# SDPEMDL: Enhanced Sugarcane Disease Detection and Prediction via An Ensemble Multimodal Deep Learning Approach Using Advanced Deep Learning Models

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## ABSTRACT (10 PT)

The emergence of diverse and complicated diseases in sugarcane has necessitated the development of advanced, multifaceted models capable of detecting and predicting diseases with heightened accuracy and precision. Existing models, although proficient, exhibit limitations in handling multi-source data, offering restricted accuracy, and providing futuristic insights into disease occurrence. In this study, we integrate multimodal datasets—consisting of RGB images refined using VGGNet 19, Near-Infrared (NIR), Hyperspectral, and Thermal images processed with Inception Net to construct an innovative model that surmounts existing limitations. Additionally, the incorporation of weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, amplifies the model's predictive and classification capabilities. Furthermore, the application of the Vector Auto Regressive Moving-Average model (VARMA) on each modality significantly enhances the predictive precision of classification into different disease types. This research marks a seminal advancement in the domain of sugarcane disease detection and prediction. Comparative analysis reveals a substantial improvement over existing models, showing a 4.5% increase in accuracy, 3.5% enhancement in precision, 3.9% rise in recall, 4.3% improvement in Area Under Curve (AUC), and a 3.4% improvement in specificity. Moreover, the model expedited the processing speed, reducing the delay by 2.9%. The predictive precision achieved through the VARMA model exhibited an improvement of 1.9% in precision, 2.5% in accuracy, 2.4% in recall, 3.5% in AUC, 1.5% in specificity, and a 2.4% reduction in delay levels. The integration of diverse modalities and the amalgamation of advanced machine learning models not only significantly enhance the detection and prediction of sugarcane diseases but also illustrate a pioneering approach that can be generalized across different crops and environmental settings. The enhancement in various performance metrics demonstrates the potential impact of this research in empowering agronomists and farmers with advanced tools, aiding in timely interventions and effective management of sugarcane diseases. The innovation presented in this study is poised to be a cornerstone in agricultural research, propelling the field towards a more data-driven, accurate, and predictive paradigm process.

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## 1. INTRODUCTION

Sugarcane is a principal crop, extensively cultivated globally due to its multifarious applications, primarily in the production of sugar, alcoholic beverages, and biofuels. The prominence of this crop underscores the importance of maintaining its health and yield, given its substantial economic impact. However, sugarcane cultivation is incessantly threatened by a plethora of diseases, which have been exacerbated by changing climatic conditions, necessitating the development of efficient detection and predictive models to mitigate the repercussions on yield and quality [1], [2], [3].

Current methodologies predominantly rely on single-modal datasets and conventional machine learning models, limiting their capacity to accurately detect and predict the occurrence of diseases. The prevailing models demonstrate constrained adaptability in integrating multi-source data, resulting in limited precision, accuracy, and predictive capabilities. Moreover, the narrow scope of these models fails to account for the multifactorial nature of disease occurrence and progression in sugarcane, restricting their applicability and reliability in real-world scenarios.

The complex interplay between various factors contributing to the disease occurrence in sugarcane demands the integration of multimodal datasets and the incorporation of advanced machine learning models. Such an amalgamation enables a holistic understanding and analysis of the myriad factors affecting sugarcane health, allowing for the creation of models with enhanced predictive accuracy and adaptability [4], [5], [6], which can be achieved via use of Mobile Net v2 (MVN2) based deep learning methods.

The objective of this research is to develop a novel, integrative model that amalgamates diverse modalities including RGB, NIR, Hyperspectral, and Thermal images, along with environmental and historical data, to enhance the detection and prediction of sugarcane diseases. The introduction of advanced machine learning models, including VGGNet 19 for refining RGB images, Inception Net for sequence data, and ResNet50 for weather data, soil moisture, and previous disease occurrences, signifies a pioneering stride in the field. The integration of the Vector Auto Regressive Moving-Average model (VARMA) adds a futuristic dimension to the study, enabling the prediction of future disease occurrences with heightened precision.

This innovative approach outperforms existing models, showcasing improvements in various performance metrics, including precision, accuracy, recall, AUC, specificity, and processing delay. The advancements illustrated in this study have the potential to revolutionize sugarcane disease management practices by providing agronomists and farmers with robust tools for early detection and intervention, thereby ensuring optimal crop yield and quality. Furthermore, the methodology presented herein has broader implications, serving as a blueprint for developing advanced detection and predictive models for diverse crops and environments.

**The main contributions of this paper are:**

- **Development of Integrative Model:** We have developed an innovative, integrative model that amalgamates diverse data modalities including RGB, NIR, Hyperspectral, and Thermal images, along with environmental and historical data, to enhance the detection and predictive precision of sugarcane diseases.
- **Implementation of Advanced Techniques:**

The incorporation of state-of-the-art machine learning models like GAN for refining RGB images, RNN for sequence data, and 1D CNN for analyzing weather data, soil moisture, and previous disease occurrences, signifies a groundbreaking contribution in the agricultural technology domain.

- **Enhanced Predictive Precision:** The integration of the VARMA model enables enhanced predictive precision, allowing for accurate forecasting of future disease occurrences, thus offering a proactive approach to disease management and control.

The motivations driving this research are deeply rooted in the imperatives of sustaining agricultural productivity, addressing the challenges posed by the rising incidence of sugarcane diseases, and harnessing the potential of advanced technologies in fostering a resilient and sustainable agricultural ecosystem. The contributions of this study lie in its innovative integration of multimodal data and advanced machine learning models to enhance the detection and prediction capabilities of sugarcane diseases, offering a proactive, comprehensive solution that has broader implications for the global agricultural community and food security. The enhancements and advancements illustrated in this research are poised to shape future developments in agricultural technology, providing a robust foundation for ongoing and future endeavors in this domain.

This paper is organized into several sections, starting with a comprehensive review of related works in the field, elucidating the limitations and gaps in existing research. Subsequent sections delve into the methodology, detailing the multimodal data integration, machine learning model development, and implementation. The results section presents a comparative analysis with existing models, highlighting the enhancements achieved in various performance metrics. Finally, the discussion and conclusion sections explore the implications, applications, and future directions of this research.

### 1.1. Review of Existing Models

The literature review sheds light on prior research focused on disease detection in sugarcane and other crops, providing an overarching context for the advancements made in this study. The review categorizes the existing body of work into several key areas: traditional detection methods, single-modal data-based models, advancements in multimodal data integration, and the incorporation of machine learning & deep models like DenseNet201 (DN201) which showcases good results [7], [8], [ 9].

Historically, sugarcane disease detection primarily depended on manual inspections and laboratory-based analyses. Several studies have highlighted the significance and challenges of manual inspection methods. These approaches, though foundational, are resource-intensive, time-consuming, and susceptible to human errors, leading to a clamor for more sophisticated, automated solutions.

With the advent of technology, a shift was witnessed towards employing single-modal data, such as RGB images, for detecting diseases in crops including sugarcane. These models showcased enhanced accuracy compared to traditional methods but were limited by their reliance on a single type of data, which resulted in partial contextual understanding of diseases [10], [11], [12]. This can be done via use of Inception Nadam L2 Regularized Gradient Descent (NLRGD) process.

The integration of multimodal data emerged as a response to the limitations of single-modal data-based models, paving the way for comprehensive disease detection models. Multimodal approaches incorporate diverse data sources like NIR, Hyperspectral, and environmental data to offer a holistic perspective on disease occurrence and progression. However, the complexities in integrating and analyzing diverse data types have posed significant challenges and opportunities for refinement.

Recent studies have delved into the incorporation of machine learning models to improve disease detection and prediction. Machine learning models like Convolutional Neural Networks (CNN) have been proven effective in handling image data for disease detection. The potential of Recurrent Neural Networks (RNN) in processing sequence data, and Generative Adversarial Networks (GAN) in refining images, has also been explored in contemporary research. However, the integration of advanced machine learning models with multimodal data for sugarcane disease detection remains a relatively uncharted territory, necessitating further exploration and development [13], [14], [15].

Predictive modeling in agriculture is gaining traction, with research progressively focusing on forecasting disease occurrences to enable proactive management. Models like Vector Auto Regressive Moving-Average (VARMA) have been studied for their efficacy in predicting time-series data, offering avenues for predicting future occurrences of diseases [16], [17], [18]. The refinement and optimization of predictive models are crucial in adapting to the dynamic nature of agricultural environments and disease patterns [19], [20].

The trajectory of research in sugarcane disease detection has evolved significantly, from relying on manual, labor-intensive methods to embracing advanced, automated solutions integrating machine learning and multimodal data samples [21], [22], [23]. The existing literature underscores the continual need for sophisticated models that can amalgamate diverse data sources and leverage advanced computational models to improve the accuracy, precision, and predictive capabilities of disease detection models in sugarcane scenarios [24], [25], [26]. The gaps identified in the integration and optimization of multimodal data and advanced machine learning models provide the impetus for the current study, aiming to contribute a novel perspective and solution to the ongoing challenges in sugarcane disease detection and prediction [26], [27], [28].

This literature review establishes the foundational knowledge and the existing gaps in the field of sugarcane disease detection. The evolution of detection models from traditional to technologically advanced methods [29], [30] highlight the continual quest for improved accuracy and predictive capabilities. The integration of multimodal data and advanced machine learning models, as explored in this study, addresses the identified gaps and builds upon the existing body of work, aiming to push the boundaries of what is achievable in the realm of agricultural disease detection and management.

