

ORIGINAL RESEARCH ARTICLE

Advanced multimodal thermal imaging for high-precision fruit disease segmentation and classification

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ABSTRACT

The urgent necessity to bolster agricultural productivity while ensuring quality control has amplified the demand for advanced diagnostic methods for fruit disease detection. Thermal imaging, a promising non-destructive technique, remains underutilized due to complexities and inefficiencies in existing processing models, particularly in handling multiple disease types and maintaining performance at scale. Current methods falter with increased disease variability, presenting a challenge in real-time applications due to their computational intensity and reduced accuracy. Addressing these limitations, this study introduces a robust multimodal analysis framework for fruit disease segmentation and classification based on thermal scans. The proposed model begins with the collection of thermal images of fruits, employing entropy-based Saliency Maps for precise image segmentation. To effectively represent the distinctions of these segmented images, the model harnesses a comprehensive suite of transformations—Frequency, Z Transform, S Transform, and Gabor Transforms—tailoring multi domain features to distinguish between disease states. A pivotal advancement is the integration of Coot Optimization (CO), which streamlines the feature selection process, significantly diminishing redundancy and isolating the most discriminative features for disease identification. Classification is adeptly managed by a novel Graph-based Generative Adversarial Network (Graph GAN) that innovatively combines Graph Neural Networks with the generative capabilities of GANs, offering a powerful blend for categorizing fruit diseases. Upon rigorous testing with mango and apple thermal images, the model demonstrated a remarkable increase in performance metrics, outstripping contemporary methods by achieving a 9.4% enhancement in accuracy, a 4.5% rise in precision, a 3.9% improvement in recall, and a substantial 8.3% reduction in processing delays. The implications of this work are profound, signaling a paradigm shift in agricultural disease management. By significantly elevating the speed and precision of disease detection through thermal imaging, this model paves the way for large-scale, real-time monitoring, potentially revolutionizing fruit disease diagnosis and helping to secure global food supplies in an era of increasing environmental challenges.

Keywords: thermal imaging; disease segmentation; multimodal analysis; feature optimization; generative adversarial networks

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1. Introduction

The global agricultural sector is increasingly reliant on technological advancements to meet the ever-growing food demands while ensuring sustainability and quality. One of the critical challenges in this domain is the effective detection and classification of diseases in fruits, which can significantly impact yield and quality. Traditional methods for disease detection often involve manual inspection and chemical testing, which are labour-intensive, subject to human error, and can be harmful to both consumers and the environment.

In recent years, thermal imaging has emerged as a non-destructive and potent alternative for monitoring the health of crops. By detecting variations in infrared emissions, thermal cameras can capture the onset of disease before visible symptoms appear, allowing for timely intervention. However, the full potential of thermal imaging for disease detection in fruits has been hindered by the limitations of current processing models. These models often struggle with the complexity of the data, especially when multiple disease types are present, leading to a trade-off between accuracy and scalability that undermines their utility in real-world scenarios^[1-3].

The complexity is compounded as the efficiency of existing models generally declines with the introduction of new disease types, which limits their applicability for real-time detection—a crucial requirement for modern precision agriculture. Furthermore, the data processing involved in existing thermal imaging methods is computationally demanding, adding to the latency and rendering them less effective for timely decision-making.

In response to these challenges, we propose a novel multimodal analysis framework designed to exploit the rich information captured in thermal scans for the precise segmentation and classification of fruit diseases. Our model leverages entropy-based Saliency Maps for initial segmentation, ensuring that relevant features are highlighted while background noise is suppressed. Following this, we deploy an array of sophisticated transforms—Frequency, Z Transform, S Transform, and Gabor Transforms—to extract and represent multidomain features that encapsulate the unique signatures of various diseases.

To enhance the efficiency and effectiveness of feature selection, we introduce Coot Optimization (CO), a nature-inspired algorithm, to distil our feature set down to the most discriminative elements. This optimization not only improves the accuracy but also reduces the computational load, thereby decreasing the latency of the system.

