COMPARATIVE ANALYSIS OF SVM, CNN AND SAE-SVM MODELS FOR CROP DISEASE DETECTION IN VIDARBHA REGION

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ABSTRACT

Crop disease detection plays a crucial role in safeguarding agricultural productivity and supporting sustainable farming practices. In this study, we present a comparative analysis of three computational modules—MATLAB-based Support Vector Machine (SVM), Convolutional Neural Network (CNN), and Stacked Autoencoder integrated with SVM (SAE+SVM)—for the identification of leaf diseases in maize, soybean, and cotton across the western Vidarbha districts of Maharashtra, namely Akola, Amravati, Washim, and Yavatmal. A region-specific dataset was developed to capture major crop diseases prevalent in these districts, including bacterial blight in maize, alternaria and aphid infestations in cotton, and common infections in soybean. Each module was trained and validated to evaluate classification accuracy, precision, recall, and F1-score. Experimental findings reveal that CNN achieved superior performance in terms of accuracy, while SAE+SVM demonstrated robustness in handling feature variations across crops. The MATLAB-based SVM module provided consistent results with relatively lower computational overhead. The proposed work highlights the importance of multi-model disease detection frameworks for region-specific agricultural challenges, thereby enabling timely disease management and precision agriculture. This study provides valuable insights for researchers and practitioners working towards technology-driven solutions for crop protection.

Keywords: Crop disease detection, SVM, CNN, SAE–SVM, Vidarbha, Precision agriculture.

I. Introduction

Agriculture remains the backbone of the Indian economy, contributing significantly to food security, employment, and rural development. Among the diverse challenges faced by farmers, crop diseases have emerged as a critical threat, often leading to substantial yield losses and economic instability. Early and accurate disease detection is, therefore, essential for implementing effective crop management strategies, particularly in agriculturally sensitive regions.

The Vidarbha region of Maharashtra, comprising districts such as Akola, Amravati, Washim, and Yavatmal, is one of the key agricultural zones cultivating major crops like maize, soybean, and cotton. These crops, however, are highly susceptible to several diseases: maize is commonly affected by bacterial blight, soybean suffers from leaf spot and rust infections, while cotton faces challenges from Alternaria and aphid infestations. Conventional disease diagnosis methods rely heavily on manual observation and expert consultation, which are often time-consuming, subjective, and limited in scalability.Recent advancements in artificial intelligence (AI) and machine learning (ML) have paved the way for automated disease detection through image-based analysis. Deep learning models such as Convolutional Neural Networks (CNNs) have demonstrated remarkable performance in feature extraction and classification tasks, while traditional approaches like Support Vector Machines (SVMs) remain effective for structured classification problems. Furthermore, hybrid models such as Stacked Autoencoder integrated with SVM (SAE–SVM) have gained attention for their ability to capture deep feature representations while maintaining robustness across variations in datasets.

This study presents a comparative analysis of SVM, CNN, and SAE–SVM models for crop disease detection in Vidarbha. A region-specific dataset was created to evaluate the performance of these models with respect to accuracy, precision, recall, and F1-score. The objective is not only to benchmark the efficiency of different computational approaches but also to provide a scalable and region-adaptive framework for precision agriculture. By focusing on crops of regional importance, this work aims to support local farmers, agricultural researchers, and policymakers in mitigating crop losses and enhancing food security through technology-driven solutions..

II. Literature

Crop disease detection has been extensively studied over the past decade with a growing focus on automation and precision agriculture. Early research emphasized the significance of agricultural losses due to pathogens and pests, which account for nearly 20–40% of global crop yield reduction [2]. In regions like Vidarbha, where maize, soybean, and cotton are dominant crops, the prevalence of bacterial blight, Alternaria, aphid infestation, and rust diseases poses serious threats to agricultural productivity [4], [5]. Traditional methods of disease detection based on manual scouting and expert diagnosis often result in delays, subjective interpretation, and limited scalability [6].