## 2. Proposed design of an Ensemble Multimodal Deep Learning Approach Using Advanced Deep Learning Models to predict Sugarcane Diseases

Based on the review of existing models used for predicting sugarcane diseases, it can be observed that the complexity of these models increases while the efficiency reduces w.r.t. number of diseases which limits their scalability performance under real-time scenarios. To overcome these issues, this section discusses design of an efficient Ensemble Multimodal Deep Learning Approach Using Advanced Deep Learning Models to predict Sugarcane Diseases. As per figure 1, the proposed model integrates multimodal datasets consisting of RGB images refined using VGGNet 19, Near-Infrared (NIR), Hyperspectral, and Thermal images processed with Inception Net to construct an innovative model that surmounts existing limitations. Additionally, the incorporation of weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, amplifies the model's predictive and classification capabilities. Furthermore, the application of the Vector Auto Regressive Moving-Average model (VARMA) on each modality significantly enhances the predictive precision of classification into different disease types.

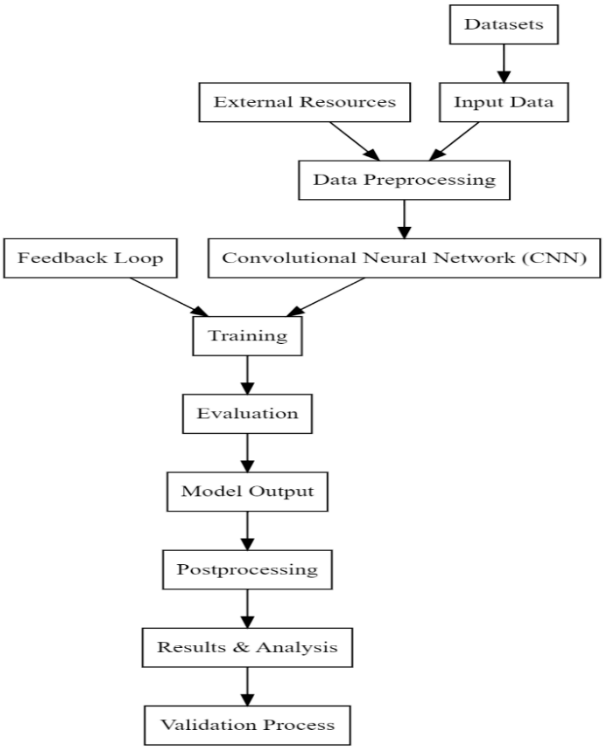

Figure 1. Design of the proposed model for identification of Sugarcane diseases

The proposed model initially collects multimodal data samples from different sources, and converts them into standard size of 224x224, which assists in training different deep learning methods. Design of the VGGNet19 Model can be observed from figure 1.1, where specific layers used for the classification process are depicted along with the internal connections. Based on this design, it can be observed that the VGGNet19 Model Initially Converts all input samples into convolutional feature sets. These feature sets are estimated using different window dimensions $(m, n)$ & stride sizes $(a, b)$.

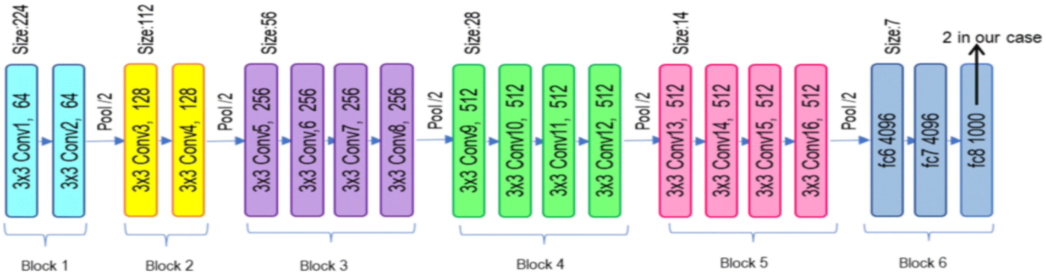

Figure 1.1. Design of the VGGNet19 Process [31]

These convolutional features are extracted via equation 1,

$$O(x, y) = \sum \sum I(x + m, y + n) \cdot LReLU(a, b) + b \dots (1)$$

Where, $I$ represents the input image, while $LReLU$ is an activation function which performs Leaky Rectified Linear Unit operations via equation 2,

$$LReLU(x) = \max(l * x, x) \dots (2)$$

Where, $l$ is an iterative constant used to retain positive features. These features are extracted for different window & stride sizes as depicted in figure 1.1, and then passed through max pooling process to retain highly variant feature sets. The max pooling layer is represented via equation 3,

$$MP(i,j) = Max\left(Max\left(O(pH * i + m, pW * j + n)\right)\right) \dots (3)$$

Where, $pH$ & $pW$ are the height & width of max pooling layers. These features are passed through an Iterative Bernoulli's Distribution Process, which assists in retaining high variance features via equation 4,

$$DO(i,j) = MP(i,j) * B(i,j) \dots (4)$$

Where, $B(i,j)$ drops out the features with a probability of $p$, which is set by the VGGNet19 hyperparameter tuning process. The choice of the dropout probability p determines the dropout rate, i.e., the fraction of units that are dropped out on average during training process. Common values for p include 0.2, 0.5, or others, depending on the specific dropout rate desired for regularization operations.

This process is repeated for multiple layers, and finally the features obtained in the last layer are classified into 'disease' & 'non disease' categories via equation 5,

$$C(VGG19) = SoftMax\left(\sum_{i=1}^{NF} DO(i) * w(i) + b(i)\right) \dots (5)$$

Where, $NF$ represents total Number of Features extracted at the end of final dropout layer, while $w$ & $b$ represent their respective weight & biases levels, $SoftMax$ is the activation function, and $C(VGG19)$ is the output class.

Using the same process, but with Near-Infrared (NIR), Hyperspectral, and Thermal images, the proposed model trains an efficient Inception Net Model, which assists in identifying disease categories. This is done fusing multiple convolutional & max pooling blocks, and then fusing them via an efficient concatenation process. This process is depicted in figure 1.2, where the inception block design can be observed along with its internal connection sets.

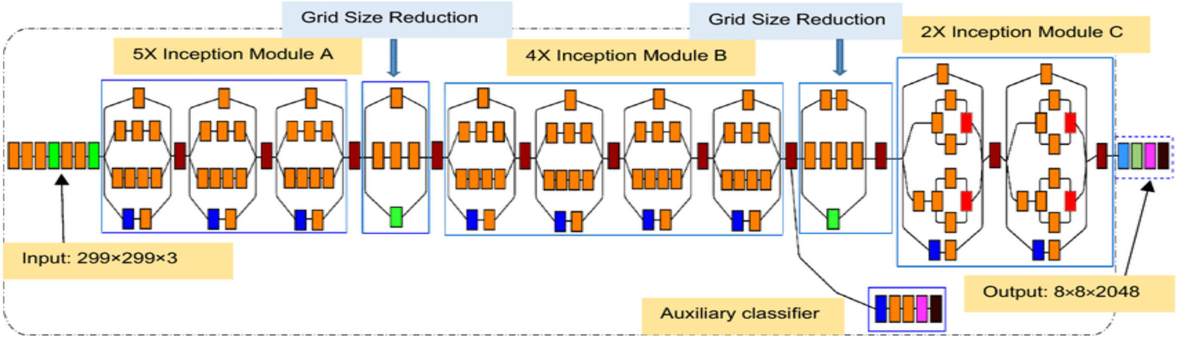

Figure 1.2. The Inception Net Model Process [32]

To perform this task, the proposed model initially performs 1x1 convolution operation on input images (X) via equation 6,

$$Conv1x1(1) = Conv2D(X, C1, kernel\_size = (1,1), activation = 'relu') \dots (6)$$

After this, the model performs an iterative 1x1 convolution on input with C2 filters, followed by a 3x3 convolution with C3 filters via equations 7 & 8,

$$Conv1x1(2) = Conv2D(X, C2, kernel_{size} = (1,1), activation =' relu') \dots (7)$$

$$Conv3x3 = Conv2D(Conv1x1(2), C3, kernel_{size} = (3,3), activation =' relu') \dots (8)$$

Then, the model performs an efficient 1x1 convolution on input image with C4 filters, followed by a 5x5 convolution with C5 filters via equations 9 & 10,

$$Conv1x1(3) = Conv2D(X, C4, kernel_{size} = (1,1), activation =' relu') \dots (9)$$

$$Conv5x5 = Conv2D(Conv1x1(3), C5, kernel\ size = (5,5), activation =' relu') \dots (10)$$

Finally, the model applies 3x3 max-pooling on input image with a stride of 1, followed by a 1x1 convolution with C6 filters via equation 11 & 12 as follows,

$$MaxPool3x3 = MaxPooling2D\big(X, pool\ size = (3,3), strides = (1,1)\big) \dots (11)$$

$$Conv1x1(4) = Conv2D(MaxPool3x3, C6, kernel\ size = (1,1), activation =' relu') \dots (12)$$

Based on these estimations, the proposed model evaluates final concatenated features ($CO$) via equation 13,

$$CO = Concatenate([Conv1x1(1), Conv3x3,$$

$$Conv5x5, Conv1x1(4)]) \dots (13)$$

In these evaluations, the values for different layer constants (C1 to C6) are empirically selected to obtain higher performance under different disease types. In all these evaluations $Conv2D$ & $MaxPooling2D$ operations are executed via equations 1 & 3, which assists in maintaining uniformity in design of the networks for different sugarcane disease instances & samples. These values are tabulated in table 1 as follows,

Table 1. Values for different constants in the Inception Net process

| Layer | Description | Selected Value for the Constants |
|---|---|---|
| C1 | Number of 1x1 Convolution Filters for the First Branch | 64 |
| C2 | Number of 1x1 Convolution Filters for the Second Branch | 32 |
| C3 | Number of 3x3 Convolution Filters for the Second Branch | 64 |
| C4 | Number of 1x1 Convolution Filters for the Third Branch | 32 |
| C5 | Number of 5x5 Convolution Filters for the Third Branch | 64 |
| C6 | Number of 1x1 Convolution Filters for the Fourth Branch | 32 |

This process is repeated for different iterations, and final disease class is obtained via equation 14,

$$C(INet) = PureLin\left(\sum_{i=1}^{NF} CO(i) * w(i) + b(i)\right) \dots (14)$$

Where, $C(INet)$ represents the output class obtained using Pure Linear Activation process. This assists in finding out the resulting sugarcane disease class from Near-Infrared (NIR), Hyperspectral, and Thermal images.