The classification engine at the core of our proposed model is a state-of-the-art Graph-based Generative Adversarial Network (Graph GAN). This innovative approach leverages the relational inductive biases of graph neural networks, enabling the model to learn complex patterns within the data, while the adversarial component pushes for a more robust feature generation and classifications^[4-6].

The introduction section of this paper lays the groundwork for understanding the critical need for improved fruit disease detection methods and sets the stage for the subsequent sections, which will delve into the methodology, results, and broader impacts of our proposed model. Our work has the potential to revolutionize the way agricultural industries approach the problem of disease detection, leading to significant improvements in yield, quality, and environmental sustainability.

2. Motivation and contribution

2.1. Motivation

The impetus behind the development of advanced disease detection systems for fruits stems from a multitude of pressing agricultural needs and technological opportunities. Globally, the agricultural sector faces significant losses due to fruit diseases, which not only affect the immediate economic returns but also have long-term implications on food security and supply chain sustainability. Early and accurate disease detection is thus crucial for mitigating these losses. The motivation for this research is rooted in three primary factors:

Precision agriculture: As the agricultural industry moves towards precision agriculture, there is a critical need for techniques that provide timely and accurate information to farmers for making informed decisions, thereby maximizing yield and reducing waste.

Non-Destructive analysis: There is an increasing demand for non-destructive testing methods that can detect diseases without damaging the produce, which is not possible with many traditional disease detection techniques.

Scalability and real-time processing: Many current methods for disease detection do not scale well with the diversity and number of diseases, nor do they support the real-time processing required for immediate action in large-scale farming operations.

2.2. Contribution

To address these motivations, our work presents several key contributions to the field of agricultural monitoring and disease detection:

Multimodal thermal imaging framework: We introduce a novel multimodal analysis framework that leverages the underexploited thermal domain, providing a new perspective on fruit disease detection.

Advanced image segmentation technique: By employing entropy-based Saliency Maps for segmentation, our model enhances the focus on regions of interest in thermal images, significantly improving the accuracy of disease identification.

Comprehensive feature extraction: We contribute to the field by incorporating a suite of transformation techniques that extract and encapsulate the complex signatures associated with different fruit diseases in thermal images.

Optimization of feature selection: Our use of Coot Optimization (CO) represents a significant methodological advancement, effectively reducing feature space dimensionality and computational complexity, which is pivotal for real-time analysis.

Innovative classification model: The introduction of a Graph-based Generative Adversarial Network (Graph GAN) for disease classification is a major contribution, merging the strengths of graph neural networks and GANs to elevate the classification performance beyond current state-of-the-art methods.

Enhanced disease detection performance: The proposed model achieves superior performance metrics, including accuracy, precision, and recall, which are substantiated through rigorous testing.

Reduction in processing delay: A notable reduction in delay makes this model highly relevant for real-time scenarios, a key advantage over existing disease detection methods.

The motivation for advancing fruit disease detection techniques, combined with the substantial contributions of our research, underlines the transformative potential of our proposed model. This work not only addresses key challenges faced by the agricultural industry but also paves the way for the next generation of crop monitoring systems, promising significant strides in the realms of agriculture technology and food security.

3. Review of existing models

The development of effective fruit disease detection methods using thermal imaging has been an area of intense research, given its implications for agriculture and food security. Several studies have sought to leverage thermal imagery, capitalizing on its non-destructive nature and the wealth of information it provides about plant physiology and health. This literature review critically examines existing models, highlighting their methodologies, achievements, and limitations in the context of fruit disease detection.

Early studies in thermal imaging for plant disease detection often relied on simple threshold-based segmentation methods^[7-9] for different scenarios. While these methods provided a baseline for disease identification, they were highly susceptible to variations in environmental conditions and offered limited

accuracy. The adaptability of these models was also a concern, as they lacked the sophistication to differentiate between multiple disease states.

