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Tomato leaf disease detection and management using VARMAx-CNN-GAN integration

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ABSTRACT

In contemporary agriculture, farmers confront substantial challenges in maintaining crop yields and mitigating agricultural losses attributable to diseases. The existing methods for diagnosing and managing tomato leaf diseases often exhibit deficiencies in terms of accuracy, robustness, and interpretability. Typically, these methods are reactive, addressing symptoms after the disease has already impacted the plants, resulting in delayed and often ineffective interventions. The precision of disease localization and severity estimation plays a crucial role in efficient disease treatment; regrettably, existing post-processing techniques frequently fall short in this regard. While these methods have their flaws, our proposed method uses the best parts of deep learning and vector autoregressive moving average processes with eXogenous regressors (VARMAx processes) to quickly and accurately find tomato leaf diseases. Our approach represents an innovative solution to the challenges currently confronting the agriculture sector, thanks to its proactive attributes, improved categorization capabilities, and advanced post-processing stages. Convolutional neural networks (CNNs) and generative adversarial networks (GANs), built upon the "VARMAx-CNN-GAN Integration" framework, form the core of our method. In this integrated model, convolutional neural networks serve the purpose of extracting features and performing early disease classification, whereas generative adversarial networks come into play for generating synthetic images, expanding the dataset, and enhancing the model's ability to generalize. The "VARMAx-CNN-GAN Integration" model improves disease classification and decision-making for farmers and agronomists by providing insights into critical leaf images. Compared to traditional methods, it improves precision, accuracy, recall, AUC, and delay in identifying tomato diseases. The approach also shows potential for disease prevention, revolutionizing tomato leaf disease identification and management.

1. Introduction

Tomatoes are a vital global crop, crucial for food security, but various leaf diseases threaten their productivity. Traditional detection methods lack accuracy and timeliness, leading to significant crop and economic losses. Current approaches are reactive and often misdiagnose diseases due to reliance on visible symptoms. Deep learning models like the Modified-Xception-based Multi-Level Feature Fusion (MXF) can address these issues. Deploying such models on resource-constrained agricultural devices presents challenges like limited processing power and memory. However, optimization techniques, hardware acceleration, and efficient inference strategies can make deployment feasible. Memory management through model caching and compression, and energy-efficient strategies can further improve performance. A federated learning framework can facilitate collaborative training, maintaining data localization and privacy. Traditional post-processing in disease detection lacks precision and interpretability, hindering effective disease management. Our research integrates IoT, deep learning, and "VARMAx-CNN-GAN Integration" mechanisms for early detection and management of tomato leaf diseases. This approach uses a fusion of CNNs, GANs, and autoencoders for accurate disease classification and saliency mapping for better disease localization and severity estimation. Extensive experiments show the model's effectiveness over existing methods.

The paper includes a literature review, methodology, experimental setup, results, comparative analysis, and concludes with implications for enhancing agricultural practices and reducing tomato leaf disease losses.

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2. Literature review

The detection and management of tomato leaf diseases have been extensively researched, utilizing methods ranging from traditional visual inspection to advanced machine learning models. Historically, visual inspection by trained agronomists and farmers has been the primary method, relying on physical symptoms of plants (Nandhini and Ashokkumar, 2021; Thanammal et al., 2022; Huang et al., 2023; Moussafir et al., 2022). While simple and equipment-free, this approach is often subjective, time-consuming, and inaccurate, especially in early disease stages (Gurubelli et al., 2022; Nawaz et al., 2022; Vengaiah and Konda, 2023; Hanamasagar et al., 2021). Spectral analysis techniques have improved detection accuracy and timeliness by leveraging light properties reflected or transmitted by leaves (Lee et al., 2022; Thangaraj et al., 2021,2023; Djimeli-Tsajio et al., 2022). However, these require expensive, specialized equipment, limiting their use in resource-limited settings (Wang et al., 2021; Novak et al., 2021; Guo et al., 2023; Gadekallu et al., 2021).

Traditional machine learning models like Support Vector Machines, Decision Trees, Random Forests, and k-Nearest Neighbors have also been applied to detect diseases (Martins et al., 2021; Balafas et al., 2023; Lobin et al., 2022; Ahmed et al., 2021,2023). Despite their advancements, these models struggle with the variability and complexity of disease symptoms (Sahu et al., 2023; Sunil et al., 2023; Kaur et al., 2023; Al Hashimi et al., 2022; Hosny et al., 2023).Deep learning models, particularly CNNs like Multivariate Normal Deep Learning Neural Network (MNDLNN), have been employed to address these limitations, enhancing classification accuracy by learning intricate patterns from images (Bora et al., 2023; Gajjar et al., 2022; Vengaiah and Konda, 2023; Mondal et al., 2022; Joseph, et al., 2024). However, these models require large datasets and may struggle with generalizing to new disease variants, as well as with interpretability issues (Kurmi et al., 2021; Moupojou et al., 2023; Garg and Singh, 2023; Liu and Wang, 2020. Table 1 describes the review of existing models used to estimate the tomato leaf diseases.

Preemptive disease detection systems use weather, soil, and historical data to predict potential disease outbreaks. However, data availability and quality can limit these models, and they may struggle with real-world variability. Validation on a dataset involving diverse conditions, tomato varieties, and disease types shows precision, accuracy, recall, and specificity values. Current methods for diagnosing and managing tomato leaf diseases have shortcomings, including accuracy, robustness, and interpretability. Post-processing methods often fail to meet the need for accurate disease detection. Some of the more advanced systems integrate IoT devices with machine learning models for continuous monitoring and disease detection. These systems, along with (Chavan and Balani, 2022; Balani et al., 2022; Vengaiah and Konda, 2024) can provide real-time alerts and recommendations for disease management, enhancing the timeliness of interventions. However, existing models can be complex to set up and maintain, particularly in large-scale farming operations.