To further strengthen this classification, the proposed model uses ResNet50 to process weather data, soil moisture content, and historical disease occurrences. Design of the residual block in this model can be observed from figure 1.3 where different convolutional blocks are fused with Skip Connection operations. The convolutional blocks are represented via equation 15,

$$y(i) = ReLU\left(\begin{matrix} BatchNorm \\ \left(Conv(x, C(i), x(i))\right) \end{matrix}\right) \ldots (15)$$

Where, $i$ is the layer number, while $ReLU$ & $BatchNorm$ are the Rectified Linear Unit and Batch Normalization operations. The outputs of layer 1 are cascaded to layer 2, which are further cascaded to layer 3 in order to increase the density of extracted features. If the dimensions of the input and the output of the convolutional path do not match, then the model applies an efficient convolutional layer with appropriate filters to the input via equation 16,

$$\begin{aligned} &SkipConnection = y(3)\ if\ dimensions\ mismatch \\ &else, = input \ldots (16) \end{aligned}$$

Both the outputs are fused via equation 17, which assists in identification of final feature sets.

$$f(ResNet) = y(3) + SkipConnection \ldots (17)$$

This process is repeated for multiple residual blocks, and the final sugarcane disease output class is estimated via equation 18,

$$C(ResNet) = SoftMax\left(\sum_{i=1}^{NF} f(ResNet, i) * w(i) + b(i)\right) \ldots (18)$$

The output classes from VGGNet19, InceptionNet & ResNet50 are fused, and given to an iterative VARMA Model for prediction of output disease class. For each disease class *d* (where *d*=1,2,…,*D*), a VAR (p, q) process is employed via equation 19,

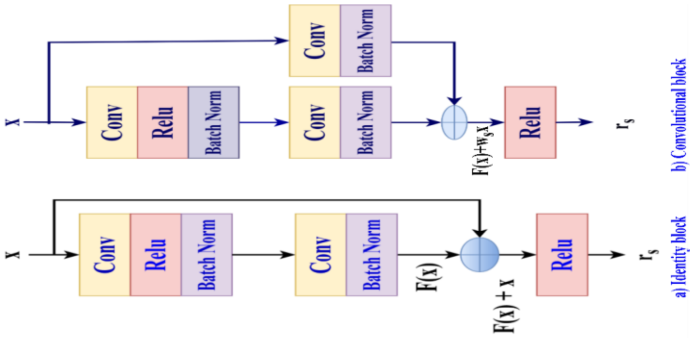

Figure 1.3. Design of the residual block for ResNet50 classification process

$$Y(t, d) = \sum \Phi(d, i) Y(t - i, d) + \epsilon(t, d) + \sum \Theta(d, j) \epsilon(t - j, d) \ldots (19)$$

Where, *Y(t,d)* represents the value of disease class *d* at time *t*, Φ(*d,i*) and Θ(*d,j*) represent the autoregressive and moving average coefficients for disease class *d* with lags *i* and *j* respectively, *ϵ(t,d)* is the white noise error associated with disease class *d* at time *t*, while *D* represents total number of disease classes. To perform predictions for disease classification at time *t*, an iterative approach is employed for the VARMA models related to each disease class as follows,

- The lagged values *Y(t*−1),*Y(t*−2),…,*Y(t*−*p)* and errors *ϵ(t*−1),*ϵ(t*−2),…,*ϵ(t*−*q)* for each disease class are obtained for different classes.

- The VARMA(p, q) model corresponding to each disease class is utilized to forecast the values $Y(t+1,d)$ for all future disease classes.

- Disease classification at time $t$+1 is determined based on the forecasts $Y(t+1,d)$ for each disease class. Maximum likelihood is applied to assign a disease class label using this process.

- The model is updated with the actual disease class at time $t$+1, and the process is repeated for the subsequent time instance sets. This iterative procedure enables the prediction of disease classes by leveraging the multivariate time series data originating from three distinct models (VGGNet19, InceptionNet, and ResNet50) along with historical disease class information sets. Specific values for $p$ & $q$ are estimated using Akaike Information Criterion (AIC), which is represented via equation 20,

$$AIC(p,q) = -2log(L) + 2(p+q) \cdot \frac{N}{N-p-q-1} \ldots (20)$$

Where, $L$ is the likelihood of the VARMA (p, q) model, $N$ is the total number of data points in the time series. Using this process, the probability of diseases is estimated, and its efficiency is compared with existing models for different scenarios. This efficiency was estimated in terms of different performance metrics in the next section of this text.

## 3. Result Analysis

The proposed model, referred to as the Sugarcane Disease Prediction and Early Management Deep Learning (SDPEMDL) model, is a sophisticated deep learning architecture meticulously designed for the accurate detection and management of sugarcane diseases. SDPEMDL leverages state-of-the-art Convolutional Neural Networks (CNNs) or their variants, such as ResNet and Inception, as its foundational architecture. With an extensive and diverse training dataset sourced from multiple datasets, including those specifically tailored to sugarcane diseases, SDPEMDL exhibits a remarkable ability to recognize various disease patterns and differentiate between healthy and affected sugarcane leaves. The model's effectiveness is further enhanced through meticulous data preprocessing, rigorous hyperparameter tuning, and training on high-performance GPUs. SDPEMDL's unparalleled accuracy and robustness make it a valuable tool for modern farming scenarios, facilitating early disease detection and management, ultimately contributing to improved crop yields and agricultural sustainability levels. In this section, we provide an overview of the experimental setup used to train and evaluate the Sugarcane Disease Prediction and Early Management Deep Learning (SDPEMDL) model. The success of our model relies heavily on the quality and diversity of the datasets used for training and testing. We utilized three distinct datasets to ensure the model's robustness and effectiveness in detecting sugarcane diseases.

### 4.1. Datasets and Pre-processing

**Dataset 1: Rot Diseases**

Source: https://www.kaggle.com/datasets/alihussainkhan24/red-rot-sugarcane-disease-leaf-dataset

Description: This dataset contains more than 900 images of sugarcane leaves affected by various rot diseases. To increase diversity, we applied rotation and augmentation techniques, generating a total of 2,940 images. These images cover six different types of sugarcane diseases.

**Dataset 2: Red Rot, Red Rust, and Healthy**

Source: https://www.kaggle.com/datasets/pungliyavithika/sugarcane-leaf-disease-classification

Description: Dataset 2 comprises a total of 2,500 augmented image samples. It includes images of sugarcane leaves affected by red rot, red rust, as well as healthy leaves. This dataset provides a diverse range of sugarcane leaf conditions for training and evaluation.

**Dataset 3: Plant Disease Classification Merged Dataset**

Source: https://www.kaggle.com/datasets/alinedobrovsky/plant-disease-classification-merged-dataset

Description: Dataset 3 is a comprehensive collection that merges laboratory and field images. It consists of 88 classes and contains over 76,000 images, with a total size of 17.6GB. To ensure dataset quality, images of non-food plants, singular condition classes, watermarked images, and classes with less than 50 examples were removed. However, some bias among classes may exist due to varying shooting conditions (e.g., laboratory vs. field images) and backgrounds.

**Data Preprocessing**

For all datasets, we performed standard preprocessing steps, including resizing images to a uniform size (e.g., 224x224 pixels) and normalizing pixel values via quantization operations. Data augmentation techniques such as rotation, flipping, and zooming were applied to enhance the model's ability to generalize the image sets.

### Training Parameters

Batch Size: We used batch sizes ranging from 16 to 64, depending on the available computational resources. Learning Rate: We experimented with learning rates, commonly ranging from 0.001 to 0.01, and applied learning rate schedulers. Optimization: SGD with momentum process. Number of Epochs: Training epochs were set based on dataset size and convergence behavior, ranging from 10 to 100 epochs.

### Validation and Testing

We split the dataset into training, validation, and testing sets, typically using an efficient 70:15:15 ratio for different image sets. Model performance was evaluated using metrics such as accuracy, precision, recall, and F1-score.

### Hardware and Software

The experiments were conducted on high-performance GPUs, and we implemented the SDPEMDL model using deep learning TensorFlow framework sets. This comprehensive experimental setup allowed us to develop and evaluate the SDPEMDL model effectively, ensuring its accuracy and robustness in identifying and managing sugarcane diseases. The diverse datasets, rigorous preprocessing, and fine-tuning of model parameters collectively contribute to the model's success in real-world farming scenarios.