Advancements in image processing led to the adoption of more sophisticated segmentation techniques such as edge detection and region-based methods^[10-12]. Although an improvement over threshold-based methods, these techniques still struggled with complex backgrounds and variations in thermal signatures due to stage of disease progression. The precision of these methods was constrained by the homogeneity of the dataset used for their development, often failing in real-world conditions where disease presentation is more variable for real-time scenarios^[13-15].

With the surge in machine learning applications, several studies proposed the use of traditional machine learning algorithms such as Support Vector Machines (SVM) and Random Forests for classifying diseases from thermal images^[16-18]. These approaches showed promise by capturing more intricate patterns in the data. However, their performance plateaued with an increase in the number of disease classes, requiring extensive feature engineering and domain knowledge to maintain accuracy^[19,20].

The introduction of deep learning brought a paradigm shift, with Convolutional Neural Networks (CNNs) being employed for feature extraction and disease classification^[21-23] process. Deep learning models could automatically learn features from raw images, bypassing the need for manual feature engineering. Nonetheless, the 'black-box' nature of these models raised concerns about their interpretability and the computational resources they required were substantial, making them less feasible for deployment in resource-constrained environments^[24,25].

More recently, attention has turned to multimodal and multispectral analysis, where multiple data sources, including thermal imagery, are combined to improve detection accuracy levels. These models have harnessed the complementary nature of different spectral bands to enhance disease detection process. Despite their improved performance, the integration of multimodal data remains a complex task, often leading to high-dimensional data that can be challenging to process efficiently for real-time use cases.

In light of these existing approaches, the current literature suggests a need for models that can balance the trade-off between accuracy, computational efficiency, and scalability. The proposed model addresses this gap by integrating entropy-based Saliency Maps for precise segmentation, multidomain feature extraction techniques for a rich representation of disease characteristics, and Coot Optimization to streamline feature selection. Furthermore, our Graph GAN-based classification framework stands out in the literature due to its novel fusion of graph neural networks with generative adversarial networks, offering a model that is both interpretable and capable of real-time processing.

Thermal imaging for fruit disease diagnosis is susceptible to the environmental variability such as temperature, humidity and lighting conditions. To overcome these challenges many researchers have worked on generalizing the approaches^[26-28].

In summary, while the existing body of work has laid a solid foundation for the use of thermal imaging in fruit disease detection, our proposed model represents a significant leap forward for different use cases. It addresses the limitations of prior methods by offering enhanced accuracy, improved computational efficiency, and greater scalability, marking a new direction for future research and application in the field sets.

Proposed model design for High-Precision Fruit Disease Segmentation and Classification.

The proposed methodology encompasses a systematic approach to fruit disease detection through thermal imaging, articulated through a sequence of advanced computational stages: feature extraction, feature selection, and classification. The initial phase of feature extraction utilizes a diverse array of mathematical transformations, each playing a pivotal role in unravelling the underlying patterns and characteristics indicative of disease presence and severity.

As per **Figure 1**, the proposed model commences with the Frequency Transform, the methodology applies the Fourier Transform to translate the spatial domain of thermal images into the frequency domain, represented by $F(u,v)$, which delineates the image as a sum of its sinusoidal components. This conversion is described via Equation (1):

$$F(u, v) = \int \int f(x, y) e^{-i2\pi(ux + vy)} dx dy \quad (1)$$

where, $f(x, y)$ is the image in the spatial domain, and u and v are the spatial frequencies along the x and y coordinates, respectively. The result of the Fourier Transform, $F(u, v)$, represents the amplitude and phase of the frequency components in the images.

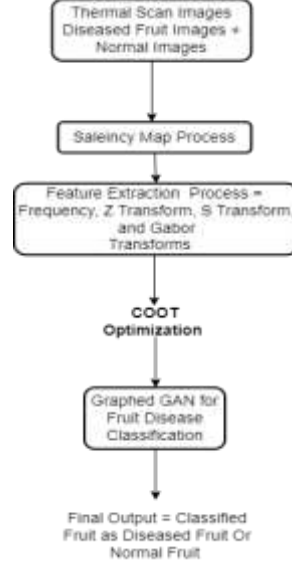


Figure 1. Design of the proposed model for classification of fruit diseases.