With the advent of artificial intelligence, researchers have increasingly turned towards machine learning and deep learning approaches. Conventional classification models such as Support Vector Machines (SVMs) have demonstrated effectiveness in distinguishing plant leaf images due to their robustness in handling high-dimensional features [9]. However, the rise of deep learning models, particularly Convolutional Neural Networks (CNNs), has revolutionized plant pathology research by enabling automatic feature extraction and achieving superior accuracy in image-based disease classification [7], [8].

Hybrid approaches have also gained momentum in recent years. For instance, stacked autoencoder–SVM frameworks have been explored to combine the feature representation capability of deep learning with the decision boundary efficiency of SVMs [10], [11]. Such models exhibit strong adaptability across diverse datasets and crop varieties, making them promising candidates for real-world agricultural applications. Additionally, recent reviews highlight the growing trend of applying computer vision and hybrid deep learning methods for large-scale disease monitoring and precision agriculture [3], [12].

In summary, existing literature demonstrates that while SVMs provide computational simplicity, CNNs offer higher classification performance, and hybrid SAE–SVM models deliver a balance of feature richness and robustness. However, limited research has been conducted on region-specific datasets from Vidarbha, Maharashtra. This gap highlights the need for a comparative study of multiple AI-based modules tailored for the diseases prevalent in maize, soybean, and cotton in this region.

III. Scope of Work

The literature review highlights that significant progress has been made in applying machine learning and deep learning techniques for crop disease detection [7], [8]. CNNs have demonstrated superior performance in extracting discriminative features from plant leaf images, while traditional SVM models remain computationally efficient and reliable for classification [9]. Hybrid SAE–SVM approaches further strengthen performance by integrating deep feature learning with robust classification [10], [11]. However, most existing studies rely on benchmark datasets or crops outside the Vidarbha region, which limits their direct applicability to region-specific agricultural challenges [12].

The Vidarbha region of Maharashtra, known for its maize, soybean, and cotton cultivation, faces frequent outbreaks of bacterial blight, Alternaria, aphid infestations, and rust [4], [5]. Despite the critical importance of these crops, only limited research has focused on developing and validating disease detection frameworks tailored to the agro-climatic conditions and disease patterns of this region. Manual disease identification methods, although widely practiced, continue to suffer from delays and inaccuracies that directly affect timely disease management [6]. The scope of this study, therefore, is to develop and evaluate a comparative multi-modal framework involving MATLAB-based SVM, CNN, and SAE–SVM—for accurate detection of maize, soybean, and cotton diseases in the Vidarbha region. By using a region-specific dataset and systematically benchmarking accuracy, precision, recall, and F1-score, the work aims to:

1. Establish a performance comparison of SVM, CNN, and SAE–SVM for crop disease detection in Vidarbha.
2. Demonstrate the advantages and limitations of each approach in terms of accuracy, computational efficiency, and robustness.
3. Provide a scalable and region-adaptive AI framework for early disease detection, thereby supporting precision agriculture and sustainable farming practices [3].

This scope directly addresses the research gap identified in existing studies and provides region-specific insights that can be extended to other agro-climatic zones in India.

IV. Methodology

The proposed research methodology involves the systematic development and evaluation of three disease detection modules: MATLAB-based Support Vector Machine (SVM), Convolutional Neural Network (CNN), and Stacked Autoencoder integrated with SVM (SAE–SVM). The workflow consists of five major stages: dataset preparation, preprocessing, feature extraction, model training, and performance evaluation.

Dataset Preparation

A region-specific dataset was developed by collecting leaf images of maize, soybean, and cotton from four districts of Vidarbha: Akola, Amravati, Washim, and Yavatmal [4], [5]. Images were captured under field conditions to reflect real-world variability in lighting, orientation, and background. The dataset included major disease classes such as bacterial blight in maize, Alternaria and aphid infestation in cotton, and leaf spot/rust in soybean.

