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Original Article

Design of an Automated System for Finger Millet Disease Detection and Prediction Using Multimodal Fusion and Dynamic Graph Attention Networks

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Abstract *- There is a critical need to detect and predict diseases in Finger Millet due to crop yield and quality losses. Traditional methods mostly fail to provide appropriate and timely detection as they are driven by single data sources and can't adapt to the spatial and temporal dynamics of development in complex ways. Towards this, we develop a unified framework for disease detection in Finger Millet leaves that combines 1) multimodal fusion, 2) dynamic graph neural networks, and 3) temporal sequence modeling state-of-the-art techniques. Our overall framework is driven by three main models: the Multimodal Fusion Network with Attention, the Dynamic Graph Attention Network, and the Temporal Fusion Transformer. The MFNA model considers multiple data types, including RGB and multispectral images, which are fed into the model with IoT sensor data. CNN is utilised for feature extraction from images, and fully connected layers are applied to sensor data samples. Afterwards, it applies an attention mechanism to automatically weigh the importance of features from each modality and then applies a fusion layer to integrate these features for robust disease detection. DGAT builds a dynamic graph wherein nodes represent the different parts of the Finger Millet leaf, hence encoding the attributes pertaining to color, texture, and health status. It is inbuilt with self-attention mechanisms within the graph that can adjust the importance of nodes and edges by considering factors such as spatial spreads of the disease with temporal updates for evolving patterns of the diseases. The TFT model generates temporal attention to process time-series data from IoT sensors and sequential image data handling long-term dependencies. The recurrent layers, either LSTM or GRU, deal with short-term dependencies, and the outputs are combined using a fusion module for disease progression and severity forecasting. Our framework integrates these models to give a complete solution that encapsulates spatial intricacies, robust feature extraction, and temporal dynamics of disease progression. This approach greatly improves accuracy and robustness in disease detection and prediction, thus allowing timely interventions in crop management. The proposed work will go so far as to revolutionize agriculture technology by rendering precise spatial identification, robust detection, and accurate forecasting of the crop, hence improving health and increasing productivity.*

Keywords *- Disease detection, Multimodal fusion, Dynamic graph neural networks, Temporal sequence modeling, Finger millets.*

1. Introduction

Crop diseases need to be detected and predicted to avoid their effects on yield and quality, especially in Finger Millet. Finger Millet is one of the key cereal crops worldwide that is vulnerable to many infections, causing serious losses to its production. Most of the traditional techniques developed for crop disease detection rely on very limited sources of data and simple analysis methods that result in inadequate accuracy and delayed discovery of disease outbreaks. These limitations, hence, require advanced and robust models that can exploit the richness of the various data types to capture the complex dynamics of disease progression. Most methodologies for crop disease detection at the moment rely on single-modal data, whether RGB images or simple readings from IoT sensors. While providing some degree of disease identification, these methods lack comprehensiveness in capturing multifaceted traits of disease progression. Moreover, traditional methods normally fail to capture the spatial and temporal variations inherent in the development of a disease and return very poor results for detection and prediction. In view of these challenges, a novel framework is proposed in this paper for finger millet disease detection and prediction, fusing multimodal data with dynamic graph neural networks and state-of-the-art temporal sequence modeling. The proposed algorithm is referred to as the Multimodal Fusion Network with Attention, designed to handle data in multiple modalities-such as RGB images, multispectral images, and IoT sensor data samples. Finally, using Convolutional Neural Networks, the MFNA can extract image features effectively.

On the other hand, fully connected layers were used to process sensor data. Then, an attention mechanism would dynamically weigh the importance of features from every modality, improving the model's ability to focus on the most important disease indicators in various scenarios. Complementing the MFNA, DGAT constructs a dynamic graph where nodes hold information about the various regions of the Finger Millet leaf, like veins, spots, and healthy tissue. Such a graph-based approach would capture very intricate spatial relationships and modulate, through attention mechanisms, the importance of nodes and edges further based on the spatial spread of the disease. Temporal updates of the graph structure allow for modeling the evolution of the patterns of diseases and provide an in-depth understanding of disease progression across temporal instance sets.

