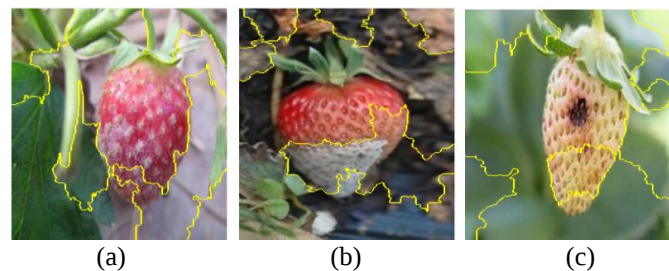


Figure 5. LIME-based saliency map visualisations for disease prediction (a) grey mould, (b) powdery mildew, and (c) anthracnose fruit rot

5. DISCUSSION

Results show that the hybrid GNN-MLP model outperforms the evaluated traditional machine-learning, CNN-based, and YOLO-based baselines. Its accuracy and macro-F1 score indicate that it can represent irregular spatial characteristics of strawberry disease symptoms that are difficult for grid-based CNNs to encode explicitly. Previous strawberry studies have shown that CNN-based systems can achieve strong detection performance [6], [12], [13], while YOLO-based detectors provide effective localisation [11], [28]. The proposed model extends these approaches by explicitly modelling lesion-to-lesion spatial relationships through graph reasoning. This design is consistent with graph-based learning studies that demonstrate the value of non-Euclidean representations for plant structures [9], [15], [27]. The stable 5-fold cross-validation performance also indicates good generalisation across data splits. Moreover, the LIME and Grad-CAM outputs highlight biologically relevant lesion areas that justify trustworthy by-design agricultural AI [17], [22].

There are various advantages of the proposed framework. First, the GNN ingredient model learns patterns of adjacency among lesions (i.e., lesion fragmentation and dynamic evolution) that single images cannot sufficiently encode, which CNNs fail to represent robustly. Second, the synthetic hyperspectral preprocessing enhances sensitivity to early biochemical changes, confirming results shown in previous hyperspectral and multispectral studies [2], [14], [15], [16]. Third, the MLP fusion head: the semantic images used for global semantic cues help to stabilise decision boundaries. Lastly, integrated XAI renders the predictions transparent and trustworthy, combating the interpretability gap observed in contemporary literature [5], [10], [17], [22]. The analysis has some limitations. The dataset does not include multi-year temporal variation that may be important for performance in extreme environmental conditions. Although synthetic hyperspectral simulation is sufficient, it's only an approximation of the real one. The model has not been evaluated in the presence of significant occlusions or complicated co-infection situations, which can affect its overall accuracy in real life. In the future, the system can be further developed by acquiring multi-season real-field data, adding actual multispectral or hyperspectral sensors, and considering disease severity estimation and temporal development modelling. Running the model on low-end edge devices and coupling it with IoT-based sensing systems, as investigated in related work [23], [24], may be another potential venue for real field use.

6. CONCLUSION

In this study, a hybrid GNN-MLP model combined with synthetic hyperspectral simulation and explainable AI was proposed to solve the issue of real-field position strawberry disease detection. The model achieved high accuracy, precision, recall, and macro-F1 performance, indicating strong generalisation to heterogeneous datasets. The enhancement-based, graph-based relational modelling and semantic fusion proposal network was able to accurately capture irregular lesion structures that traditional CNN/YOLO based

methods cannot cope with. The experimental results demonstrate the stability and competitiveness of our method by 5-fold cross-validation as compared with those of classical machine-learning methods, lightweight CNN models, transformer-based models, and classic GNN variants. Such interpretability was reinforced by the addition of LIME and Grad-CAM, which consistently showed biologically meaningful symptom regions and would support adoption in a smart-farming environment.

This technique, however, still has limitations. The absence of data with multi-season variation in the dataset and the use of synthetic simulated hyperspectral images are still approximations of real spectral imaging. The potential role of extreme occlusion, co-infection, and environmental stress is a matter for further investigation. In the future, the dataset will be expanded with field samples across a multi-season and/or multi-region range by integrating real multispectral or hyperspectral sensors, advancing it to disease-severity estimation, and deploying on edge devices for real-time monitoring. Finally, the demonstrated system offers a stable, interpretable, and computationally affordable method for practical strawberry disease detection in precision agriculture.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognise individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C : Conceptualization

M : Methodology

So : Software

Va : Validation

Fo : Formal analysis

I : Investigation

R : Resources

D : Data Curation

O : Writing - Original Draft

E : Writing - Review & Editing

Vi : Visualization

Su : Supervision

P : Project administration

Fu : Funding acquisition

CONFLICT OF INTEREST STATEMENT

The authors declare that they have no conflict of interest.

DATA AVAILABILITY

The datasets used in this study are available upon reasonable request from the corresponding author.

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