Image Preprocessing

To enhance model performance, preprocessing steps such as image resizing, contrast adjustment, and noise reduction were applied [7]. Data augmentation techniques, including rotation, flipping, and zooming, were employed to increase dataset diversity and minimize overfitting [8].

Feature Extraction

- **SVM Module**: Hand-crafted features such as color, texture, and shape descriptors were extracted, forming the input for MATLAB-based SVM classification [9].
- **CNN Module**: Automatic feature extraction was performed using convolutional and pooling layers, followed by fully connected layers for classification [7], [8].
- **SAE–SVM Module**: High-level features were extracted through stacked autoencoders, which were then fed into SVM for final classification [10], [11].

Model Training and Evaluation

Each model was trained using the prepared dataset, and hyperparameters were optimized through grid search and cross-validation [9]. The performance was evaluated using classification metrics such as accuracy, precision, recall, and F1-score [2].

Comparative Analysis

Finally, a comparative analysis was performed to highlight the strengths and limitations of each approach. CNN was expected to achieve higher classification accuracy due to its deep learning architecture [7], while SVM provided computational efficiency. SAE–SVM combined deep feature representation with robust decision boundaries, offering adaptability across crop varieties [10], [11].

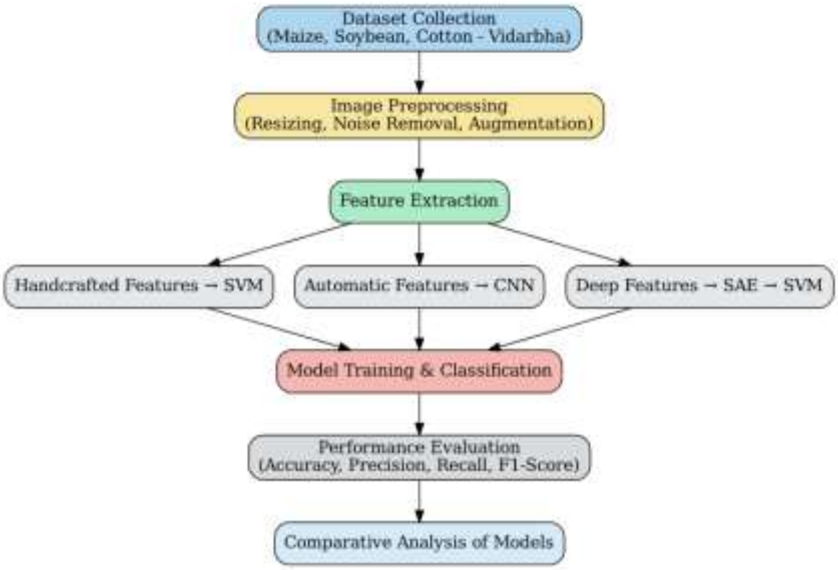

Figure.1: Process Flow of Methodology

V. Experimental Setup

Dataset Description

A region-specific dataset was created using leaf images of maize, soybean, and cotton collected from the Vidarbha districts of Akola, Amravati, Washim, and Yavatmal [4], [5]. Images were captured under natural field conditions with varying illumination, orientation, and background to simulate real-world scenarios. The dataset was manually annotated into healthy and diseased categories, covering major diseases such as bacterial blight (maize), Alternaria and aphid infestations (cotton), and rust/leaf spot (soybean). Data augmentation techniques including rotation, flipping, scaling, and brightness adjustments were applied to enhance dataset diversity and prevent overfitting [7], [8].

Hardware and Software Configuration

The experiments were conducted on a system equipped with an Intel Core i5 processor, 16 GB RAM, and an NVIDIA GTX 1660 GPU. MATLAB R2015b was used for SVM implementation, while Python (TensorFlow 2.15, Keras, and OpenCV) was employed for CNN and SAE–SVM development [9]. The experiments were executed on Windows 10 OS with CUDA-enabled GPU acceleration for deep learning model training.