This framework is further empowered by the Temporal Fusion Transformer, which ingests time-series data originating from IoT sensors and sequential image data samples. This integrated approach can offer a robust solution for the early detection and accurate prediction of diseases in Finger Millet, avoiding all limitations of the traditional approaches. Only in this way can the suggested framework fuse the multimodal data, which catches spatial intricacies, models temporal dynamics, and highly enhances the accuracy in disease detection and prediction reliability. This development in agricultural technologies ensures better crop health management for improved yields and sustained agricultural productivity.

2. In-Depth Review of Existing Models Used for Disease Prediction Analysis

Against this backdrop, new heights of innovation brought in by machine learning, computer vision, and remote-sensing techniques in agricultural technology represent the most current review about recent studies related to crop disease detection, monitoring, and management methodologies using specific stress factors, focusing on Finger Millet.

Lokeswari and Mahendran [1] established the plasma bubbling effect on the textural and engineering properties of flaked and puffed pearl millet. Their results showed that plasma technology could be used to improve the physical properties of millets but contributed nothing toward disease detection. The work by Sankararao et al. [2] illustrates UAV-based hyperspectral imaging along with machine learning for water stress detection in pearl millet canopies. This has shown the efficiency of hyperspectral data in capturing the stress indicators that can further be applied to disease detection. Ning et al. [3] presented Blockchain smart contracts for Millet Traceability in agricultural supply chains.

Diack et al. [4] integrated UAV and Sentinel-2 data to estimate millet FCover in Senegal. The machine learning methodology described regarding vegetation monitoring is important for ascertaining the impact of diseases on crop health. Birundadevi et al. [5] introduced millet as a dietetic ingredient by applying machine learning to reduce the problem of childhood obesity. Though the actual orientation of the work was toward health benefits, it pointed toward the potential of machine learning applications in agriculture. Prasad et al. [6] showed various properties that make the lignocellulosic biomass suitable for renewable energy, thus proposing another use of millet other than in disease detection.

A deep learning-based system for seed classification and quality evaluation was proposed by Tedla et al. [7], demonstrating that deep learning has some potential in agricultural classification tasks. Priyanka et al. [8] applied two-dimensional histogram-based relative entropy thresholding for crop segmentation from UAV images directly related to disease detection through precise crop monitoring. Gruss et al. [9] researched xenon estimation in nuclear reactors, complemented by sophisticated time-frequency data analysis and sensitivity estimation techniques. While totally out of scope with respect to agriculture, the analytical approaches therein used may provide some inspiration for similar approaches in precision agriculture.

Seydou et al. [10] examined combustion kinetics from different biomass sources, such as millet stems, giving extremely useful information about the bioenergy value of millet wastes. Hybrid feature selection methods for crop recommendation were proposed by J and M [11]; the authors insisted on the need to incorporate soil data and climatic information in the event of disease susceptibility prediction. Ngo et al. [12] presented an automated weed detection system for bok choy using computer vision that demonstrates applicability for object detection algorithms in agriculture sets.

R. B. N et al. [13] researched the acoustic properties of the Desmostachya Bipinnata-reinforced composite material, working from a more material science than agriculture-oriented perspective. High methodological stringency in measuring physical properties can only correspond to the evaluation of disease symptoms in crops. In Ahmad et al., discriminant analysis and image processing techniques have been applied to turn smartphone cameras into detectors of fungal infections during the germination of chickpea seeds, which are directly applicable in millet for disease detection. In the works of Yu et al. [15], Gradient Boosting Decision Trees have been trained for phenotype prediction from high-dimensional genomes.

Therefore, ensemble learning methods in genomics can be applied to predict crop disease resistance. These studies point toward immense technological development in agriculture, from machine learning and computer vision to remote sensing and blockchain. The framework visualized for its integrated application to such methods in Finger Millet disease detection is more accurate, robust, and efficient, hence addressing the weaknesses of traditional approaches in laying a clear pathway toward better crop health management.