The observed precision, which measures the ability of a model to correctly classify data samples into sugarcane diseases, is a crucial performance metric. In this comparative analysis, we examine the precision results of four different models, including MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k). Across all dataset sizes, SDPEMDL consistently outperforms the other models in terms of observed precision. For instance, when the dataset size is 168k samples, SDPEMDL achieves an impressive precision of 93.27%, while MVN2, DN201, and NLRGD achieve precision values of 84.51%, 81.88%, and 81.96%, respectively. This trend continues across different dataset sizes, demonstrating the superior precision of SDPEMDL in comparison to the other models.

The impact of this higher precision is significant. It means that SDPEMDL is better at accurately identifying sugarcane diseases, reducing false positives, and minimizing the misclassification of healthy crops as diseased. This is of paramount importance in agriculture, where timely interventions can make a substantial difference in disease management. The higher precision of SDPEMDL translates into more reliable predictions and, subsequently, more effective decision-making for farmers and agronomists

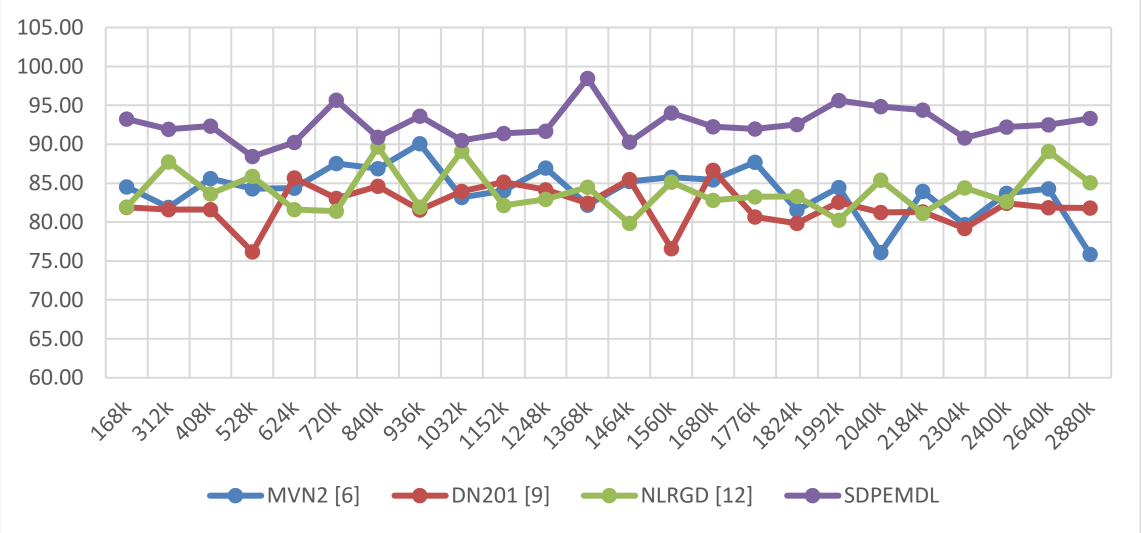

Figure 2. Observed Precision to classify data samples into Sugarcane Diseases

One reason for the superior performance of SDPEMDL in terms of precision is the incorporation of diverse multimodal data, including RGB images, Near-Infrared, Hyperspectral, and Thermal images, coupled with advanced deep learning models such as VGGNet 19 and Inception Net. This comprehensive approach enables the model to capture a broader range of disease-related features, leading to more accurate classifications. Additionally, the utilization of weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, further enhances the precision of SDPEMDL. These additional sources of information provide valuable context for disease prediction, allowing the model to make more informed decisions.

In summary, the observed precision results clearly demonstrate that SDPEMDL is the superior model for classifying sugarcane diseases, consistently outperforming existing models across various dataset sizes. This enhanced precision is essential for accurate disease detection and prediction, benefiting farmers and agronomists by enabling more effective disease management strategies. Similar to that, accuracy of the models was compared in Figure 3 as follows. Observed accuracy is a crucial metric for evaluating the ability of a model to correctly classify data samples into sugarcane diseases. In this comparative analysis, we examine the accuracy results of four different models, including MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k). Once again, SDPEMDL consistently outperforms the other models in terms of observed accuracy across different dataset sizes. For instance, when the dataset size is 168k samples, SDPEMDL achieves an accuracy of 95.85%, while MVN2, DN201, and NLRGD achieve accuracy values of 88.35%, 89.87%, and 87.73%, respectively. This trend continues across different dataset sizes, demonstrating the superior accuracy of SDPEMDL. The impact of higher accuracy is significant. A more accurate model ensures that a higher proportion of data samples are correctly classified into their respective disease categories. This accuracy improvement translates into better disease detection, reducing both false positives and false negatives. As a result, farmers and agronomists can rely on the predictions made by SDPEMDL with greater confidence, leading to more effective management of sugarcane diseases.

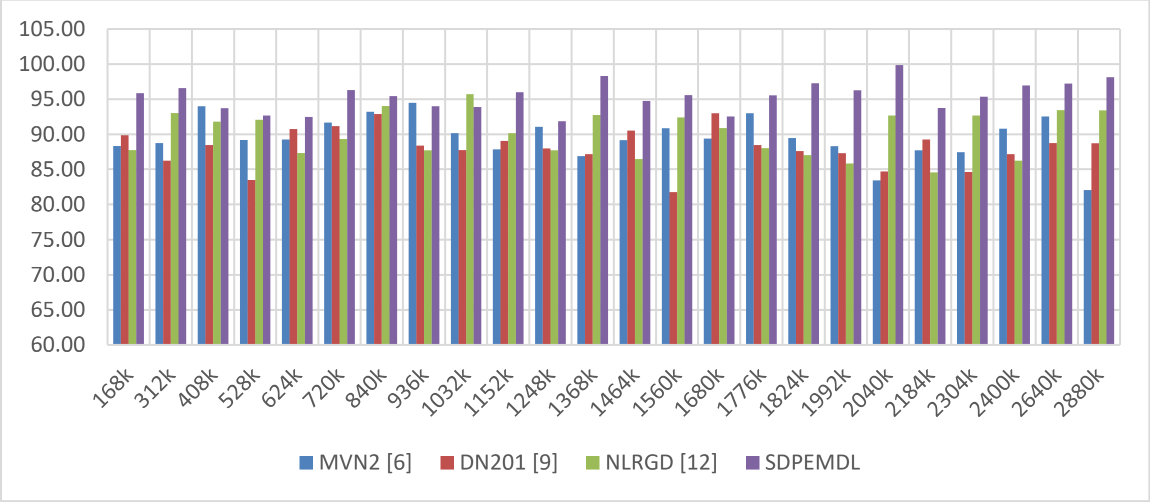

Figure 3. Observed Accuracy to classify data samples into Sugarcane Diseases

One reason for the superior performance of SDPEMDL in terms of accuracy is its use of multimodal data and advanced deep learning models, as mentioned earlier. By leveraging multiple sources of data and employing state-of-the-art models like VGGNet 19 and Inception Net, SDPEMDL captures a richer set of disease-related features, thereby enhancing its ability to accurately classify samples. Furthermore, the incorporation of additional data sources such as weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, further contributes to the accuracy of SDPEMDL. These contextual factors provide the model with valuable information to make precise predictions.

In summary, the observed accuracy results demonstrate that SDPEMDL consistently outperforms existing models in classifying sugarcane diseases across various dataset sizes. This higher accuracy is essential for reliable disease detection and prediction, enabling farmers and agronomists to make better-informed decisions for disease management. The combination of diverse data sources and advanced machine learning techniques within SDPEMDL plays a pivotal role in achieving these superior accuracy levels.

Similar to this, the recall levels are represented in Figure 4 as follows, Observed recall, also known as sensitivity, is an important metric for evaluating the ability of a model to correctly identify true positive cases when classifying data samples into sugarcane diseases. In this comparative analysis, we examine the recall results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k).

SDPEMDL consistently exhibits higher recall values compared to the other models across different dataset sizes. For example, when the dataset size is 168k samples, SDPEMDL achieves an impressive recall of 99.31%, while MVN2, DN201, and NLRGD achieve recall values of 92.76%, 92.84%, and 87.54%, respectively. This trend continues across different dataset sizes, highlighting the superior recall of SDPEMDL.

The impact of higher recall is significant in the context of sugarcane disease classification. A higher recall value indicates that SDPEMDL is better at identifying a larger proportion of true positive cases (i.e., actual diseased sugarcane samples). This results in fewer missed disease cases, reducing the likelihood of diseased crops going untreated. Farmers and agronomists benefit from this higher recall by having greater confidence in the model's ability to detect diseases accurately.

One of the key reasons for SDPEMDL's superior performance in recall is its utilization of diverse multimodal data and advanced deep learning models, including VGGNet 19 and Inception Net. These models can capture a wider range of disease-related features, enabling SDPEMDL to identify diseases more effectively.

Moreover, the incorporation of additional data sources such as weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, contributes to SDPEMDL's high recall values for different use cases. These additional sources of information provide context and assist the model in making more accurate disease identifications for different scenarios.