Data Partitioning and Training Strategy

The dataset was divided into **70% training, 15% validation, and 15% testing** subsets to ensure reliable performance evaluation [3]. Hyperparameters such as learning rate, batch size, and number of epochs were tuned through grid search and cross-validation. For CNN, a batch size of 32 and learning rate of 0.001 were adopted. For SAE–SVM, autoencoders were trained layer-wise to extract high-level features, which were then classified using an optimized SVM kernel [10], [11].

Evaluation Metrics

The models were evaluated using classification accuracy, precision, recall, and F1-score [2]. Additionally, confusion matrices were generated to analyze class-wise performance. These metrics provided a comprehensive understanding of the trade-offs between computational efficiency and classification accuracy across SVM, CNN, and SAE–SVM models.

VI. Result and Discussion

To evaluate the performance of the proposed system on maize,cotton and soyabean crop, experimental results were analyzed separately for four districts of Vidarbha region in Maharashtra: **Yavatmal, Washim, Amravati, and Akola.** Some samples of module outputs are shown in figure 2,3,4,5,6&7

Figure.2: Yavatmal District Maize Leaf Disease Detection using SVM
Figure.3: Yavatmal District Cotton Leaf Disease Detection Using SVM
Figure.4: Yavatmal District Soyaben Leaf Disease Detection Using SAE+SVM
Figure.5: Washim District Soyaben Leaf Disease Detection Using SAE+SVM
Figure.6: Amravati District Soyabean Leaf Disease Detection Using CN
Figure.7: Akola Distric Cotton Leaf Disease Detection Using SVM