3. Proposed model

After conducting an extensive review of existing models for tomato leaf disease identification, we discovered that their efficiency diminishes when applied to multiple datasets, and their complexity further constrains their scalability levels. To overcome these issues, this section discusses the design of a "VARMAx-CNN-GAN Integration" for early detection and management of tomato leaf diseases. As shown in Fig. 1, the proposed model integrates CNNs for feature extraction and initial disease classification with GANs for generating synthetic images,

Table 1
Review of existing models used to estimate tomato leaf diseases.

Method	Findings	Limitations	Research Gaps
SVM (Aishwarya et al., 2023)	High accuracy in classifying tomato diseases.	Limited by feature extraction and training data.	Kernel selection and adaptation to large datasets.
CNN (Russel and Selvaraj, 2022)	Exceptional feature learning.	Need significant computational resources and data.	Transfer learning potential and architecture optimization.
RF (Zhang and Chen, 2023)	Robust against noisy datasets.	Struggles with imbalanced datasets and interpretability.	Parameter tuning and addressing class imbalance.
DT (Bhagat and Kumar, 2023)	Simple and interpretable.	Prone to overfitting and instability.	Ensemble methods for stability and generalization.
KNN (Uppada and Kumar, 2023)	Effective proximity-based grouping.	Performance drops with high-dimensional data.	Tailored distance metrics and handling high-dimensional data.
NB (Zhou et al., 2022)	Efficient probabilistic categorization.	Assumes feature independence.	Advanced probabilistic methods for complex relationships.
MLP (Zhou et al., 2021)	Adapts to intricate patterns.	Prone to overfitting without regularization.	Regularization techniques and hybrid models.
GAN (Roy, 2023)	Produces diseased leaf images.	Vulnerable to mode collapse.	GAN training stability and conditional GANs.
PCA (Ahmed et al., 2022)	Enables dimensionality reduction.	Loss of interpretability and sensitivity to scaling.	Advanced PCA variants for nonlinear extraction.
LDA (Özbılge et al., 2022)	Facilitates multiclass discrimination.	Assumes class homoscedasticity.	Robust LDA variants and integration with feature selection.
HMM (Shafik et al., 2023)	Captures sequential progression.	Depends on data sequence quality.	Hybrid models with deep learning for sequence learning.
SVM-RFE (Wu et al., 2022)	Highlights key features.	Computationally intensive.	Efficient feature selection and noise resilience.
CNN-LSTM (Sarma et al., 2022)	Proficient in sequential feature extraction.	Prone to vanishing gradients and overfitting.	Improved mechanisms within hybrid architecture.
DT-RF (Ashwathappa et al., 2021)	Enhanced classification accuracy.	Potential redundancy and complexity.	Pruning strategies and complexity mitigation.
SAE (Rahman et al., 2023)	Unsupervised feature learning.	Sensitive to hyperparameters.	Hyperparameter optimization and regularization techniques.
ELM (Tian et al., 2023)	Rapid training and generalization.	Limited interpretability.	Enhancing interpretability and optimizing hidden neurons.
CRF (Thangaraj et al., 2022)	Sequential pattern recognition.	Dependent on feature engineering.	Deep learning integrations and parameter calibration.
ESVM (Ashwathappa et al., 2022)	Improved categorization.	Computationally intense.	Hybrid ensembles with lightweight classifiers.
GMM (Alzahrani and Alsaade, 2023)	Probabilistic clustering.	Sensitive to initialization.	Robust initialization strategies and alternative models.
RNN (Daniya and Vigneshwari, 2023)	Excels in sequential learning.	Vanishing gradient issues.	New activation functions and transfer learning methods.

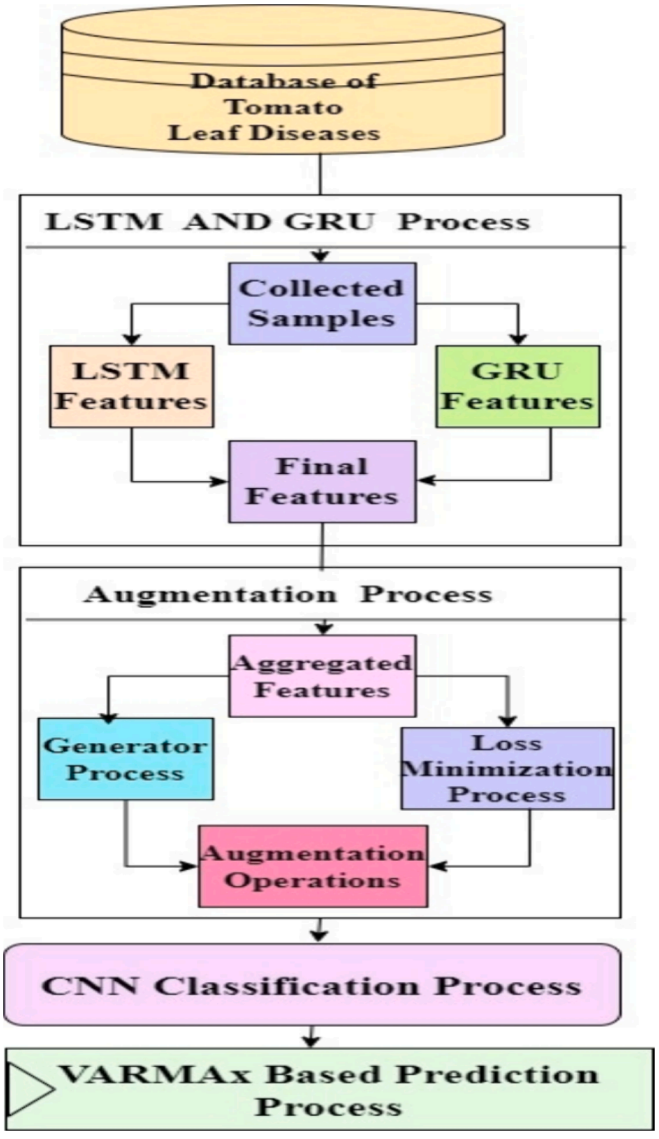

Fig. 1. Design of the proposed model for prediction of Tomato Diseases from Leaf Image Sets.