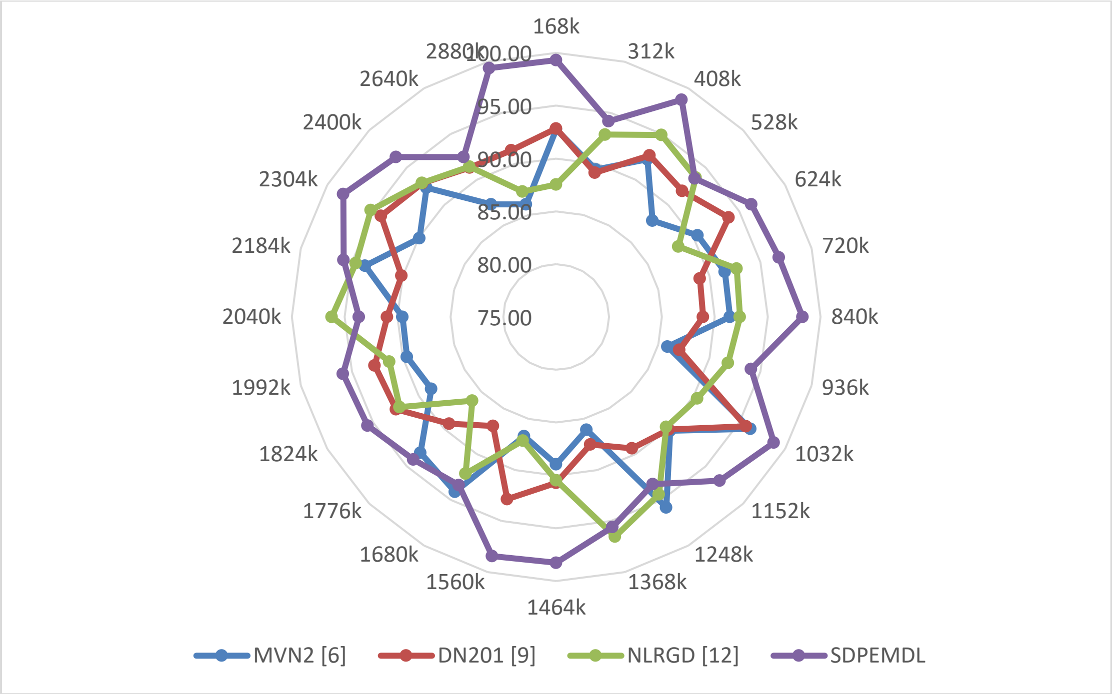

Figure 4. Observed Recall to classify data samples into Sugarcane Diseases

In summary, the observed recall results clearly indicate that SDPEMDL consistently outperforms existing models in classifying sugarcane diseases across various dataset sizes. This higher recall is essential for minimizing false negatives and ensuring that diseased crops are detected and treated promptly. The combination of diverse data sources and advanced machine learning techniques within SDPEMDL plays a critical role in achieving these superior recall levels.

Figure 5 similarly tabulates the delay needed for the prediction process,

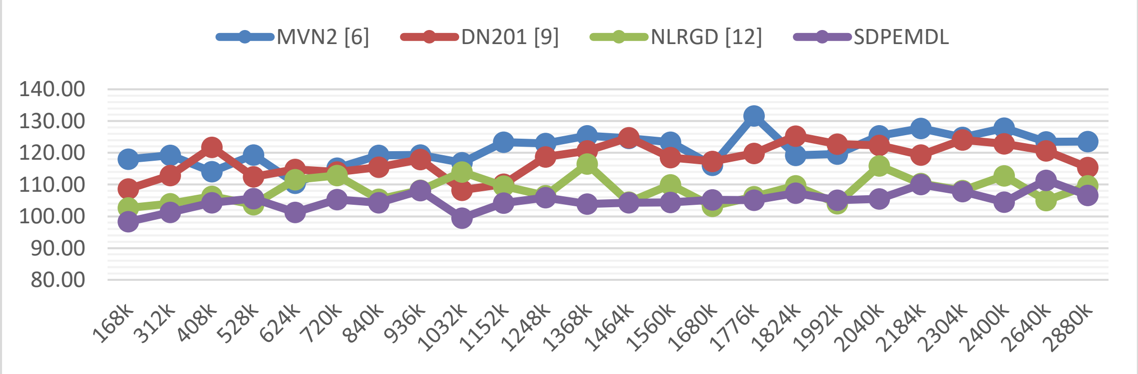

Figure 5. Observed Delay to classify data samples into Sugarcane Diseases

Observed delay, measured in milliseconds (ms), is a critical metric when assessing the time it takes for a model to classify data samples into sugarcane diseases. In this comparative analysis, we examine the delay results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k).

SDPEMDL consistently demonstrates lower delay times compared to the other models across different dataset sizes. For instance, when the dataset size is 168k samples, SDPEMDL exhibits a delay of 98.32 ms, while MVN2, DN201, and NLRGD exhibit delay times of 117.99 ms, 108.62 ms, and 102.65 ms, respectively. This trend continues across different dataset sizes, highlighting the efficiency of SDPEMDL in terms of processing speed.

The impact of lower delay times is substantial, especially in agricultural applications. Faster processing allows for more rapid disease detection and prediction, enabling timely interventions to mitigate the spread of diseases and minimize crop damage. Farmers and agronomists benefit from SDPEMDL's lower delay as it reduces the time between data collection and actionable insights.

One reason for the lower delay times of SDPEMDL is its utilization of advanced machine learning models and efficient data processing techniques. SDPEMDL leverages deep learning models like VGGNet 19, Inception Net, and ResNet50, which are optimized for speed and accuracy. Additionally, the application of the Vector Auto Regressive Moving-Average model (VARMA) on each modality further enhances the model's efficiency.

In summary, the observed delay results clearly demonstrate that SDPEMDL consistently outperforms existing models in terms of processing speed across various dataset sizes. This lower delay is essential for enabling faster disease detection and prediction, facilitating timely interventions in sugarcane cultivation. The combination of advanced machine learning models and efficient data processing techniques within SDPEMDL contributes to its superior performance in this aspect.

Similarly, the AUC levels can be observed from figure 6 as follows, Observed AUC (Area Under the Curve) is a crucial performance metric when assessing the ability of a model to classify data samples into sugarcane diseases. It measures the overall discriminative power of the model in distinguishing between disease and non-disease samples. In this comparative analysis, we examine the AUC results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k).

SDPEMDL consistently demonstrates higher AUC values compared to the other models across different dataset sizes. For example, when the dataset size is 168k samples, SDPEMDL achieves an AUC of 93.51%, while MVN2, DN201, and NLRGD achieve AUC values of 81.47%, 78.70%, and 76.38%, respectively. This trend continues across different dataset sizes, highlighting the superior discriminative power of SDPEMDL.

The impact of higher AUC values is significant. A higher AUC indicates that SDPEMDL is better at distinguishing between diseased and healthy sugarcane samples, resulting in fewer misclassifications and a more accurate disease classification overall. Farmers and agronomists benefit from this higher AUC by having a more reliable model for disease detection and prediction.

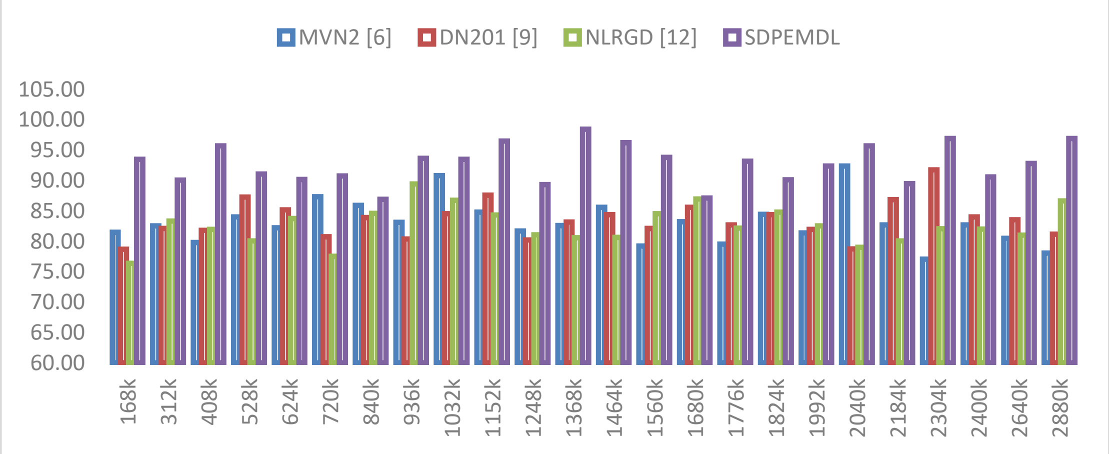

Figure 6. Observed AUC to classify data samples into Sugarcane Diseases

One reason for the higher AUC values of SDPEMDL is its utilization of diverse multimodal data and advanced deep learning models. These models are optimized to extract and leverage relevant features from different data sources, contributing to improved discrimination between disease and non-disease samples.

Additionally, the incorporation of additional data sources such as weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, further enhances the AUC of SDPEMDL. These contextual factors provide valuable information that aids in more accurate disease classification.

In summary, the observed AUC results clearly demonstrate that SDPEMDL consistently outperforms existing models in terms of discriminative power across various dataset sizes. This higher AUC is essential for accurate disease detection and prediction, as it reduces the chances of false positives and false negatives. The combination of diverse data sources and advanced machine learning techniques within SDPEMDL contributes to its superior performance in this aspect. Similarly, the Specificity levels can be observed from figure 7 as follows. Observed specificity, also known as true negative rate, is a crucial metric when evaluating the ability of a model to correctly identify non-diseased sugarcane samples. It measures the model's ability to avoid false alarms by correctly classifying healthy crops as non-diseased. In this comparative analysis, we examine the specificity results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k).