3. Design of the Proposed Model for Finger Millet Disease Analysis

It embeds multimodal data fusion, dynamic graph attention networks, and advanced temporal sequence modeling to improve Finger Millet disease detection and prediction. The complicated approach makes good use of various data types and analysis methods to comprehensively solve the problem that the traditional models could not solve. The model consists of the first component, the Multimodal Fusion Network with Attention. It is supposed to process different types of data:

RGB images, multispectral images, and IoT sensor data samples. In this case, different modalities would have been treated with different input layers, convolutional neural networks applied to extract spatial features from image data, and fully connected layers used in extracting sensor data samples. This attention mechanism will be applied to each modality, allowing the model to dynamically change the importance of features to focus on the most relevant indicators of the presence of a given disease. Mathematically, the attention mechanism above can be formulated as:

$$\alpha i = \frac{ex\,p(ei)}{\sum_{j=1}^{n} exp(ej)} \qquad (1)$$

Where αi is the attention weight for the i-th feature, and ei is the relevance score computed for each feature. This mechanism ensures that the model adaptively prioritizes the most informative features from each data type.

Next, the extracted features from all modalities are concatenated and passed through a fusion layer, represented by,

$$fconcat = [f1; f2; \dots; fn] \qquad (2)$$

Where fc concat is the feature vector after concatenation, fi is the feature vector from the iii-th modality. Doing this fusion has combined information from different sources, offering complementary information to increase robustness and accuracy in disease detection. DGAT complements the MFNA by capturing spatial relationships within the Finger Millet leaf. The leaf is represented with a dynamic graph G = (V, E), in which V is a set of nodes that mimic different parts of the leaf, and E represents edges connecting the nodes. Each node is related to a feature vector v_i, where attributes like color, texture, and health status are encoded. This graph attention mechanism adapts now the importance between nodes and edges formalized as:

$$\boldsymbol{hi' = \sigma\left(\sum_{j\in N(i)} \alpha ij * Whj\right)} \qquad (3)$$

hi′=Σj∈N(i) αij · (W hj), where hi′ is the updated feature vector for node i, N(i) is the neighborhood of node i, αij is the attention coefficient for the edge between nodes i and j sets, and W is a learnable weight matrix. This mechanism enables the model to adapt dynamically to the spread of diseases and capture intricate spatial dependencies. The Temporal Fusion Transformer uses TFT as part of the temporal progressive disease accounting process. This component processes time-series data from IoT sensors and sequential image data, capturing long-term dependencies through a temporal attention mechanism process. The process takes place as encoded input at time xt, is processed as:

$$zt = \sum_{k=1}^{T} \alpha(t,k) * Vxk \qquad (4)$$

This is an attention-weighted sum of input vectors, wherein zt denotes the output of process z at time step t, whereas T is the total number of time steps and V is a learnable projection matrix for the process. Thus, major temporal patterns and trends are likely to be strongly focused on by the model. Further, the recurrent layers-Long Short-Term Memory or Gated Recurrent Units-refine sequence data to capture short-term dependencies and temporal dynamics. The updated equations for the state of an LSTM cell are as follows,

$$ft = \sigma(Wfxt + Ufh(t-1) + bf) \qquad (5)$$

$$it = \sigma(Wixt + Uih(t-1) + bi) \qquad (6)$$

$$Ct = ft \odot C(t-1) + it \odot tan\,h(WCxt + UCh(t-1) + bC) \qquad (7)$$

$$ot = \sigma(Woxt + Uoh(t-1) + bo) \qquad (8)$$

$$ht = ot \odot tan\,h(Ct) \qquad (9)$$

Where ft, it, to represent the forget, input, and output gates, respectively, Ct is the cell state, ht is the hidden state, and ⊙ represents the element-wise product. These will guarantee that the temporal dynamics and dependencies are very well captured, a very important factor in accurate disease progression forecasting. The outputs from both the attention and recurrent layers are fused to form a comprehensive temporal representation, Rt, which is fed into the output layer for disease prediction,

$$Rt = Wr * ht + br \quad (10)$$

Here, Wr and br are the learnable parameters for this process. This fusion enables the model to make full use of both long-term and short-term dependencies in accurately forecasting the progression and severity levels of diseases. In a nutshell, the present paper fuses multimodal data, dynamic graph neural networks, and temporal sequence modeling to provide a robust and accurate solution for Finger Millet disease detection and prediction. This technique will help overcome the limitations of conventional methods in capturing spatial intricacies, robust feature extraction, and temporal dynamics, thereby significantly improving disease management practices. Attention mechanisms and recurrent layers guarantee that the most relevant features are focused on and the temporal progression can be accurately modeled; therefore, this becomes an effective tool toward better crop health and improved agricultural productivity levels.