augmenting the dataset, and enhancing generalization. The GAN model augments leaf images by upsampling via bicubic sampling and iterating through the GAN model. Initially, the model estimates cross-entropy between image samples of different classes, as detailed in equation (1).,

$$L(I^1, I^2) = f^1 * \log(f^2) + [1 - f^2] * \log(1 - f^1) \cdots \quad (1)$$

Where, $I^1 \& I^2$ are the images from different classes, while, $f^1 \& f^2$ are their features which are estimated via use of Long-Short-Term Memory (LSTM) & Gated Recurrent Unit (GRU) operations. The feature extraction process is represented in Fig. 2, where both LSTM & GRU is cascaded to improve density of features.

The cascaded model estimates LSTM output features via equation (2),

$$f(LSTM) = var(f * I(t-1) + i * C) \cdots \quad (2)$$

Where, $var(x)$ represents variance of the signal which is estimated via equation (3), while $f, i \& C$ represents intermediate features, which are estimated via equations (4), 5, & 6, as follows,

$$var(x) = \sqrt{\sum_{i=1}^{N} \frac{\left(x(i) - \sum_{j=1}^{N} \frac{x(j)}{N}\right)^2}{N}} \cdots \quad (3)$$

Where, N represents total number of values in the input x for different signals.

$$f = var\left(I * U^f + h(t-1) * W^f\right) \cdots \quad (4)$$

$$i = var\left(I * U^i + h(t-1) * W^i\right) \cdots \quad (5)$$

$$C = tanh(I * U^g + h(t-1) * W^g) \cdots \quad (6)$$

Where, h represents an Iterative Kernel Matrix, which is used to identify high-density features. This matrix is updated via equation (7),

$$h(t) = \tanh(var(f * I(t-1) + i * C)) * var(I * U^o + h(t-1) * W^o) \cdots \quad (7)$$

where, $U \& W$ represents constants of the LSTM process. These output features are further augmented using GRU operations via equation (8),

$$f(final) = (1 - z) * h_t' + z * h(t) \cdots \quad (8)$$

Where, z is estimated via equation (9),

$$z = var(W_z * [h(t) * f(LSTM)]) \cdots \quad (9)$$

This process is repeated with new values of h till condition (10) is fulfilled, which indicates convergence of the feature extraction operations.

$$|f(final, t+1) - f(final, t)| < \epsilon \quad (10)$$

Where, ϵ is an Iterative error threshold, which is used to maximize feature variance for LSTM & GRU operations. Based on this evaluation, the maximum levels of loss are estimated via equation (11),

$$L(Max) = Max\left[\log\left(f^1\right) + \log(1 - f^2)\right] \cdots \quad (11)$$

While, the minimum level of loss is estimated via equation (12),

$$L(Min) = Min\left[\log\left(f^1\right) + \log(1 - f^2)\right] \cdots \quad (12)$$

Using these evaluations, the final loss function is estimated via equation (13) as follows,

$$L = Min\left[Max\left[\log\left(f^1\right) + \log\left(1 - f^2\right)\right]\right] \cdots \quad (13)$$

The loss level is used to estimate generator probability via equation (14),

$$P(G) = \frac{I^1}{L(Max)} - I^2 \cdots \quad (14)$$

This probability is used to control augmentation operations by estimation of probability for each augmentation type via equation (15),

$$P(out) = E\left(I^1\right) * \log\left[\frac{I^1}{0.5 * \left(I^1 - P(G)\right)}\right] + E\left(I^2\right) * \log\left[\frac{P(G)}{0.5 * \left(I^2 - P(G)\right)}\right] \quad (15)$$

Using the $P(out)$ levels, augmentation probability is estimated via equation (16),

$$AP(i) = P(out) * Max(A(i)) \cdots \quad (16)$$

Where, $A(i)$ represents the parameters for different augmentation types. These types include Zooming, Rotating, Sheering, Shifting, and Brightness changes. The augmented images are classified into different tomato leaf diseases using an efficient 2D CNN process as shown in Fig. 3. This process fuses different Convolution Layers with Max Pooling & Drop Out

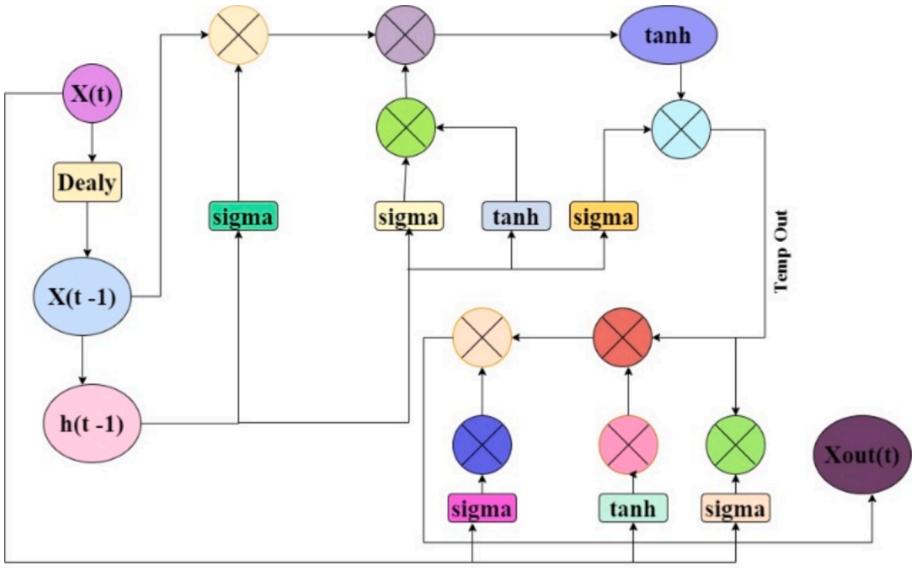

Fig. 2. Cascade of LSTM & GRU for extraction of GAN Features.