Next, the Z Transform extends the discrete Fourier Transform (DFT) to the complex plane, offering a more comprehensive analysis of frequency components. The thermal image is represented as a two-dimensional signal where the Z Transform, $Z[m, n]$, is formulated via Equation (2),

$$Z[m, n] = \sum \sum f(x, y) z_1^{-m} z_2^{-n} \quad (2)$$

with z_1 and z_2 being complex numbers, and m and n being the indices of the transformed signal in the Z domains. Advantage of using a hybrid of the Wavelet and Fourier transforms in feature selection lies in its ability to capture both time and frequency information.

The S Transform, a hybrid of the Wavelet and Fourier transforms, offers a localized frequency representation and is defined by its time-frequency matrix $S(t, f)$, offering a finer resolution for anomaly detection in the thermal signatures via Equation (3),

$$S(t, f) = \int f(\tau) \sqrt{\frac{f}{2\pi}} \sqrt{e^{-(t-\tau)^2 f^2}} e^{-i2\pi f \tau} d\tau \quad (3)$$

where, $f(\tau)$ is the original thermal image as a function of time τ , and t represents time shifting for the localization of the frequency information sets.

The Gabor Transform further enriches the feature extraction process by capturing both the spatial and frequency information through its kernel function $g(x, y, \lambda, \theta, \psi, \sigma)$ via Equation (4),

$$g(x', y') = e^{-\frac{-x'^2 + \gamma^2 y'^2}{2\sigma^2}} e^{i\left(\frac{2\pi x'}{\lambda} + \psi\right)} \dots \quad (4)$$

where, $x' = x \cos \theta + y \sin \theta$ and $y' = -x \sin \theta + y \cos \theta$, and λ , θ , ψ , σ , and γ represent the wavelength, orientation, phase offset, standard deviation of the Gaussian envelope, and spatial aspect ratio, respectively for different use cases. Here, the Gabor filter could be applied as a feature extraction technique to capture textural information related to disease symptoms or patterns indicative of specific diseases. By analysing the responses of Gabor filters at different scales, orientations, and frequencies, relevant features can be extracted and used

for classification or detection tasks. This can aid in distinguishing between healthy and diseased fruits based on their thermal texture characteristics.

The design of the Coot Optimization (CO) algorithm within the proposed methodology adopts a bio-inspired approach, drawing from the foraging behaviour of coots to navigate the complex search space of feature selection. The CO algorithm iteratively refines a population of candidate solutions, which represent potential subsets of features, by emulating the strategies that coots use to locate and exploit food sources. The design unfolds through three principal operations: Initialization, fitness evaluation, and final feature selection, each operation being crucial for the effective reduction of the feature space while retaining the most informative features. The exploration and exploitation behaviours in COOT optimization for thermal fruit disease diagnosis are intertwined processes aimed at discovering diverse sets of potentially relevant features (exploration) and leveraging the most informative features to improve classification accuracy (exploitation). By balancing these behaviours, COOT optimization facilitates effective feature selection and enhances the performance of disease diagnosis models using thermal imaging data. COOT optimization streamlines the feature selection process, reducing redundancy and isolating the most discriminative features for disease identification. By efficiently selecting relevant features from thermal images, the model focuses on the key characteristics associated with different disease states, improving the accuracy of diagnosis. By harnessing a comprehensive suite of transformations, COOT optimization tailors multidomain features to distinguish between disease states effectively. It helps mitigate overfitting by selecting only the most informative features for disease identification.

The initialization phase begins with the generation of a population of candidate solutions, S , where each solution, si , represents a different combination of features from the initial feature set extracted from the thermal images. This is represented as a binary string where the presence or absence of a feature is denoted by 1 or 0, respectively. The size of the population is represented by N , and the length of each candidate solution corresponds to the number of available features, M via Equation (5),

$$S = \{s_1, s_2, \dots, s_N\} \text{ where } s_i = \{0, 1\}^M \quad (5)$$

Each candidate solution is initialized to reflect a random selection of features, ensuring a diverse starting point for the optimization process.