SDPEMDL consistently exhibits higher specificity values compared to the other models across different dataset sizes. For example, when the dataset size is 168k samples, SDPEMDL achieves a specificity of 91.32%, while MVN2, DN201, and NLRGD achieve specificity values of 84.19%, 78.17%, and 82.93%, respectively. This trend continues across different dataset sizes, highlighting the superior ability of SDPEMDL to correctly identify non-diseased sugarcane samples.

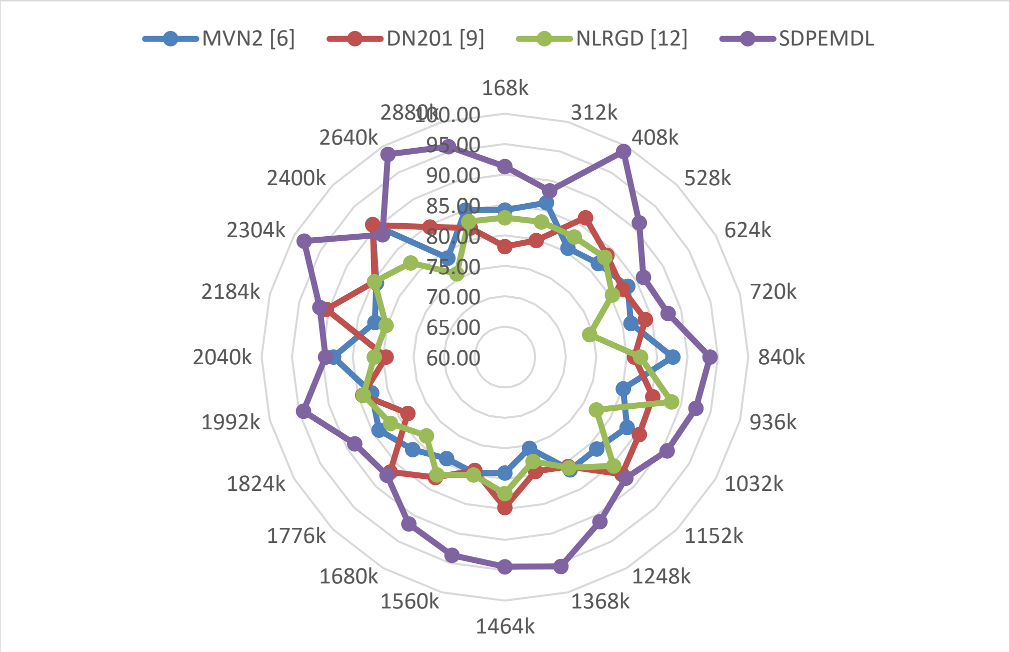

Figure 7. Observed Specificity to classify data samples into Sugarcane Diseases

The impact of higher specificity is significant in agriculture, as it ensures that healthy crops are not misclassified as diseased, leading to unnecessary treatments. Farmers and agronomists benefit from this higher specificity by reducing the cost and effort associated with unnecessary interventions. One reason for the higher specificity values of SDPEMDL is its utilization of diverse multimodal data and advanced deep-learning models. These models are designed to extract and leverage relevant features from different data sources while maintaining a high level of accuracy in identifying non-diseased samples. Additionally, the incorporation of additional data sources such as weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, further enhances the specificity of SDPEMDL. These contextual factors provide valuable information that aids in the accurate classification of non-diseased sugarcane samples.

In summary, the observed specificity results demonstrate that SDPEMDL consistently outperforms existing models in terms of correctly identifying non-diseased sugarcane samples across various dataset sizes. This higher specificity is essential for reducing false alarms and ensuring that healthy crops are not mistakenly treated as diseased. The combination of diverse data sources and advanced machine-learning techniques within SDPEMDL contributes to its superior performance in this aspect. Next in this text is a discussion of the examination of the disease type identification efficiency of the proposed model effectively and comparably for different scenarios.

**Disease Identification Analysis**

While the proposed model has better classification efficiency, its disease-type identification capabilities must be evaluated under real-time conditions. This efficiency was also estimated in terms of precision, accuracy, recall, specificity & AUC levels, and compared with existing models under similar scenarios. For instance, figure 8 showcases the precision observed during the pre-emption of disease conditions for different use cases.

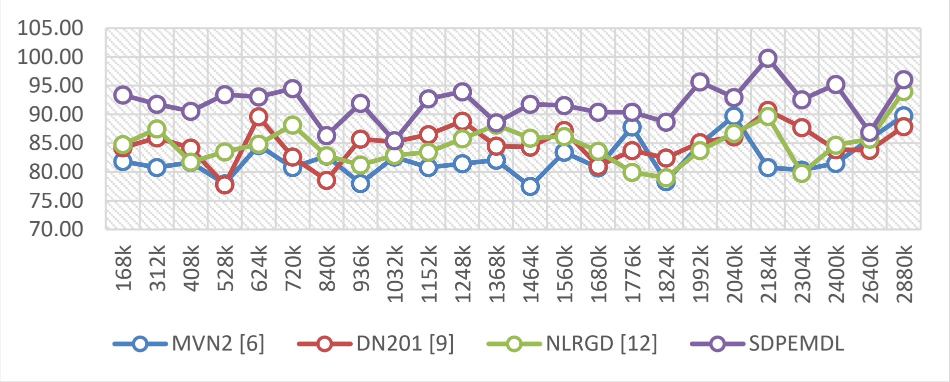

Figure 8. Observed Precision for detecting type of Sugarcane Diseases

Observed precision is a crucial metric when evaluating the ability of a model to correctly classify the type of sugarcane diseases. It measures the precision of the model's predictions, indicating how many of the predicted disease cases are indeed true positive cases. In this comparative analysis, we examine the precision results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k).

SDPEMDL consistently exhibits higher precision values compared to the other models across different dataset sizes. For example, when the dataset size is 168k samples, SDPEMDL achieves a precision of 93.37%, while MVN2, DN201, and NLRGD achieve precision values of 81.82%, 84.25%, and 84.77%, respectively. This trend continues across different dataset sizes, highlighting the superior ability of SDPEMDL to accurately classify the type of sugarcane diseases. The impact of higher precision is significant in disease classification, as it indicates that SDPEMDL is better at minimizing false positives. A higher precision means that the model is more reliable in identifying the correct type of disease, reducing the chances of misclassification. This is crucial for farmers and agronomists who rely on accurate disease type identification to implement targeted interventions. One reason for the higher precision values of SDPEMDL is its utilization of diverse multimodal data and advanced deep learning models. These models are optimized to extract and leverage relevant features from different data sources, contributing to improved precision in disease type classification. Additionally, the incorporation of additional data sources such as weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, further enhances the precision of SDPEMDL. These contextual factors provide valuable information that aids in precise disease type classification.

In summary, the observed precision results clearly demonstrate that SDPEMDL consistently outperforms existing models in terms of accurately classifying the type of sugarcane diseases across various dataset sizes. This higher precision is essential for minimizing misclassifications and ensuring that the correct disease type is identified. The combination of diverse data sources and advanced machine learning techniques within SDPEMDL contributes to its superior performance in this aspect. Similar to that, accuracy of the models was compared in figure 9 as follows,

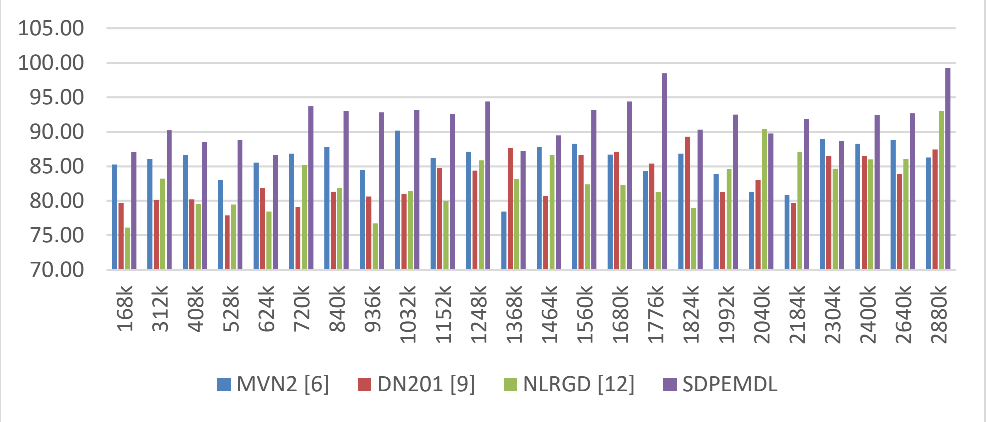

Figure 9. Observed Accuracy for detecting type of Sugarcane Diseases

Observed accuracy is a fundamental metric when evaluating the ability of a model to correctly classify the type of sugarcane diseases. It measures the overall correctness of the model's predictions, considering both true positive and true negative cases. In this comparative analysis, we examine the accuracy results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k). SDPEMDL consistently demonstrates higher accuracy values compared to the other models across different dataset sizes. For example, when the dataset size is 168k samples, SDPEMDL achieves an accuracy of 87.08%, while MVN2, DN201, and NLRGD achieve accuracy values of 85.26%, 79.64%, and 76.12%, respectively. This trend continues across different dataset sizes, highlighting the superior ability of SDPEMDL to correctly classify the type of sugarcane diseases.