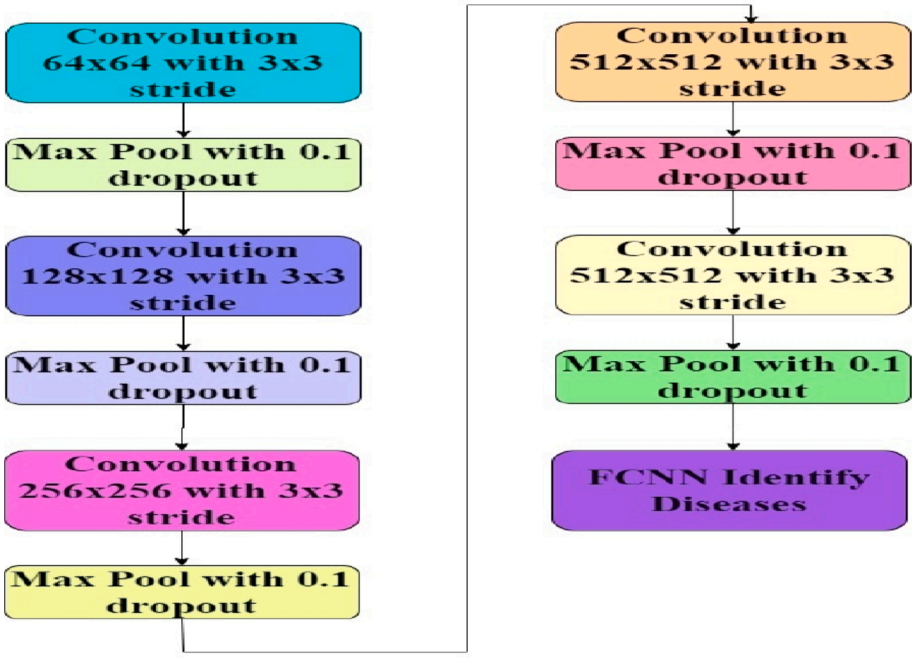

Fig. 3. Design of the 2D CNN Process for identification of tomato leaf diseases.

layers for conversion of LSTM & GRU features into high-density feature sets.

The 2D CNN process initially extracts Convolutional features via equation (17),

$$Conv(f) = \sum_{a=-\frac{m}{2}}^{\frac{m}{2}} \sum_{b=-\frac{n}{2}}^{\frac{n}{2}} f(i-a, j-b) * LReLU\left(\frac{m}{2}+a, \frac{n}{2}+b\right) \tag{17}$$

Where, m, n are the window dimensions, which range from 64×64 to 512×512 for different layers, while a, b are stride sizes, and LReLU is an Iterative Leaky Rectilinear Unit, which is represented via equation (18),

$$LReLU(x, y) = \max((x+y) * la, (x+y)) \cdots \tag{18}$$

Where, la is an augmented leaky rectilinear constant, which is used to retain positive feature sets. The feature extraction process is repeated for multiple layers, and the final features are converted into disease classes using SoftMax activation via equation (19),

$$C(disease) = SoftMax\left(\sum_{i=1}^{Nf} Conv(i) * w(i) + b(i)\right) \tag{19}$$

Where, $w\&b$ are the weights & biases for individual features, while $\boldsymbol{N_f}$ represents the total features which are extracted at the final convolutional layer, thereby assisting in improving feature variance levels.

An efficient "VARMAx-CNN-GAN Integration" model has been designed to predict tomato plant diseases from feature patterns. We leverage the strengths of LSTM and GRU models to extract high-density temporal features from surveillance data. The fused outputs of these models, capturing intricate spatio-temporal patterns, serve as inputs for

the "VARMAx-CNN-GAN Integration" model, a robust time series forecasting process. This model uses the history of fused LSTM and GRU outputs to predict future values, considering interactions between variables and exogenous influences. The Vector AutoRegressive (VAR) component plays a crucial role by regressing each variable in the fused outputs against its past values to find temporal dependencies, as described in Equation (20) for variable i at time t.

$$Y\{i,t\} = ci + \sum A\{i,j\}Y\{i,t-j\} + \sum\sum B\{i,j,k\}Y\{i,t-j\} + \varepsilon\{i,t\} \tag{20}$$

Where, *Yi,t*: This represents the value of the variable *i* (disease type), which proposed work are trying to predict, *ci* is the intercept term specific to the variable *i*, indicating the base value sets, *Ai,j* are coefficients that reflect the influence of the past values of variable *i* on its current value sets. The index *j* refers to the number of past temporal instance sets. *Bi,j,k* are coefficients capture the impact of the past values of variable *i* on itself, considering the influence of other past temporal instance sets. The indices *j* and *k* indicate different lags. $\in i,t$ term represents the error or residual at time *t* for the variable *i*, which accounts for the difference between the predicted and actual value sets.

Exogenous inputs, which represent external factors (including temperature, rainfall, pH levels, and soil parameters) affecting the disease behavior, are integrated into the "VARMAx-CNN-GAN Integration" framework process via equation (21),

$$Y\{i,t\} = ci + \sum A\{i,j\}Y\{i,t-j\} + \sum B\{i,j,k\}Y\{i,t-j\} + \sum C\{i,l\}X\{l,t\} + \varepsilon\{i,t\}\cdots \tag{21}$$

The "VARMAx-CNN-GAN Integration" model was used for disease detection in tomato plant segments. It improved accuracy by capturing changes in variables over time, allowing for multivariate analysis and understanding complex interactions. VARMAx models are flexible, allowing for both linear and nonlinear relationships, and can include exogenous variables, enhancing predictive accuracy and effectiveness in disease prediction and management strategies.