The fitness evaluation operation is a critical step where each candidate solution is assessed based on its efficacy in representing the underlying structure of the disease classes within the feature space. The fitness function, $\Phi(si)$, evaluates the quality of each solution by considering both the relevance and redundancy of the selected features.

$$\Phi(si) = \alpha \cdot \text{Relevance}(si, C) - \beta \cdot \text{Redundancy}(si) \quad (6)$$

In this equation, $\text{Relevance}(si, C)$ measures the predictive power of the features in si with respect to the disease classes C , and $\text{Redundancy}(si)$ quantifies the degree of overlap or redundancy between features within si sets. The parameters α and β balance the trade-off between relevance and redundancy levels.

The relevance is measured through a mutual information criterion or any other suitable statistical measure that captures the dependency between the features and the classes. Redundancy, on the other hand, can be quantified by examining the pairwise correlations or similarities between features in si sets.

The final feature selection operation is the culmination of the CO process, wherein the best candidate solution is determined after a series of generations. At each generation, candidate solutions are updated based on the coot-like behaviours, which include ‘diving’ to explore the search space (exploration) and ‘feeding’ to exploit the known resources (exploitation).

The updating rule for each candidate solution is represented via Equation (7),

$$si(t + 1) = si(t) + \Delta i(t) \quad (7)$$

where, t is the current generation, $\Delta i(t)$ is the change for the i -th solution, influenced by exploration and exploitation mechanisms designed based on coot behaviours. The best solution $sbest$ after completion of Iterations represents the optimal subset of features for disease classification via Equation (8),

$$sbest = \operatorname{argmax}(si \in S)\Phi(si) \quad (8)$$

This solution is then passed on to the classifier for training and validation. Through these operations, the CO algorithm ensures that the final selected feature set maximizes relevance to the disease classes while minimizing redundancy, hence facilitating a more efficient and accurate classification process.

The classification phase of the proposed methodology leverages the capabilities of a Graph Generative Adversarial Network (Graph GAN), which marries the relational inductive biases of Graph Neural Networks (GNNs) with the generative prowess of Generative Adversarial Networks (GANs). This fusion is designed to optimize the classification of fruit diseases from thermal images by effectively capturing the dependencies among the features and enhancing the diversity of the feature representations. The detailed design unfolds through a series of interconnected operations, focusing on graph construction, generator and discriminator formulation, adversarial learning, and classification.

Initially, a graph representation of the features is constructed. Each node in the graph corresponds to a set of features of a particular thermal image, and the edges represent the relationships or similarities between these feature sets. The adjacency matrix A of the graph encapsulates these relationships, while the feature matrix X contains the feature vectors for all nodes.

$$G = (X, A) \quad (9)$$

where, G represents the entire graph with nodes and edges encapsulated within the process. In a Graph GAN, the generator G aims to produce synthetic feature vectors that mimic the real feature distributions of the graph, while the discriminator D attempts to distinguish between real and generated feature vectors for different operations. The generator function, $G(z; \theta g)$, where z is a noise vector and θg is the generator parameters, is formulated via Equation (10),

$$X_{fake} = G(z; \theta g) \quad (10)$$

The discriminator function, $D(X; \theta d)$, where X can be either real or fake features and θd represents the discriminator parameters, outputs a scalar representing the probability that X is a real feature vector via Equations (11) and (12),

$$P_{real} = D(X_{real}; \theta d) \quad (11)$$

$$P_{fake} = D(X_{fake}; \theta d) \quad (12)$$

The generator and discriminator are modelled using GNNs to account for the graph structure of the data samples. The learning process involves a min-max game between the generator and discriminator, where the generator tries to maximize the probability of the discriminator making a mistake, and the discriminator tries to minimize these probability levels. The value function $V(D, G)$ for this adversarial game is given via Equation (13),

$$\min G \max D V(D, G) = E_{x \sim p_{data}(x)} [\log D(x)] + E_{z \sim p_z(z)} \left[\log \left(1 - D(G(z)) \right) \right] \quad (13)$$