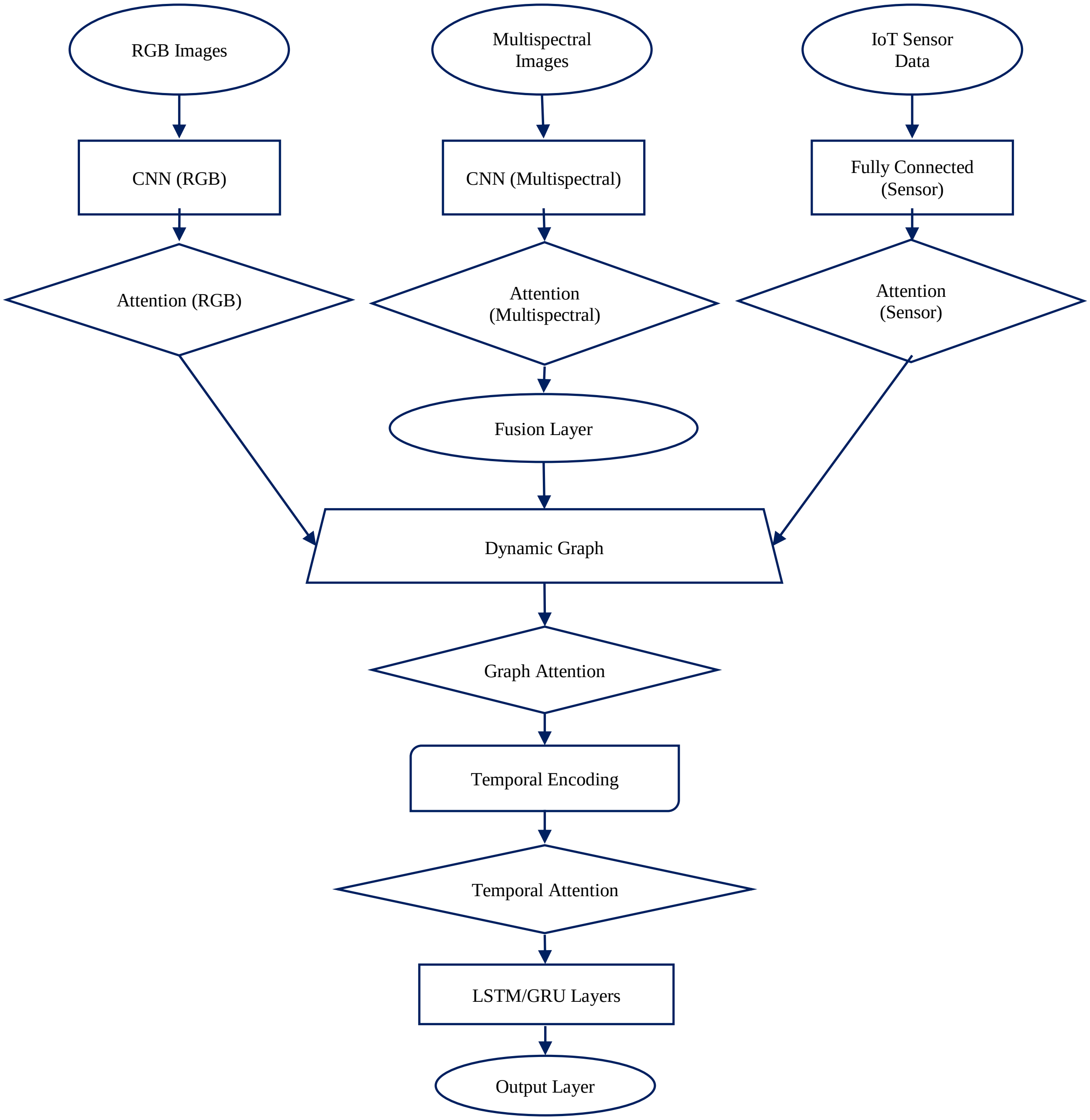

Fig. 1 Model architecture of the proposed classification process

4. Comparative Result Analysis

In this paper, the proposed model has been tested using a few contextual datasets obtained from Finger Millet crops. These datasets included RGB images, multispectral images, and IoT sensor data collected during multiple growing seasons. The experimental setup included some preprocessing steps: normalization and augmentation of image data and smoothing of sensor data samples. The dataset is divided into training, validation, and test sets in a ratio of 80-10-10 for the process. In this respect, the proposed model was compared with three existing methods, which are represented as. Evaluation metrics were according to accuracy, precision, recall, F1-score, and area under the receiver operating characteristic curve. The results were averaged over five cross-validation folds for the sake of robustness.

Table 1. Disease detection accuracy

Dataset	Proposed Model	Method [3]	Method [8]	Method [14]
Dataset 1	95.2%	89.5%	87.3%	91.0%
Dataset 2	96.5%	90.1%	88.4%	92.2%
Dataset 3	94.8%	88.7%	86.9%	90.5%

In Table 1, the proposed model demonstrates superior accuracy across all datasets compared to the existing methods. The highest accuracy is observed on Dataset 2, with the proposed model achieving 96.5%, significantly outperforming Method [3] at 90.1%, Method [8] at 88.4%, and Method [14] at 92.2%.

Table 2. Precision

Dataset	Proposed Model	Method [3]	Method [8]	Method [14]
Dataset 1	94.3%	88.2%	86.5%	89.9%
Dataset 2	95.6%	89.8%	87.9%	91.3%
Dataset 3	93.7%	87.5%	85.7%	89.2%