4. Result analysis and experimentation

The proposed model combines CNN and GAN operations to improve tomato leaf disease classification and prediction. Using a dataset of 350,000 images, it was divided into training (65 %), validation (15 %), and testing (20 %) sets. Preprocessing involved resizing, data augmentation, and normalization. Models such as MXF[5], MIR[23], MNDLNN [24], and custom designs were evaluated using cross-entropy loss and the Adam optimizer, focusing on specificity, precision, and accuracy. Experiments ran on high-end GPUs with TensorFlow and PyTorch. Efficiency was enhanced by optimizing architecture, reducing parameters, and using pruning, quantization, data pipeline optimization, parallelization, and transfer learning to ensure robust performance.

4.1. Performance of the classification process

Based on this strategy, the Precision, Accuracy, Recall, and Specificity levels were estimated via equations (22), 23, 24 & 25 as follows,

$$Precision = \frac{TP}{TP + FP} \tag{22}$$

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}\cdots \tag{23}$$

$$Recall = \frac{TP}{TP + FN}\cdots \tag{24}$$

$$Specificity = \frac{TN}{TN + FP} \tag{25}$$

True Positive (TP) indicates correctly predicted positive instances, True Negative (TN) indicates correctly predicted negative instances, False Positive (FP) indicates incorrectly predicted positive instances, and False Negative (FN) indicates incorrectly predicted negative instances. The precision obtained during disease classification was compared with MXF [5], MIR [23], & MNDLNN [24], and the VARMAX-CNN-GAN combination also helps to improve the pre-emptive capabilities for identifying tomato leaf diseases. Fig. 4a displays the precision observed for identification of different diseases using various methods at different data sizes (ranging from 240 K to 3 M). MXF [5] shows precision ranging from 82.38 % to 87.31 %, with the highest precision of 87.31 % at 2280 K data. MIR [23] demonstrates a steady increase in precision from 86.26 % at 240 K to 92.54 % at 3 M. MNDLNN [24] similarly shows an increasing trend, starting at 86.25 % and reaching 93.54 % at 3 M. VARMAx-CNN-GAN consistently outperforms the other methods, with precision values between 92.33 % and 99.37 %, and the highest precision of 99.37 % at 3 M data. Overall, VARMAx-CNN-GAN exhibits superior performance across all data sizes compared to the other methods. Similarly, Fig. 4b presents the precision observed for the pre-emption of diseases using various methods at different data sizes (ranging from 240 K to 3 M). MXF [5] shows precision ranging from 73.60 % to 82.94 %, with the highest precision of 82.94 % at 2280 K data. MIR [23] demonstrates precision varying between 78.20 % and 86.34 %, reaching its peak precision of 86.34 % at 3 M. MNDLNN [24] shows fluctuations in precision, starting at 82.34 % at 240 K and achieving its highest precision of 86.88 % at 3 M. VARMAx-CNN-GAN consistently outperforms the other methods, with precision values between 87.48 % and 94.55 %, and the highest precision of 94.55 % at 1320 K data. Overall, VARMAx-CNN-GAN demonstrates the highest precision for the pre-emption of diseases across most data sizes compared to the other methods.

The Fig. 5(a) shows the accuracy of various disease identification methods at different data sizes. MXF[5], MIR[23], and MNDLNN[24] show varying accuracy rates at different data sizes (ranging from 240 K to 3 M). VARMAx-CNN-GAN consistently outperforms these methods, with an accuracy of 97.61 % at 3 M data, and demonstrating superior accuracy across all data sizes. The Fig. 5(b) shows the accuracy observed for the pre-emption of diseases using various methods at different data sizes (ranging from 240 K to 3 M). MXF [5] shows accuracy ranging from 81.41 % to 89.79 %, with the highest accuracy of 89.79 % at 1800 K data. MIR [23] demonstrates an increasing trend in accuracy from 73.51 % at 720 K to 89.70 % at 3 M. MNDLNN [24] shows fluctuating accuracy, starting at 68.22 % at 240 K and achieving its highest accuracy of 83.23 % at 2280 K. VARMAx-CNN-GAN consistently outperforms the

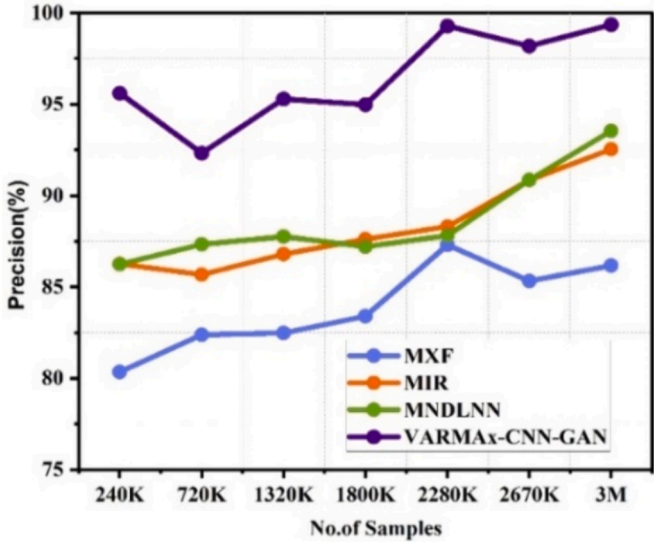

Fig. 4a. Precision observed for identification of different diseases.