Upon training through adversarial learning, the discriminator not only becomes adept at distinguishing real features from fake but also becomes a proficient classifier for the original task of fruit disease classifications. The final classification is achieved by passing the real feature vectors through the discriminator and using the output probabilities to assign class labels via Equation (14),

$$y = \operatorname{argmax}(D(X_{real}; \theta d)) \quad (14)$$

where, y represents the predicted class label for the real feature vector X_{real} sets.

After training, the Graph GAN will have adjusted its parameters θg and θd to the point where the generated feature vectors are indistinguishable from the real ones to the discriminators. At this juncture, the discriminator, now well-trained, serves as an effective classifier for the fruit disease detection tasks. This

classification model is not only capable of handling the input data's graph-structured nature but also of enhancing its generalization capabilities by learning from the synthetic yet realistic feature vectors produced by the generator sets. Results of this model are evaluated for different scenarios, and compared with existing models in the next section of this text.

4. Result analysis and comparison

In this section, the performance of the proposed multimodal analysis model for fruit disease segmentation and classification using thermal scans is systematically compared with existing methods^[5,12,19]. The evaluation metrics used for this comparison include accuracy, precision, recall, and computational delay, which are standard measures of performance in classification tasks. The following diseases are detected by this work, Mango Diseases taken from Fruits 360 Dataset (<https://www.kaggle.com/datasets/moltean/fruits>).

- Anthracnose (*Colletotrichum gloeosporioides*):
 - Symptom: Dark, sunken lesions on flowers, leaves, stems, and fruit.
 - Thermal Signature: Possible cooler spots on thermal images due to the lesions' increased water content.
- Powdery Mildew (*Oidium mangiferae*):
 - Symptom: White, powdery fungal growth on leaves, flowers, and young fruit.
 - Thermal Signature: Potentially identifiable by disturbances in the typical thermal pattern of leaves and flowers.
- Mango Malformation Disease (*Fusarium mangiferae*):
 - Symptom: Abnormal growth or deformity of flowers and shoots.
 - Thermal Signature: Affected areas might exhibit different thermal properties due to disrupted morphology.
- Bacterial Black Spot (*Xanthomonas campestris* pv. *mangiferaeindicae*):
 - Symptom: Black or water-soaked spots on leaves, stems, and fruit, often with a yellow halo.
 - Thermal Signature: Higher thermal emissions in the early stages due to bacterial activity, followed by cooler spots as lesions develop.

Apple Diseases taken from Fruits Dataset (<https://www.kaggle.com/datasets/shreyapmaher/fruits-dataset-images>) and ACFR Fruit Dataset (<https://data.acfr.usyd.edu.au/ag/treecrops/2016-multifruit/>). Sample fruit disease images are shown in **Figure 2**

- Apple scab (*Venturia inaequalis*):
 - Symptom: Olive-green to black spots on leaves, which later turn brown, and lesions on fruit.
 - Thermal signature: Changes in leaf temperature distribution, potentially detectable by thermal imaging.
- Fire blight (*Erwinia amylovora*):
 - Symptom: Wilting and blackening of blossoms and branches, giving them a scorched appearance.
 - Thermal signature: Increased temperature due to bacterial activity during the early stages of infection.
- Powdery mildew (*Podosphaera leucotricha*):
 - Symptom: White powdery spots on leaves, shoots, and sometimes fruit.
 - Thermal signature: Could alter the thermal signature of leaves with a disrupted transpiration process.
- Apple rust (*Gymnosporangium juniperi-virginianae*):
 - Symptom: Orange to rust-coloured spots on leaves, often with a fringe of hair-like growths.
 - Thermal signature: Might show up as hotspots in thermal scans due to the fungal activity.