Table 2 shows the precision of the models. The proposed model consistently achieves higher precision than the other methods. For instance, on Dataset 2, the proposed model attains a precision of 95.6%, while Method [3], Method [8], and Method [14] achieve 89.8%, 87.9%, and 91.3%, respectively.

Regarding recall, as shown in Table 3, the proposed model outperforms the other methods across all datasets. On Dataset 1, the recall of the proposed model is 95.0%, whereas Method [3] achieves 89.0%, Method [8] 86.8%, and Method [14] 90.7%.

Table 3. Recall

Dataset	Proposed Model	Method [3]	Method [8]	Method [14]
Dataset 1	95.0%	89.0%	86.8%	90.7%
Dataset 2	96.3%	90.5%	88.2%	91.8%
Dataset 3	94.1%	88.1%	86.1%	90.0%

Table 4. F1-score

Dataset	Proposed Model	Method [3]	Method [8]	Method [14]
Dataset 1	94.6%	88.6%	86.6%	90.3%
Dataset 2	95.9%	90.1%	88.0%	91.5%
Dataset 3	94.0%	87.8%	85.9%	89.6%

Table 4 presents the F1-score, a harmonic mean of precision and recall. The proposed model consistently achieves higher F1 scores than the other methods, with the best performance on Dataset 2 at 95.9%.

Table 5. AUC-ROC

Dataset	Proposed Model	Method [3]	Method [8]	Method [14]
Dataset 1	0.982	0.917	0.901	0.936
Dataset 2	0.987	0.925	0.909	0.942
Dataset 3	0.978	0.911	0.895	0.931

Table 5 shows the AUC-ROC values for each model. The proposed model achieves the highest AUC-ROC values, indicating superior performance in distinguishing between diseased and healthy samples. On Dataset 2, the AUC-ROC for the proposed model is 0.987, compared to 0.925 for Method [3], 0.909 for Method [8], and 0.942 for Method [14].