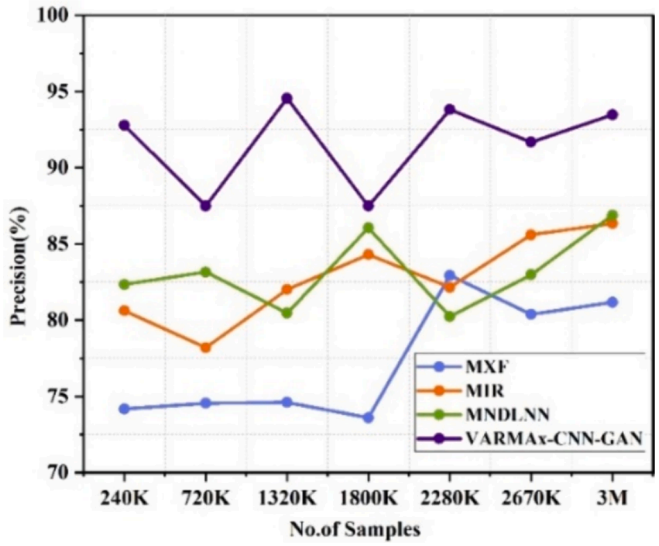

Fig. 4b. Precision for pre-emption of diseases.

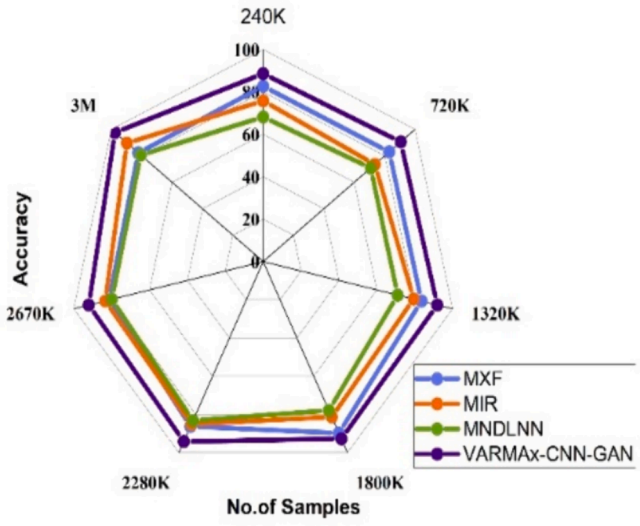

Fig. 5b. Accuracy for pre-emption of diseases.

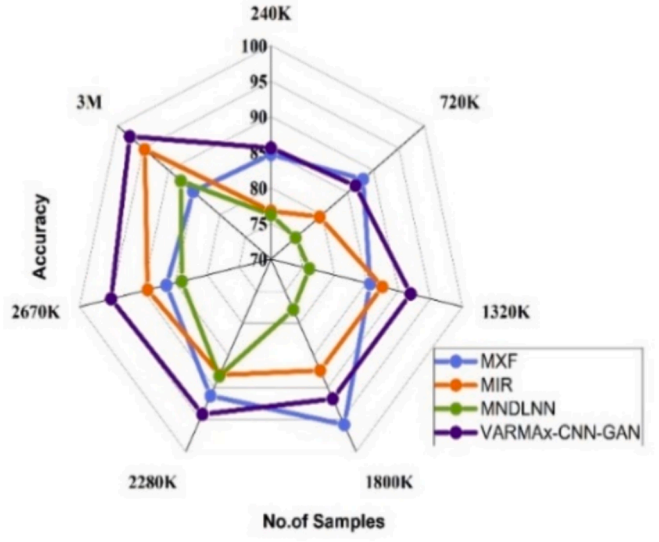

Fig. 5a. Accuracy observed for identification of different diseases.

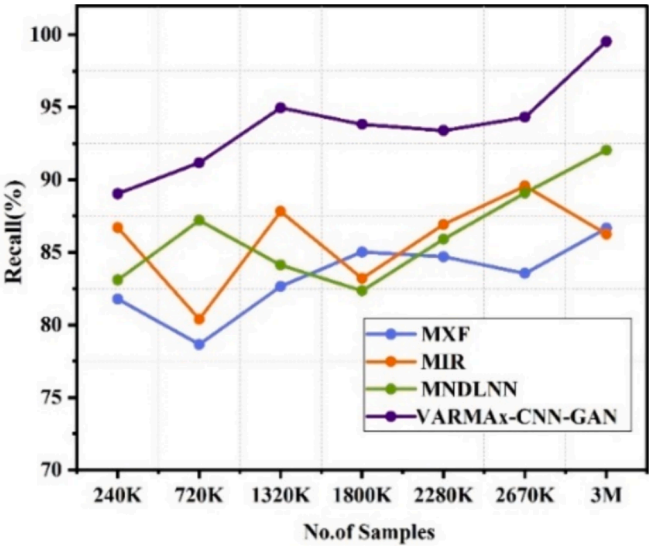

Fig. 6a. Recall observed for identification of different diseases.

other methods, with accuracy values between 85.61 % and 97.61 %, reaching the highest accuracy of 97.61 % at 3 M data. Overall, VARMAx-CNN-GAN demonstrates superior accuracy for the pre-emption of diseases across all data sizes compared to the other methods.

The Fig. 6(a) shows the recall observed for the identification of different diseases using various methods at different data sizes (ranging from 240 K to 3 M). MXF [5] shows recall values ranging from 78.65 % to 86.66 %, with the highest recall of 86.66 % at 3 M data. MIR [23] demonstrates recall values ranging from 80.39 % to 89.58 %, peaking at 89.58 % at 2670 K data. MNDLNN [24] shows recall values fluctuating between 82.35 % and 92.05 %, achieving the highest recall of 92.05 % at 3 M data. VARMAx-CNN-GAN consistently outperforms the other methods, with recall values between 89.04 % and 99.55 %, reaching the highest recall of 99.55 % at 3 M data and demonstrates the highest recall for the identification of different diseases across all data sizes compared to the other methods. Similarly, the Fig. 6(b) shows the recall observed for the observed for the pre-emption of diseases using various methods at different data sizes (ranging from 240 K to 3 M). VARMAx-CNN-GAN consistently outperforms the other methods, with recall values between 89.04 % and 99.55 %, reaching the highest recall of 99.55 % at 3 M data.