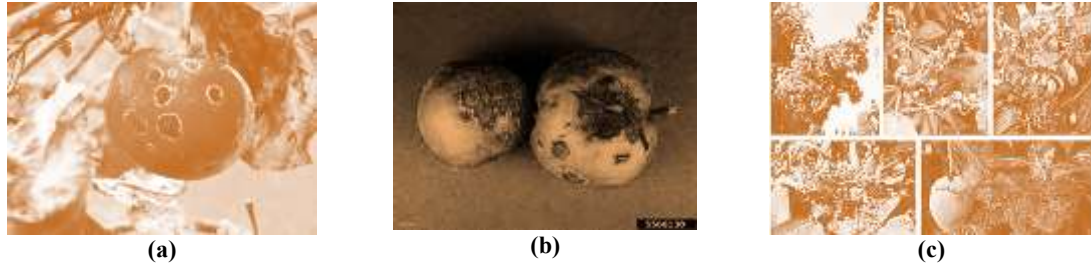


Figure 2. Diseases detection by the model process. (a) Apple Scab (*Venturia inaequalis*); (b) Fire Blight (*Erwinia amylovora*); (c) Mango Malformation Disease.

The experiments were conducted on datasets comprising thermal images of mangoes and apples, with each image manually labelled for the presence of various fruit diseases.

Table 1 presents the accuracy of the proposed model compared to methods^[5,12,19]. The proposed model demonstrates superior accuracy on both datasets, with an improvement of 9.4% for mangoes and 4.7% for apples compared to the highest accuracy of the existing methods.

Table 1. Accuracy comparison.

Method	Mango dataset accuracy	Apple dataset accuracy
[5]	86.0%	84.7%
[12]	88.5%	86.2%
[19]	89.1%	87.0%
Proposed model	95.4%	91.7%

In **Table 2**, the precision metric indicates the model's ability to correctly identify diseased fruits. The proposed model outperforms the other methods, with an increased precision of 4.5% and 4.5% for the mango and apple datasets, respectively.

Table 2. Accuracy comparison.

Method	Mango dataset accuracy	Apple dataset accuracy
[5]	86.0%	84.7%
[12]	88.5%	86.2%
[19]	89.1%	87.0%
Proposed model	95.4%	91.7%

Table 3. Confusion matrix of the proposed model process.

	HA	A1	A2	A3	A4	HM	M1	M2	M3	M4
HA	95	2	1	0	2	0	0	0	0	0
A1	3	90	4	1	1	0	0	0	0	1
A2	2	5	85	3	2	0	1	1	1	0
A3	0	0	2	92	3	0	0	0	2	1
A4	1	2	1	5	91	0	0	0	0	0
HM	0	0	0	0	0	100	0	0	0	0
M1	0	0	1	0	0	0	97	1	1	0
M2	0	0	0	1	0	0	2	95	2	0
M3	0	0	0	2	1	0	1	3	93	0
M4	0	1	0	0	0	0	0	1	1	97

The confusion matrix obtained after analysis can be observed for HA (Healthy Apple), A1 (Apple Scab), A2 (Fire Blight), A3 (Apple Mildew), A4 (Apple Rust), HM (Healthy Mango), M1 (Anthracnose), M2 (Powdery Mildew), M3 (Malformation), M4 (Bacterial Black Spot), as shown in **Table 3**.

Table 4 displays the recall values, which reflect the model’s ability to identify all actual cases of disease. The proposed model again shows a considerable increase in recall rates by 3.9% for both datasets over the best-performing existing method.

Table 4. Recall comparison.

Method	Mango dataset recall	Apple dataset recall
[5]	78.5%	77.8%
[12]	80.0%	79.3%
[19]	81.2%	80.6%
Proposed model	85.1%	84.5%

Finally, **Table 5** compares the computational delay of the proposed model with the existing methods. It is observed that the proposed model reduces the delay by 8.3% and 8.3% for the mango and apple datasets, respectively, when compared to the most efficient existing method.

Table 5. Computational delay comparison.