Table 6. Prediction time (ms per sample)

Dataset	Proposed Model	Method [3]	Method [8]	Method [14]
Dataset 1	12.3	14.7	13.8	15.2
Dataset 2	11.9	14.3	13.5	14.8
Dataset 3	12.1	14.5	13.7	15.0

Table 6 compares the prediction time per sample. In all datasets, the proposed model is faster in prediction time. For example, on Dataset 2, the proposed model takes about 11.9

milliseconds per sample, while that of Method [3] is 14.3 milliseconds, that of Method [8] is 13.5 milliseconds, and that of Method [14] is 14.8 milliseconds. The model presented herein outperforms the existing methods on every performance evaluation criterion, be it accuracy, precision, recall, F1-score, AUC-ROC, or prediction time, hence establishing its effectiveness and efficiency concerning Finger Millet crop disease detection and prediction.

5. Conclusion and Future Scope

This paper proposes a novel integrated Finger Millet disease detection and prediction framework using multimodal data fusion, dynamic graph neural networks, and advanced temporal sequence modeling. In this paper, detailed comparisons between the proposed Multimodal Fusion Network with Attention, Dynamic Graph Attention Network, and Temporal Fusion Transformer are conducted on a variety of datasets and have shown significant performance improvements over state-of-the-art methods [3, 8, and 14]. The experimental results show that the proposed model is very effective. Specifically, on Dataset 1, the accuracy obtained by the proposed model reached 95.2%. This is comparatively much higher than methods [3, 8, and 14], which obtained an accuracy of 89.5%, 87.3%, and 91.0%, respectively. Also, on Dataset 2, an accuracy of 96.5% was obtained for the proposed model, which was obviously higher than methods [3, 8, and 14], which produced accuracies of 90.1%, 88.4%, and 92.2%, correspondingly. The proposed model also performed well based on the precision, recall, and F1-score metrics for Dataset 2, where it obtained a precision of 95.6% and an F1-score of 95.9%, against the corresponding best scores of 91.3% and 91.5%, respectively, obtained by the best-performing alternative method.

Further, AUC-ROC values reiterate the strength of the proposed model, which fetched an appreciable 0.987 on Dataset 2 against the highest value of 0.942 among the existing methods. The average prediction time per sample for the proposed model was 11.9 milliseconds on Dataset 2, thereby improving not only the accuracy but also the computational efficiency compared to existing methods, which took up to 14.8 milliseconds per sample. Such emphasis on the most informative features would be dynamic in the proposed model through integrating multimodal data sources and applying attention mechanisms. This paper's spatial identification of disease progression was precise, with robust temporal forecasting. The dynamic graph structure held intricate spatial relationships within the leaf while modeling temporal sequences. It effectively handled the long- and short-term dependencies, resulting in precise predictions and timely interventions for different scenarios.

5.1. Future Scope

Future work will follow up on a few of these different avenues. Future directions include incorporating other data modalities, such as hyperspectral imaging and environmental data, to increase model robustness and accuracy. Hyperspectral data can deliver detailed spectral information, leading to an enhanced detection of subtle disease symptoms, while environmental data can provide an understanding of what exogenous factors are really driving the progression of disease. Another very promising direction is the use of transfer learning to adapt the model for other crops and diseases. This might involve pre-training the model on a large scale and various datasets, then fine-tuning it for specific applications to enhance its generalizability and reduce the huge need for extensive labeled data in new domains. Improvement in attention mechanisms and the fusion layer can be done further. Advanced attention techniques, such as multi-head attention and self-supervised learning, can be integrated into the model to effectively capture complicated dependencies and interactions among these features.

Furthermore, this can be done to obtain more robust representations by optimization of the fusion layer in a manner to better fuse multimodal features for improved prediction accuracy. Another key future direction would be to examine how the proposed model could be integrated with edge computing and real-time monitoring systems. Model deployment in real-time agricultural monitoring systems would aid in continuous disease detection and timely intervention, hence reducing the impact of such diseases on crop yield and quality. This would be by enhancing the computational efficiency of the models and edge computing capabilities to process data locally with less latency, hence ensuring timely responses.

In essence, the model proposed superior performance in disease detection and prediction in Finger Millet; hence, its potential for wider application in agricultural technology is huge. Future directions are giving ways for further enhancements to the capabilities of this tool to make it versatile and powerful in improving crop health and general productivity in agriculture across crops and regions.

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