Fig. 7(a) shows the delay in milliseconds for identifying different diseases using various methods across data sizes from 240 K to 3 M. MXF [5] delays range from 173.09 ms to 192.73 ms, peaking at 2670 K data. MIR [23] delays range from 154.27 ms to 185.66 ms, peaking at 2280 K data. MNDLNN [24] delays are more consistent, from 141.06 ms to 149.83 ms, peaking at 3 M data. VARMAx-CNN-GAN shows the lowest delays, from 127.94 ms to 142.77 ms, peaking at 3 M data, and is the fastest across all data sizes. Fig. 7(b) shows the delay for disease pre-emption, where VARMAx-CNN-GAN again shows the lowest delays, from 125.94 ms to 138.77 ms, peaking at 3 M data, consistently outperforming other methods. VARMAx-CNN-GAN also achieves the highest AUC values for disease identification (85.14 to 98.70) and pre-emption (81.09 to 92.70), peaking at 98.70 and 92.70, respectively. Comparatively, MXF [5] ranges from 75.90 to 85.73 in identification and 75.90 to 80.73 in pre-emption; MIR [23] ranges from 76.17 to 90.60 in identification and 76.17 to 84.87 in pre-emption; MNDLNN [24] ranges from 75.13 to 87.83 in identification and 75.13 to 80.15 in pre-emption.

The VARMAx-CNN-GAN consistently demonstrates high specificity

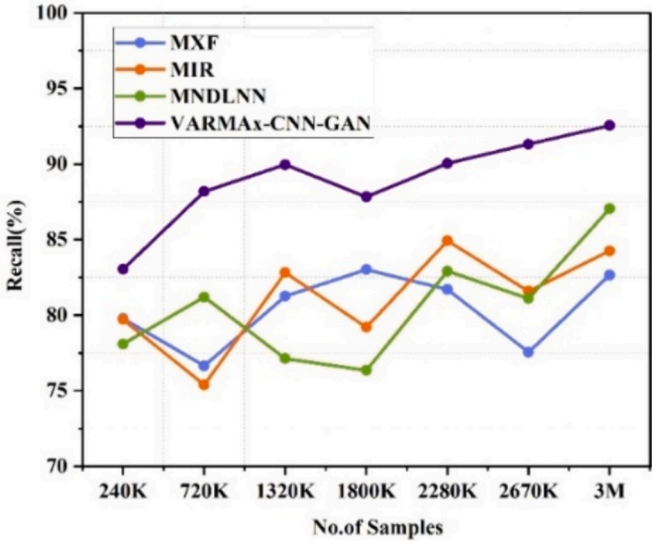

Fig. 6b. Recall for preemption of diseases.

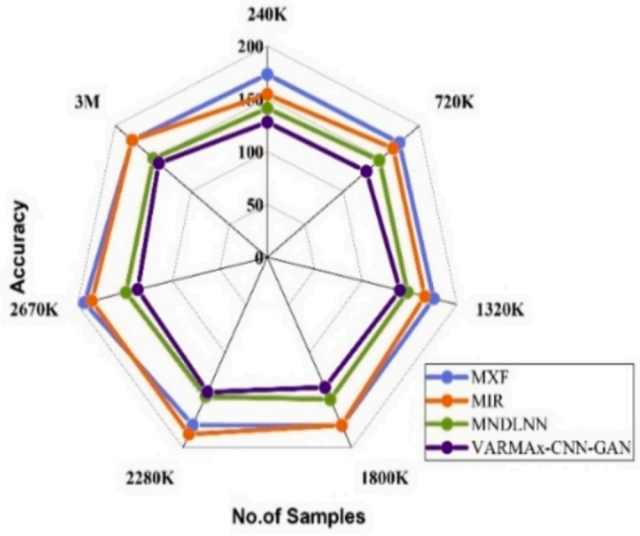

Fig. 7a. Delay observed for identification of different diseases.

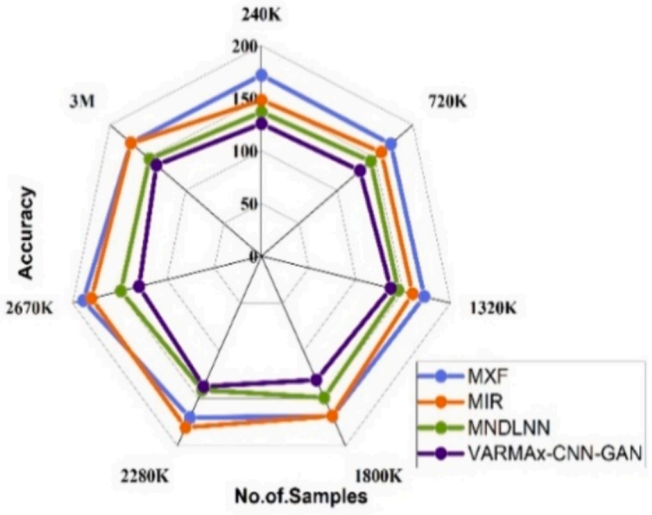

Fig. 7b. Delay for preemption of diseases.