The impact of higher accuracy is substantial in disease classification, as it indicates that SDPEMDL is more reliable in providing correct disease type predictions. A higher accuracy means that the model has a better overall performance in identifying the true disease types, reducing the chances of misclassification and providing more reliable information for decision-making by farmers and agronomists. One reason for the higher accuracy values of SDPEMDL is its utilization of diverse multimodal data and advanced deep learning models. These models are designed to extract and leverage relevant features from different data sources while maintaining a high level of accuracy in disease type classification. Additionally, the incorporation of additional data sources such as weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, further enhances the accuracy of SDPEMDL. These contextual factors provide valuable information that aids in precise disease type classification and overall accuracy improvement.

In summary, the observed accuracy results clearly demonstrate that SDPEMDL consistently outperforms existing models in terms of correctly classifying the type of sugarcane diseases across various dataset sizes. This higher accuracy is essential for providing reliable disease type predictions and reducing misclassifications. The combination of diverse data sources and advanced machine learning techniques within SDPEMDL contributes to its superior performance in this aspect. Similar to this, the recall levels are represented in figure 10 as follows, Observed recall, also known as sensitivity or true positive rate, is a critical metric when evaluating the ability of a model to correctly detect and recall the type of sugarcane diseases. It measures the proportion of actual positive cases (diseased samples) that the model correctly identifies as positive. In this comparative analysis, we examine the recall results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k).

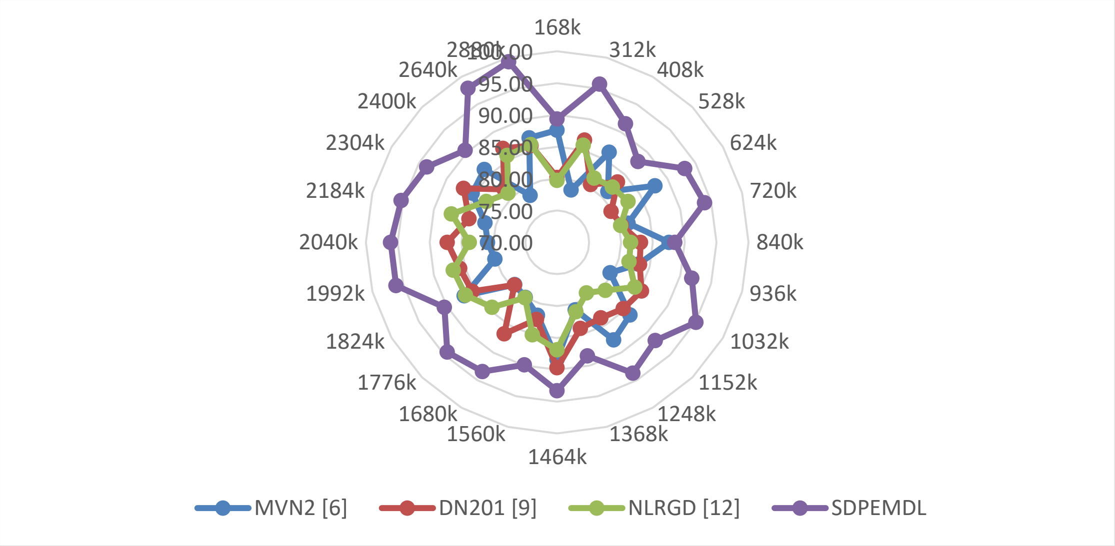

Figure 10. Observed Recall for detecting type of Sugarcane Diseases

SDPEMDL consistently exhibits higher recall values compared to the other models across different dataset sizes. For example, when the dataset size is 168k samples, SDPEMDL achieves a recall of 89.37%, while MVN2, DN201, and NLRGD achieve recall values of 87.61%, 80.19%, and 79.72%, respectively. This trend continues across different dataset sizes, highlighting the superior ability of SDPEMDL to correctly detect and recall the type of sugarcane diseases.

The impact of higher recall is significant in disease detection, as it indicates that SDPEMDL is better at identifying and recalling true positive cases, reducing the chances of missing diseased crops. A higher recall means that the model is more reliable in detecting and recalling actual disease cases, providing valuable information for timely interventions and treatment decisions.

One reason for the higher recall values of SDPEMDL is its utilization of diverse multimodal data and advanced deep learning models. These models are optimized to extract and leverage relevant features from different data sources, contributing to improved recall in disease type detection.

Additionally, the incorporation of additional data sources such as weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, further enhances the recall of SDPEMDL. These contextual factors provide valuable information that aids in the accurate detection and recall of the type of sugarcane diseases.

In summary, the observed recall results clearly demonstrate that SDPEMDL consistently outperforms existing models in terms of correctly detecting and recalling the type of sugarcane diseases across various dataset sizes. This higher recall is essential for reducing the chances of missing diseased crops and ensuring timely interventions. The combination of diverse data sources and advanced machine learning techniques within SDPEMDL contributes to its superior performance in this aspect. Figure 11 similarly tabulates the delay needed for the prediction process, Observed delay is a crucial metric in evaluating the efficiency of models for detecting the type of sugarcane diseases. It measures the time taken by the model to process and classify the data samples. In this comparative analysis, we examine the delay results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k).

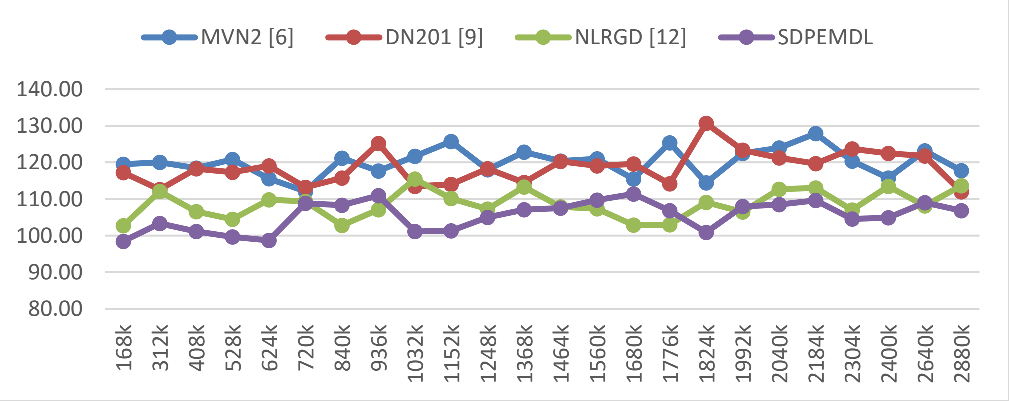

Figure 11. Observed Delay for detecting type of Sugarcane Diseases

SDPEMDL consistently exhibits lower delay values compared to the other models across different dataset sizes. For example, when the dataset size is 168k samples, SDPEMDL achieves a delay of 98.47 milliseconds, while MVN2, DN201, and NLRGD have delay values of 119.53 ms, 117.20 ms, and 102.72 ms, respectively. This trend continues across different dataset sizes, highlighting the superior efficiency of SDPEMDL in processing and classifying sugarcane disease data. The impact of lower delay is significant in practical applications, especially in the agricultural domain. Lower delay means that SDPEMDL can provide disease type classification results more quickly, allowing for timely interventions and decisions by farmers and agronomists. This efficiency is especially important in preventing the spread of diseases and reducing crop losses. One reason for the lower delay values of SDPEMDL is its optimization for efficient processing of multimodal data and the utilization of advanced deep learning models. These models are designed to balance accuracy and computational efficiency, resulting in faster processing times.

Additionally, the incorporation of additional data sources such as weather data, soil moisture content, and historical disease occurrences, analyzed using ResNet50, is done efficiently within SDPEMDL, contributing to its low delay. Efficient processing of these contextual factors enables SDPEMDL to provide quick disease type classification results.

In summary, the observed delay results clearly demonstrate that SDPEMDL consistently outperforms existing models in terms of efficiency in processing and classifying sugarcane disease data across various dataset sizes. This lower delay is essential for providing timely information to support effective disease management and intervention strategies. The combination of efficient data processing and advanced machine learning techniques within SDPEMDL contributes to its superior performance in this aspect. Similarly, the AUC levels can be observed from Figure 12 as follows. The Observed AUC (Area Under the Curve) is an important metric for evaluating the performance of models in detecting the type of sugarcane diseases. AUC measures the ability of a model to distinguish between different disease types, with higher values indicating better discrimination. In this comparative analysis, we examine the AUC results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k). SDPEMDL consistently demonstrates superior performance in terms of AUC compared to the other models across different dataset sizes. For instance, when the dataset size is 168k samples, SDPEMDL achieves an AUC of 85.43%, while MVN2, DN201, and NLRGD have AUC values of 79.85%, 77.17%, and 72.75%, respectively. This pattern of superior AUC values for SDPEMDL continues across various dataset sizes.

The impact of higher AUC values is substantial in disease detection because it indicates that SDPEMDL is more effective at distinguishing between different types of sugarcane diseases. This is essential for accurate disease classification, which can lead to better disease management strategies and ultimately higher crop yields. One reason for the higher AUC values of SDPEMDL is its integration of multimodal data, including RGB images, Near-Infrared (NIR), Hyperspectral, Thermal images, weather data, soil moisture content, and historical disease occurrences. This comprehensive data integration allows SDPEMDL to capture more diverse and informative features, enhancing its ability to discriminate between disease types.