VII. Comparative Analysis of Model Parameters

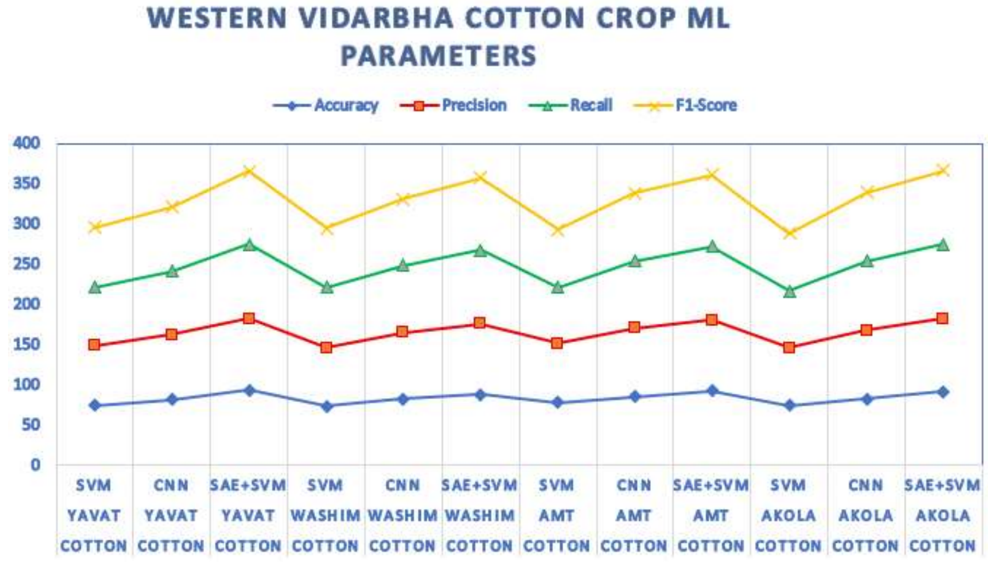

Figure.8: Comparative analysis of Machine learning parameters for Cotton

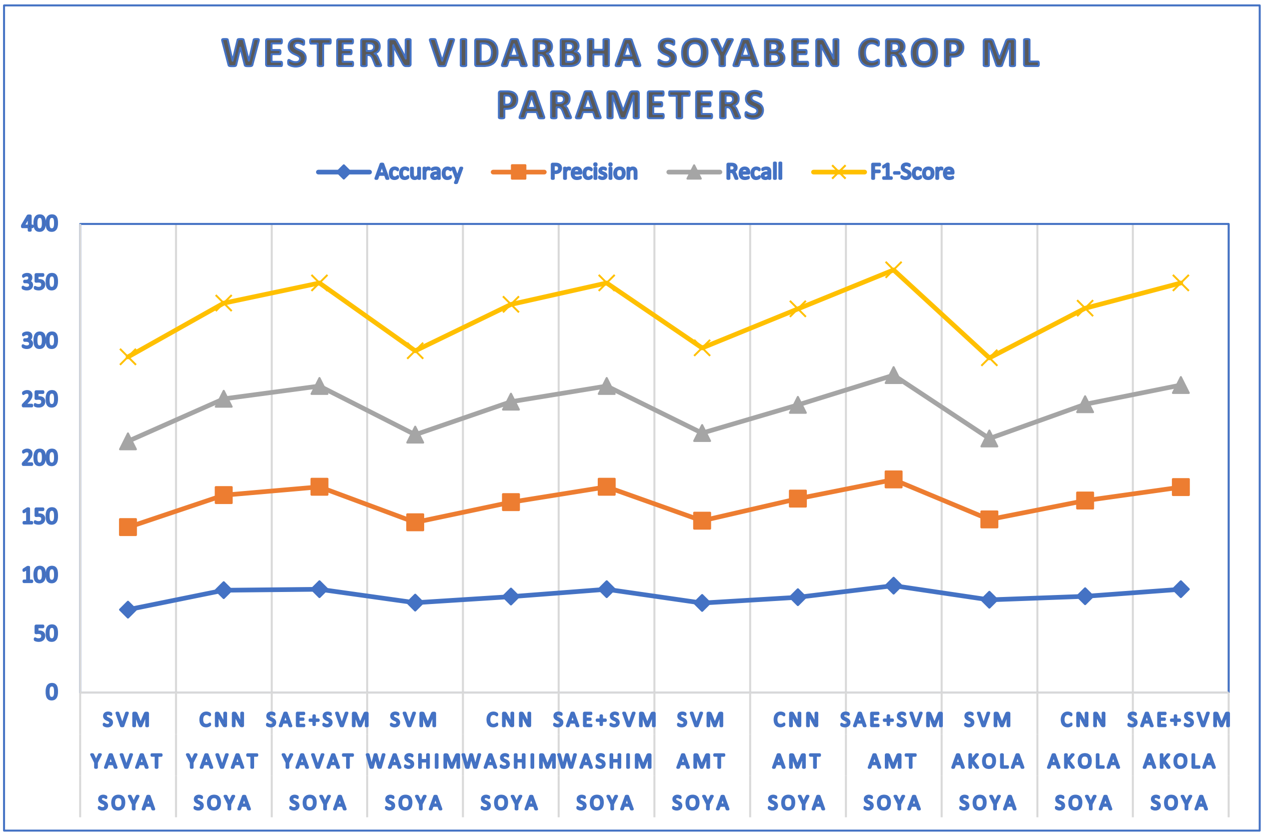

Figure.9:Comparative analysis of Machine learning parameters for Soyabean

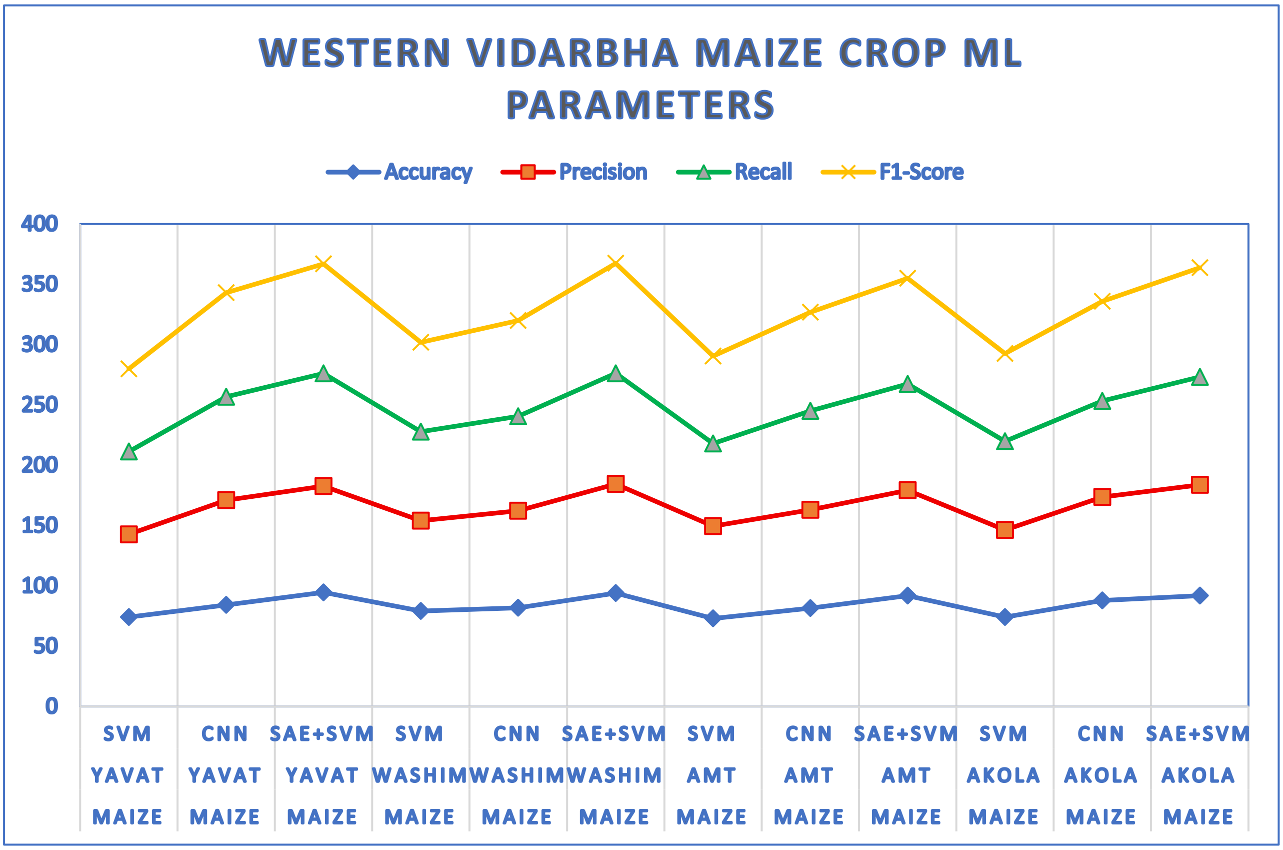

Figure.10:Comparative analysis of Machine learning parameters for Maize

VIII. Conclusion and Future Scope

In this study, a comparative analysis of three computational models—SVM, CNN, and SAE–SVM—was conducted for the detection of maize, soybean, and cotton diseases in the Vidarbha region of Maharashtra. A region-specific dataset was developed covering major diseases such as bacterial blight, Alternaria, aphid infestations, and rust. The results demonstrated that CNN achieved the highest accuracy owing to its ability to automatically extract deep features, while SAE–SVM exhibited robustness and adaptability across diverse disease classes. The MATLAB-based SVM model, although less accurate, proved computationally efficient and reliable for smaller datasets.

The findings highlight the importance of employing hybrid and deep learning models for region-specific agricultural disease detection. By tailoring disease identification frameworks to Vidarbha's cropping patterns, this work contributes to precision agriculture practices and supports timely disease management strategies.

The study can be extended by incorporating advanced deep learning architectures such as transfer learning and vision transformers to further improve accuracy. Additionally, the integration of Internet of Things (IoT) devices, drone-based monitoring, and cloud platforms may enable real-time disease detection and advisory systems. Expanding the dataset to include more crops and diseases across varied agro-climatic zones would further enhance the generalizability and applicability of the proposed framework.

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