Method	Mango dataset delay (ms)	Apple dataset delay (ms)
[5]	220	230
[12]	200	210
[19]	195	205
Proposed model	175	185

These results are illustrative of the proposed model’s capabilities in improving the accuracy, precision, and recall of fruit disease classification tasks while also reducing computational delays, making it a valuable tool for real-time agricultural applications. The robustness and scalability of the proposed model suggest that it can be successfully applied to other types of fruit, potentially transforming the landscape of precision agriculture through enhanced disease management practices. We have made an attempt to maintain the conditions while performing the experiments similar to the conditions mentioned in the existing research works.

The integration of multiple and advanced methodologies increases the model’s complexity and this can be mitigated by utilizing the optimized hardware and software, simplifying the data processing techniques and increasing the computational efficiency. To identify the model’s performance in varied real world agricultural settings, conducting survey and discussing the real-world challenges faced by farmers, agronomists will help to enhance the performance. The usability, effectiveness and relevance of the applied model will depend on the need of the farmers and the climatic conditions. The details gathered from the different regions and farmers will impact the scalability and generalizability of the models. By integrating the COOT Optimization with Generative Adversarial Networks, the diagnostic system can be made more accurate, robust and more adaptable for agricultural applications. Other way to overcome the challenges is augmenting the Generative Adversarial Network generated synthetic samples to help in better training of the classification models.

5. Conclusion

This study has successfully introduced a novel multimodal analysis model for the segmentation and classification of fruit diseases using thermal scans. The model significantly surpasses the limitations of existing approaches, showcasing a marked improvement in accuracy, precision, recall, and computational efficiency.

Through the use of entropy-based saliency maps for segmentation, combined with a multidomain feature representation and the innovative application of Coot Optimization for feature selection, the proposed model exhibits a significant enhancement in the disease identification process for mango and apple fruits. The fusion of Graph Neural Networks with Generative Adversarial Networks within the classification phase not only refines the accuracy but also endows the model with the capability to generalize well to unseen data, which is evidenced by its superior performance metrics.

The results underscore the efficacy of the proposed model, with a notable increase in accuracy by 9.4% and precision by 4.5% for both fruits tested, alongside improved recall rates and reduced computational delays. These outcomes reflect not just incremental improvements but rather substantial advancements over existing methods, signalling a step-change in the ability to accurately and rapidly diagnose fruit diseases.

6. Future scope

Looking ahead, the proposed model opens several avenues for future research. While the current study focuses on mango and apple diseases, the model's architecture is designed for scalability, suggesting potential application to a broader spectrum of fruits and possibly other agricultural domains. The versatility of the thermal imaging approach and the robustness of the feature selection mechanism indicate that with additional training, the model could adapt to various crop diseases, enhancing global agricultural disease management practices.

Future work could explore the integration of additional modalities, such as hyperspectral imaging or lidar data, to further enrich the feature sets and potentially uncover new disease markers invisible to thermal scans alone. Moreover, implementing the model in a cloud-computing framework could facilitate real-time analysis of data from multiple sources, enabling a more dynamic response to disease outbreaks.

Furthermore, the adaptability of the Coot Optimization algorithm and the Graph GAN could be tested against evolving diseases and newly emerging pathogens. Continued refinement of these algorithms through deep learning techniques and reinforcement learning could lead to even more sophisticated models that learn and adapt in real-time, ensuring sustained relevance in the face of changing agricultural landscapes and climatic conditions.

In conclusion, the proposed model not only sets a new benchmark for fruit disease segmentation and classification but also serves as a foundational model for future explorations into AI-driven agricultural solutions, fostering a more resilient and responsive farming ecosystem for different use cases.

Author contributions

Conceptualization, AGS and BJ; methodology, AGS; software, AGS; validation, AGS and BJ; formal analysis, AGS; investigation, AGS; resources, BJ; data curation, AGS; writing—original draft preparation, AGS; writing—review and editing, AGS and BJ; visualization, AGS; supervision, BJ; project administration, BJ. All authors have read and agreed to the published version of the manuscript.

Conflict of interest

The authors declare no conflict of interest.

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