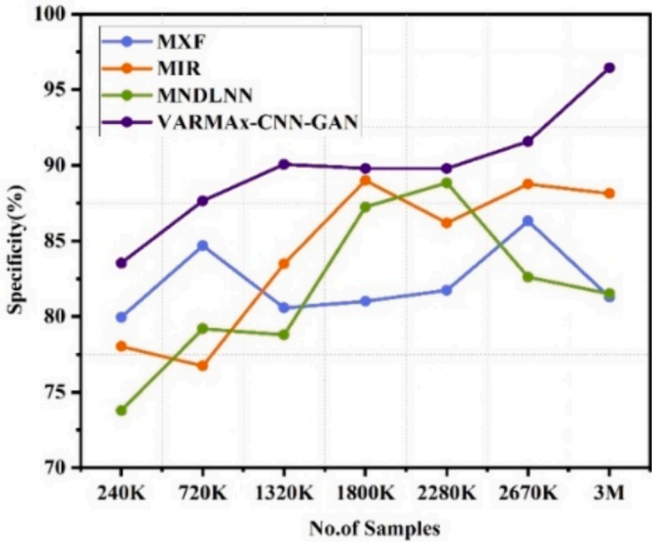

Fig. 8a. Specificity observed for identification of different diseases.

in both disease identification and prevention across varying data sizes (240 K to 3 M). For disease identification, MXF [5] achieves a maximum specificity of 86.32 % at 2670 K data, MIR [23] peaks at 89.00 % at 1800 K data, and MNDLNN [24] reaches 88.84 % at 2280 K data. In disease prevention, MXF [5] peaks at 83.32 % at 2670 K data, MIR [23] at 86.13 % at 3 M data, and MNDLNN [24] at 82.61 % at 2670 K data. VARMAx-CNN-GAN outperforms with a maximum specificity of 96.44 % for disease identification and 87.44 % for disease prevention at 3 M data. Fig. 8(a) displays the specificity observed in the detections of various diseases, whereas Fig. 8(b) illustrates the specificity in the preemption of diseases.

Table 2 shows improvements across precision, recall, accuracy, and F1-score as additional techniques (GAN and VARMAx) are incorporated into the base CNN model.

The proposed model for disease classification faces errors like false positives and false negatives due to inadequate feature representation, class imbalance, and environmental factors. To address these issues, the model may need to augment training data, improve feature representation, or incorporate advanced techniques. Strategies include data augmentation, transfer learning, and ensemble learning. Further validation and refinement are needed for real-life agricultural situations.

5. Conclusion

The approach suggested herein creates a CNN-based model for disease detection in tomato crops. Each of the three convolution and max pooling layers in the proposed CNN-based architecture contains a different number of filters. The present research undertook a thorough evaluation and comparison of four distinct classification models, assessing them across various criteria such as delay, AUC levels, and specificity. This in-depth analysis has yielded valuable insights, enriching our understanding of the effectiveness and efficiency of each model in performing classification tasks. The proposed work consistently showcased superior performance across a spectrum of metrics. Whether examining delay values, where it excelled in minimizing processing time, AUC levels, where it demonstrated impressive discrimination ability, or specificity levels, where it displayed remarkable proficiency in accurately identifying negative instances, the proposed method consistently outperformed the existing models, including MXF, MIR, and MNDLNN. This performance underscores the strength and effectiveness of the proposed approach in comparison to its counterparts. The methodology adopted in the proposed work, has proven effective in attaining optimized results. The comparative analysis

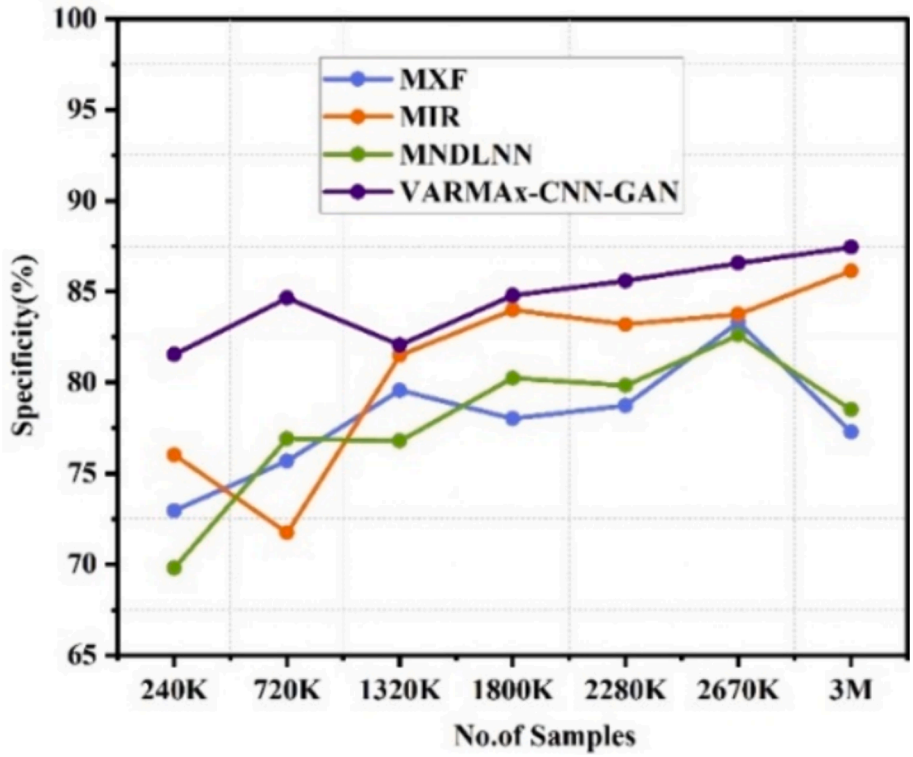

Fig. 8b. Specificity for preemption of diseases

Table 2
Performance Metrics of Model Variants.

Model Variant	Precision	Recall	Accuracy	F1-score
CNN	0.85	0.82	0.88	0.83
CNN + GAN	0.87	0.84	0.89	0.85
CNN + VARMAx	0.86	0.83	0.89	0.84
CNN + GAN + VARMAx	0.90	0.88	0.92	0.88

reflects a holistic approach where various aspects of the classification process were taken into consideration, allowing for a multifaceted understanding of the models' behaviors. The improved classification performance demonstrated by the proposed method may pave the way for new opportunities in applications where accurate, efficient, and dependable classification is crucial. This encompasses domains such as medical diagnosis, and disease detection. The enhanced model performance offers the potential to significantly benefit real-world scenarios where precise and timely classification plays a pivotal role.

CRediT authorship contribution statement

Vengaiah Cheemaladinne: Methodology. **Srinivasa Reddy K.:** Supervision.

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