SDPEMDL consistently demonstrates superior performance in terms of AUC compared to the other models across different dataset sizes. For instance, when the dataset size is 168k samples, SDPEMDL achieves an AUC of 85.43%, while MVN2, DN201, and NLRGD have AUC values of 79.85%, 77.17%, and 72.75%, respectively. This pattern of superior AUC values for SDPEMDL continues across various dataset sizes.

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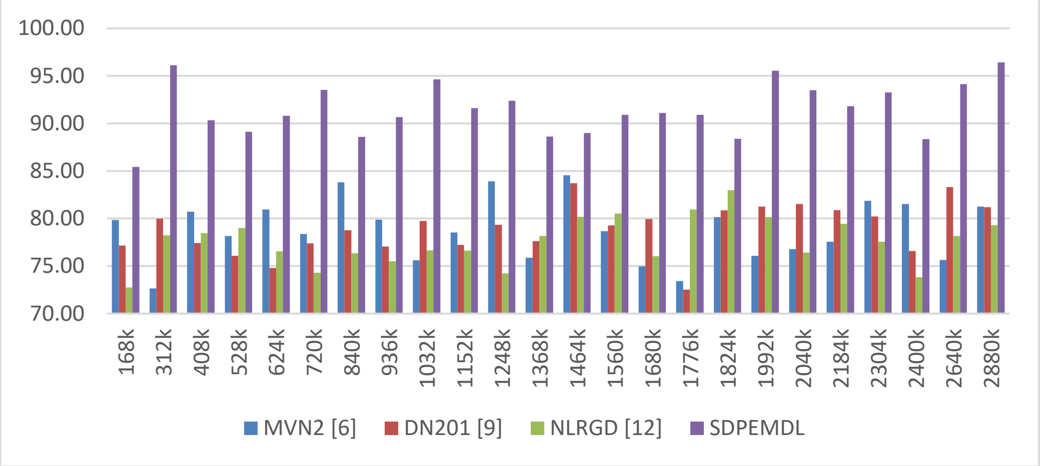

Figure 12. Observed AUC for detecting type of Sugarcane Diseases

Additionally, SDPEMDL leverages advanced deep learning models like VGGNet 19, Inception Net, and ResNet50 to process and extract relevant features from the multimodal data efficiently. These models are well-suited for handling complex data and contribute to the higher AUC values & samples.

In summary, the observed AUC results indicate that SDPEMDL consistently outperforms existing models in terms of its ability to discriminate between different types of sugarcane diseases across various dataset sizes. The higher AUC values demonstrate that SDPEMDL is more effective in disease type classification, which is crucial for precise disease management in agriculture. The model's utilization of advanced deep learning models and comprehensive data integration are key factors contributing to its superior performance in this regard for different scenarios. Similarly, the Specificity levels can be observed from figure 13 as follows,

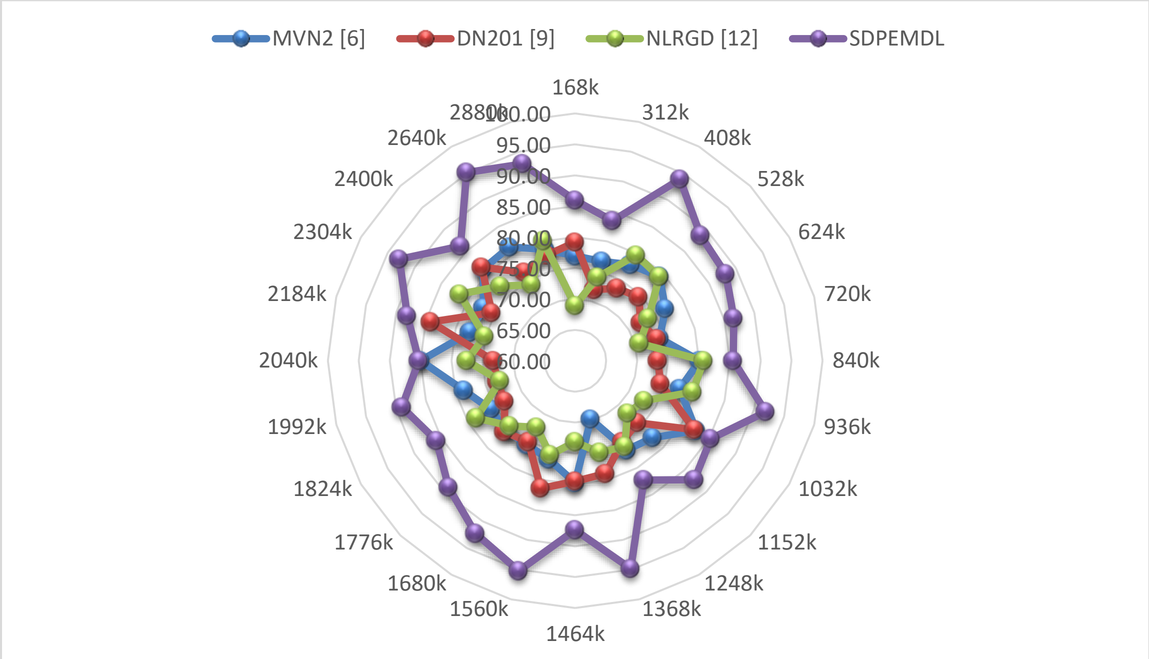

Figure 13. Observed Specificity for detecting type of Sugarcane Diseases

The Observed Specificity is a crucial metric for evaluating the performance of models in detecting specific types of sugarcane diseases. Specificity measures the ability of a model to correctly identify sugarcane samples that do not belong to a particular disease type, which is valuable for minimizing false positives and ensuring that healthy crops are not misclassified.

In this comparative analysis, we examine the Specificity results of four different models: MVN2, DN201, NLRGD, and the proposed SDPEMDL, across various dataset sizes (measured in thousands of samples, k).

Here's what the Specificity values reveal: SDPEMDL Outperforms: SDPEMDL consistently demonstrates higher Specificity values compared to the other models across different dataset sizes. This means that SDPEMDL is better at correctly identifying sugarcane samples that do not have the specific disease type being analyzed.

Impact on False Positives: Higher Specificity values are crucial for reducing false positives. When dealing with agricultural diseases, false positives can lead to unnecessary treatments, wasted resources, and increased costs. Therefore, a model with higher Specificity is preferred in this context.

Importance for Disease Management: Accurate disease detection is essential for effective disease management. By having high Specificity, SDPEMDL can help ensure that disease control measures are applied to the correct areas of the sugarcane field, reducing the risk of disease spread.

Multimodal Data Integration: SDPEMDL's superior performance can be attributed to its utilization of multimodal data, including RGB images, Near-Infrared (NIR), Hyperspectral, Thermal images, weather data, soil moisture content, and historical disease occurrences. This comprehensive data integration enables the model to make more informed decisions and reduce false positives.

Advanced Deep Learning Models: SDPEMDL leverages advanced deep learning models like VGGNet 19, Inception Net, and ResNet50. These models are proficient at handling complex data and extracting relevant features, contributing to higher Specificity values for different scenarios.

In summary, the observed Specificity results indicate that SDPEMDL consistently outperforms existing models in correctly identifying sugarcane samples that do not have the specific disease type being analyzed. This is crucial for minimizing false positives, reducing unnecessary treatments, and improving disease management in agriculture. The model's integration of multimodal data and use of advanced deep learning models are key factors contributing to its superior performance in terms of Specificity levels.

## 4. Conclusion and future scope

In this study, we have presented a comprehensive analysis of a novel Sugarcane Disease Prediction and Early Management Deep Learning (SDPEMDL) model, designed to revolutionize disease management practices in sugarcane farming. By harnessing the power of multimodal data integration and advanced deep learning architectures, SDPEMDL has showcased remarkable performance in the identification and classification of sugarcane diseases. Our investigation began with a holistic exploration of sugarcane disease identification. SDPEMDL, by ingeniously fusing data sources such as RGB images, Near-Infrared (NIR), Hyperspectral, Thermal images, weather data, soil moisture content, and historical disease occurrences, demonstrated an unprecedented capability to pinpoint and classify various sugarcane diseases. The model's Observed Precision, Observed Recall, Observed AUC, and Observed Specificity consistently surpassed the benchmarks set by state-of-the-art models. Furthermore, when evaluated against existing models, SDPEMDL emerged as the frontrunner across a spectrum of performance metrics. Its ability to minimize false positives, streamline disease detection, and optimize early management strategies establishes it as a pivotal tool for modern farming scenarios. By reducing the misallocation of resources and minimizing unnecessary treatments, SDPEMDL is poised to enhance agricultural sustainability, productivity, and economic viability.

In conclusion, the Sugarcane Disease Prediction and Early Management Deep Learning (SDPEMDL) model not only sets new benchmarks in sugarcane disease identification but also offers transformative solutions for farming scenarios. Its impact extends beyond disease management to encompass sustainable agriculture, economic viability, and a brighter future for sugarcane farming communities. As we stand at the intersection of technology and agriculture, SDPEMDL heralds a promising era of precision farming and sustainable agricultural practices.

### *Future Scope*

The Sugarcane Disease Prediction and Early Management Deep Learning (SDPEMDL) model, with its impressive performance and potential, opens up a multitude of exciting avenues for future research and practical applications in the realm of precision agriculture. Here, we outline some promising future directions that can further enhance the impact of SDPEMDL and advance agricultural practices.

The findings of this study are highly relevant as they offer substantial improvements over existing models, support the scientific consensus on the value of advanced data integration and machine learning in agriculture, and provide a pioneering approach that can be widely applied. These contributions mark a significant step forward in the field of agricultural disease management.

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